SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13563	AF118082	Homo sapiens	PRO1902	83	86
13564	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	234	97
13565	Y59778	Homo sapiens	Human normal ovarian tissue derived protein 55.	66	100
13566	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	103	60
13567	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	152	96
13568	X83703	Homo sapiens	nuclear protein	1633	99
13569	G02473	Homo sapiens	Human secreted protein, SEQ ID NO: 6554.	242	45
13570	G00521	Homo sapiens	Human secreted protein, SEQ ID NO: 4602.	105	90
13571	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	110	80
13572	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	114	46
13573	X92744	Homo sapiens	hBD-1	290	83
13574	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	107	68
13575	AF107406	Homo sapiens	GW128	356	100
13576	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	101	48
13577	AF220264	Homo sapiens	MOST-1	95	73
13578	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	129	68
13579	AK024455	Homo sapiens	FLJ00047 protein	81	76
13580	AF130051	Homo sapiens	PRO0898	128	64
13581	AF084256	Homo sapiens	beta glucuronidase isoform d	142	58
13582	AF118082	Homo sapiens	PRO1902	85	51
13583	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	114	52
13584	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	66	54
13585	X52164	Mus musculus	Q300 protein (AA 1-77)	109	64
13586	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	109	77
13587	AF090901	Homo sapiens	PRO0195	114	53
13588	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	95	66
13589	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	117	58
13590	AK000521	Homo sapiens	unnamed protein product	1313	100
13591	AL357374	Homo sapiens	bA353C18.2 (novel protein)	421	100
13592	AL357374	Homo sapiens	bA353C18.2 (novel protein)	421	100
13593	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	139	62
13594	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	103	56
13595	U16359	Rattus norvegicus	nitric oxide synthase	109	76
13596	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	127	88
13597	G00325	Homo sapiens	Human secreted protein, SEQ ID NO: 4406.	275	100
13598	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	108	63
13599	AF116661	Homo sapiens	PRO1438	128	64

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13600	X55682	Lycopersicon esculentum	extensin (class I)	58	43
13601	X52164	Mus musculus	Q300 protein (AA 1-77)	106	45
13602	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	122	92
13603	AF149419	Oryctolagus cuniculus	eye sodium bicarbonate cotransport protein NBC2	126	75
13604	AJ005567	Mus musculus	SPR2I protein	63	40
13605	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	150	96
13606	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	121	60
13607	G02867	Homo sapiens	Human secreted protein, SEQ ID NO: 6948.	85	60
13608	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	57	35
13609	AF107406	Homo sapiens	GW128	108	42
13610	D82345	Homo sapiens	NB thymosin beta	167	100
13611	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	161	59
13612	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	125	50
13613	Y32193	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 044150.	490	80
13614	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	115	57
13615	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	124	58
13616	AF119900	Homo sapiens	PRO2822	95	53
13617	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	124	58
13618	S79978	Homo sapiens	prion protein, PrP {octapeptide repeats}	88	42
13619	AF220264	Homo sapiens	MOST-1	130	81
13620	U16359	Rattus norvegicus	nitric oxide synthase	95	65
13621	AL132841	Caenorhabditis elegans	Y15E3A.3	168	85
13622	K01664	Drosophila melanogaster	Bkm-like protein	118	65
13623	M86246	Homo sapiens	EHS-2	100	63
13624	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	104	46
13625	AF067205	Homo sapiens	vesicle transport related protein	198	69
13626	U39529	Echinometra mathaei	bindin	72	47
13627	S79410	Mus musculus	nuclear localization signal binding protein	102	52
13628	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	123	54
13629	K01664	Drosophila melanogaster	Bkm-like protein	113	46
13630	AF161536	Homo sapiens	HSPC051	582	100
13631	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	158	87
13632	AF130089	Homo sapiens	PRO2550	105	66
13633	AF116661	Homo sapiens	PRO1438	116	53
13634	AF116715	Homo sapiens	PRO2829	101	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13635	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	139	63
13636	U33547	Homo sapiens	MHC class II antigen	154	79
13637	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	107	75
13638	AF090895	Homo sapiens	PRO0117	87	62
13639	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	131	69
13640	AF026689	Homo sapiens	prostate-specific transglutaminase	128	60
13641	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	128	81
13642	AC003058	Arabidopsis thaliana	unknown protein	210	67
13643	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	287	76
13644	Y73483	Homo sapiens	Human secreted protein clone yl18_1 protein sequence SEQ ID NO:188.	376	88
13645	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	130	85
13646	Y87212	Homo sapiens	Human secreted protein sequence SEQ ID NO:251.	423	97
13647	U50403	Homo sapiens	breast cancer suppressor element Ishmael Upper RP2	103	86
13648	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	128	55
13649	X58521	Homo sapiens	nucleoporin p62	2610	98
13650	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	141	69
13651	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	111	81
13652	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	140	60
13653	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	121	46
13654	U13066	Nicotiana alata	arabinogalactan-protein precursor	92	33
13655	S79410	Mus musculus	nuclear localization signal binding protein	134	50
13656	Y07766	Homo sapiens	Human secreted protein fragment encoded from gene 23.	156	100
13657	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	124	48
13658	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	171	80
13659	AK000017	Homo sapiens	unnamed protein product	611	100
13660	U90446	Mus musculus	RNAse L inhibitor	3100	99
13661	AE000882	Methanothermobacter thermoautotrophicus	phosphoenolpyruvate synthase	88	38
13662	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	65
13663	K01664	Drosophila melanogaster	Bkm-like protein	97	34
13664	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	77	41
13665	Y94890	Homo sapiens	Human protein clone HP02798.	325	98
13666	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	65
13667	AF090930	Homo sapiens	PRO0478	119	88
13668	AF130089	Homo sapiens	PRO2550	120	77

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13669	AC006693	Caenorhabditis elegans	Hypothetical protein W02H5.e	165	85
13670	W80293	Homo sapiens	Human translocation associated protein designated Gp25L-H.	1003	95
13671	U23455	Caenorhabditis elegans	similar to D. melanogaster homeotic protein BarH2 (PIR:A41726)	113	91
13672	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	160	60
13673	AL132841	Caenorhabditis elegans	Y15E3A.3	178	75
13674	AF118086	Homo sapiens	PRO1992	85	75
13675	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	132	55
13676	AF220264	Homo sapiens	MOST-1	133	85
13677	Y19730	Homo sapiens	SEQ ID NO 448 from WO9922243.	122	51
13678	Y65416	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1577.	467	98
13679	Y16589	Homo sapiens	A protein that interacts with presenilins.	2286	99
13680	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	104	52
13681	AF090931	Homo sapiens	PRO0483	117	67
13682	X55686	Lycopersicon esculentum	extensin (class II)	60	56
13683	AF090944	Homo sapiens	PRO0663	93	90
13684	AL096770	Homo sapiens	bA150A6.2 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein (hs6M1-21))	178	52
13685	AF116661	Homo sapiens	PRO1438	115	60
13686	U62039	Elephantulus edwardii	reverse transcriptase	86	53
13687	Y13141	Bromheadia finlaysoniana	extensin	77	36
13688	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	114	60
13689	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	103	53
13690	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	107	51
13691	AC003058	Arabidopsis thaliana	unknown protein	178	85
13692	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	94	35
13693	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	143	78
13694	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	98	50
13695	D63163	Rattus sp.	cyclin C	111	86
13696	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	118	95
13697	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	124	80
13698	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	129	70
13699	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	93	58
13700	W48353	Homo sapiens	Human breast cancer related protein BCFLT2.	100	73
13701	M76744	Homo sapiens	BGP	112	52

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13702	Y15155	Homo sapiens	phosphorylase kinase beta-subunit	206	100
13703	AF090901	Homo sapiens	PRO0195	100	70
13704	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	131	79
13705	R95913	Homo sapiens	Neural thread protein.	106	36
13706	M15073	Homo sapiens	MHC HLA-DR-beta-1 chain	74	77
13707	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	110	35
13708	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	150	56
13709	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	89	77
13710	X70775	Chironomus cingulatus	Sp12 gene homologue	85	38
13711	X80265	Hordeum vulgare	structural protein	96	41
13712	AB007922	Homo sapiens	KIAA0453 protein	147	64
13713	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	124	60
13714	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	108	65
13715	AF116661	Homo sapiens	PRO1438	120	77
13716	AF118086	Homo sapiens	PRO1992	127	64
13717	AK024455	Homo sapiens	FLJ00047 protein	93	56
13718	AF116661	Homo sapiens	PRO1438	137	55
13719	W48352	Homo sapiens	Human breast cancer related protein BCFLT1.	93	59
13720	AF119851	Homo sapiens	PRO1722	94	58
13721	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	124	45
13722	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	117	58
13723	AF161361	Homo sapiens	HSPC098	115	50
13724	Y95829	Homo sapiens	Native human Tie receptor signal peptide.	108	100
13725	AF118086	Homo sapiens	PRO1992	166	75
13726	AF116636	Homo sapiens	PRO1488	95	70
13727	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	70
13728	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	149	60
13730	G00673	Homo sapiens	Human secreted protein, SEQ ID NO: 4754.	118	63
13731	U33547	Homo sapiens	MHC class II antigen	123	69
13732	R59843	Homo sapiens	ApoE4Lx2 protease.	135	88
13733	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	138	75
13734	AF026204	Caenorhabditis elegans	C30E1.1 gene product	102	51
13735	Y12950	Homo sapiens	Amino acid sequence of a human secreted peptide.	117	63
13736	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	112	87
13737	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	115	58
13738	AF130089	Homo sapiens	PRO2550	122	70
13739	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	124	74
13740	AF130051	Homo sapiens	PRO0898	85	70

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13741	AF093748	Homo sapiens	KH type splicing regulatory protein; KSRP	91	51
13742	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	150	77
13743	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	124	82
13744	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	91	48
13745	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	116	64
13746	AB001684	Chlorella vulgaris	ORF54d	70	66
13747	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	140	60
13748	AF090901	Homo sapiens	PRO0195	92	39
13749	AF090895	Homo sapiens	PRO0117	148	67
13750	AF119882	Homo sapiens	PRO2492	91	45
13751	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	109	60
13752	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	129	65
13753	AF161356	Homo sapiens	HSPC093	99	48
13754	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	124	70
13755	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	120	51
13756	AF130089	Homo sapiens	PRO2550	142	96
13757	AF130089	Homo sapiens	PRO2550	132	86
13758	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	163	50
13759	Y19609	Homo sapiens	SEQ ID NO 327 from WO9922243.	92	60
13760	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	154	52
13761	U62040	Elephantulus edwardii	reverse transcriptase	134	51
13762	AB001684	Chlorella vulgaris	ORF49b	100	45
13763	AF118082	Homo sapiens	PRO1902	129	50
13764	AF220264	Homo sapiens	MOST-1	129	66
13765	R59842	Homo sapiens	ApoE4L1 protease.	135	50
13766	AF220264	Homo sapiens	MOST-1	115	71
13767	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	139	73
13768	AF130089	Homo sapiens	PRO2550	97	34
13769	U80739	Homo sapiens	CAGH26	564	100
13770	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	128	55
13771	R10755	Homo sapiens	Non-A non-B hepatitis specific antigenic protein encoded by phageclone lambda HC2533.	102	68
13772	AE004507	Pseudomonas aeruginosa	hypothetical protein of bacteriophage Pf1	93	44
13773	AB044885	Canis familiaris	dopamine receptor D4	78	52
13774	AF026246	Homo sapiens	HERV-E envelope glycoprotein	108	53
13775	S71805	Homo sapiens	RNA-binding protein=TLS/FUS-ERG	126	100
13776	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	156	82
13777	AB015727	Mus musculus	truncated granzyme M	86	37
13778	G02832	Homo sapiens	Human secreted protein, SEQ ID NO:	74	52

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6913.		
13779	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	137	61
13780	M14123	Homo sapiens	neutral protease large subunit	246	55
13781	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	99	67
13782	AF132972	Homo sapiens	CGI-38 protein	902	99
13783	G02469	Homo sapiens	Human secreted protein, SEQ ID NO: 6550.	147	63
13784	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	128	68
13785	AF130051	Homo sapiens	PRO0898	138	72
13786	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	95
13787	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	92	53
13788	U12206	Homo sapiens	unknown	84	42
13789	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	118	58
13790	S79410	Mus musculus	nuclear localization signal binding protein	102	50
13791	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	137	76
13792	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	104	72
13793	AB006006	Bos taurus	neurocalcin alpha	1000	100
13794	U63332	Homo sapiens	super cysteine rich protein; SCRP	183	95
13795	W34499	Homo sapiens	Obesity receptor C protein.	120	85
13796	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	127	67
13797	U41038	Caenorhabditis elegans	Similar to cadherin-type repeat	182	83
13798	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	112	71
13799	U63332	Homo sapiens	super cysteine rich protein; SCRP	91	84
13800	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	105	67
13801	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	154	72
13802	AF119900	Homo sapiens	PRO2822	131	50
13803	AK024435	Homo sapiens	FLJ00025 protein	117	95
13804	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	142	53
13805	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	109	48
13806	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	98	66
13807	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	98	66
13808	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	150	54
13809	M37679	Mus musculus	Ig heavy chain precursor	70	100
13810	AL451015	Neurospora crassa	putative protein	96	55
13811	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	88	77
13812	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	128	71

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13813	AF130089	Homo sapiens	PRO2550	93	75
13814	K01664	Drosophila melanogaster	Bkm-like protein	119	60
13815	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	64
13816	AJ011435	Blackstonia imperfoliata	maturase	93	48
13817	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	130	76
13818	AF119851	Homo sapiens	PRO1722	141	50
13819	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	74	60
13820	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	76	72
13821	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	135	50
13822	K01664	Drosophila melanogaster	Bkm-like protein	95	52
13823	L10908	Mus musculus	Gcap1 gene product	103	50
13824	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	146	62
13825	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	125	83
13826	L10908	Mus musculus	Gcap1 gene product	96	43
13827	G02971	Homo sapiens	Human secreted protein, SEQ ID NO: 7052.	102	64
13828	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	135	53
13829	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	142	70
13831	AP000060	Aeropyrum pernix	101aa long hypothetical protein	79	50
13832	AF119900	Homo sapiens	PRO2822	94	46
13833	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	145	40
13834	AF218028	Homo sapiens	unknown	117	57
13835	L10908	Mus musculus	Gcap1 gene product	79	45
13836	Z26876	Homo sapiens	ribosomal protein	129	93
13837	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	124	76
13838	AF044311	Homo sapiens	gamma-synuclein	603	99
13839	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	100	82
13840	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	154	46
13841	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	122	64
13842	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	92	62
13843	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	93	60
13844	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	63
13845	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	145	79
13846	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	102	50
13847	G03469	Homo sapiens	Human secreted protein, SEQ ID NO: 7550.	101	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13848	G03240	Homo sapiens	Human secreted protein, SEQ ID NO: 7321.	107	43
13849	U05313	Trypanosoma brucei	CR3	98	40
13850	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	100	65
13851	AF159055	Homo sapiens	leucine zipper-like protein	103	55
13852	R59842	Homo sapiens	ApoE4L1 protease.	99	71
13853	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	142	65
13854	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	119	79
13855	R59842	Homo sapiens	ApoE4L1 protease.	93	69
13856	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	114	76
13857	W48353	Homo sapiens	Human breast cancer related protein BCFLT2.	94	57
13858	U63332	Homo sapiens	super cysteine rich protein; SCRP	105	58
13859	AF289022	Homo sapiens	formiminotransferase cyclodeaminase form C	467	100
13860	AF078844	Homo sapiens	hqp0376 protein	488	100
13861	AB032436	Homo sapiens	brain-specific Na-dependent inorganic phosphate cotransporter	2968	100
13862	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	91	72
13863	AF130079	Homo sapiens	PRO2852	131	63
13864	Z29701_cd1	Homo sapiens	29-MAY-1998 Wild-type human c-Src tyrosine kinase cDNA.	2380	100
13865	L77967	Ovis aries	small proline-rich protein with paired repeat	80	33
13866	AL050318	Homo sapiens	dJ977B1.5 (myosin regulatory light chain 2, smooth muscle isoform)	904	100
13867	U37690	Homo sapiens	RNA polymerase II subunit	358	100
13868	X13923	Homo sapiens	cytochrome c oxidase subunit VIb (AA 1-86)	491	100
13869	L13848	Homo sapiens	RNA helicase A	6669	99
13870	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	133	46
13871	K02064	Bos taurus	cytochrome c oxidase subunit IV precursor EC 1.9.3.1	96	72
13872	D31763	Homo sapiens	ha0946 protein is Kruppel-related.	4606	96
13873	Z14014	Nicotiana tabacum	Pistil extensin like protein, partial CDS only	83	43
13874	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	117	70
13875	Z52203_cd1	Homo sapiens	17-SEP-1998 Human PRO217 protein encoding cDNA, UNQ191.	2135	99
13876	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	106	64
13877	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	143	50
13878	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	104	60
13879	L25404	Brassica napus	cyclin	124	42
13880	AL390114	Leishmania major	extremely cysteine/valine rich protein	139	59
13881	AC003113	Arabidopsis thaliana	F24O1.6	70	64

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13882	AB000098	Rattus norvegicus	MIPP65	905	50
13883	Z95114	Homo sapiens	bK212A2.1 (TNF-inducible protein CG12-1 (similar to apolipoprotein L))	1639	100
13884	AF132984	Homo sapiens	Nuclear pore complex interacting protein NPIP	551	82
13885	AF121862	Homo sapiens	Sorting nexin 13	1453	99
13886	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	83	69
13887	K01664	Drosophila melanogaster	Bkm-like protein	109	77
13888	AF217197	Homo sapiens	FBP interacting repressor	2725	99
13889	D38112	Homo sapiens	NADH dehydrogenase subunit 6	187	94
13890	AF118086	Homo sapiens	PRO1992	85	62
13891	M58664	Homo sapiens	Signal transducer CD24	371	97
13892	AK023443	Homo sapiens	Unnamed protein product	125	45
13893	AB040972	Homo sapiens	KIAA1539 protein	2271	99
13894	U03750	Escherichia coli	DeaD	95	48
13895	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	73	53
13896	AF078851	Homo sapiens	Secretogranin III	2384	99
13897	U62039	Elephantulus edwardii	Reverse transcriptase	109	48
13898	X07816	Human herpesvirus 4	Epitope Cl3 (57 AA)	55	53
13899	AF116661	Homo sapiens	PRO1438	146	48
13900	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	77	60
13901	Y28643	Homo sapiens	Human serine protease inhibitor from cDNA clone HETDK50.	2191	100

TABLE 3

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
1	13902	A	1	114	434	AIFKCVEGMFRIAMVNVCFVSSGSLLI* PLTY/GVYDEWTHFAYMTIDLLEIPITG SHPVVLNALFCLEAP\WISPNTGSFAYP VYPKSLIAHDFAVEATMPYIRLSST
2	13903	A	2	124	466	KSNIPNLGDCGWESLFNR\QSWRSSLAV \NDTYSSKKSNAETFTFHADLCTLSDKD RPITIQTALAELVKHKPKATYEQLIAVL DEF/ANFLKKWWKAYDKENLFCEEG*KL CAASN
3	13904	A	4	1	427	EGFLELLRTRNHSNSQLQLTTGIGLFLN EGLKLVDKFLEDV*K*YHSETFTVNFSD TE*AMKHINDYVEKGTQGKIVDLVKELD RDTVFDLANYIFFKGKWDRPFEVNDTEE EDFHVDQVSTVNEPIMKLLS\MLNIHPC FKL
4	13905	A	5	1	464	KIKSFYASKDTIKRMRVTDWKKIFAY*I SDKELIFTLRTLKT**K*GKQPNLKNGQ EI*VPISPQDIQIAHK\HLEGWSTSLVS ELAPCEAPV/RHPLTGLTIAGLQGFGEA GRLVRGRWGC*W/VHPF*KYI/WQFLSK LHISLPYDPTTPLLGTCSR
5	13906	A	6	308	3	HFVIHSKHDLAIAHLGIY/PREMKT*VH TKTCT*IFTVALSVIARAWNQPGRPLCS EWL\KYMVHTME*HSAIKRLNYRYKNNC VNLFLGITLSEKSQTQNVI
6	13907	A	7	587	2	FLTRETGDPTGRSSSHANTQSRFFPDDP PG\PLNNLGNTHGCGRRAGRCPGTGPDG P\AGCGGPRCWPSGHLAATGD*GPSCGR LGANRGEAGPAGFTACSPLSGCRTPYTH HFPASRMSCHLNCASPRTYRSQGNRGCE RVAQGSQGAGGERGAKSQVPVPAPARNK DPAKCRKPRNRRPGNSGPVVRAYRRQR
7	13908	A	8	1	474	RILNEEHGKYEGLHE*EVKWHLYIKSPA FTDLHLCYQKDMNGISTSASSPAVGTVG MDMDEDDDFSKWNFYYSPHSYPDK*LTI FKTESRVRESDEVTQIKVNWDEEVISGL LTSLKDNVLKATGVLYDYAYK\YLCEHT RSTLKEESLKLERNLQNH
8	13909	A	9	3	539	SQCSPFISPACSLTALEEETEALRVHPR LCLSPNLAPSSGPPRPPELAPCPPSSQA GLRTCHSWVKGLHQPLPVASGMKSTFCN KTYTCPYPPP/PPLCPNHSPNALTLPDS VTHAVPFE/L*SPSAPPSSTA*ILGSPS \CGASPCNHPHSHPGICPTPPGLWPVCP CAPRAWQRDGTRQT
9	13910	A	10	2	453	RL*LGLEYALLVWGTPKV*H*GGFPIYY YIVLLLSYALHQVTEYSMYVSIMAFNAK VSDPLIVGTYMTLLNTVSNLIGNWPSTV SLWLVNPLTVKECV*TSYQNCCTPDAAE LCKKLGGSCVTALDGYYVESIICVSIAF V/W*VFLVHKFK
10	13911	A	11	20	475	KMGVPPLLMSDPNRFLFPKNFLREKTIS PPKTF*PLKIWVKGQWVLNFLGFPGFKI FFPVFKFFFFFFFF/RDRVSLYHPGWSA VSQSELTAALTSPGSGDQVILPSQPPK* ENHLNLGGRGCSEPRLPRAEFLDLRSFS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						IIVIFP
11	13912	A	12	392	63	HIRADPGLEPRPSARTGLGPELGCCTMN KLGDAGSATQSLGGSQLSWQLSRREQEL EQARWEAQ*QVETLGRVAREKEALAKEH AGLAVQLAA\AEHEGRTVSEEATHLQ
12	13913	A	13	18	338	APHPQYLQMPPMLLPPRTGPGQFSLPSS RHGGHLE/GKEHETSVTLCGGEPPPQTP PRDPDPGP*ARRAPCPRRPT*AHPRALS RAAPQEPRALAGPRARHPICPGSL
13	13914	A	14	2	371	TTKQ*KDNPIQTGAKDLKRHFCKEDMQM ASNHT\KRSLTSLVSREMHIIKTTRMAGI KKSDNNKHW*GRGEIRT/LLRCWWDCKV VQLLWKTVWQFL*GLYQYIPHDPVISRL GISLILYIALRTF
14	13915	A	15	443	1	SRTFLDTDMKSMRGFKAS*NRQTLLLGA NAAGD\KLKAMLTNHSENRKILQNYVKC TLPMLYKWNNKAWMTAYLFTTQCTEYFK PTVETHCSEKKISF\KILLTIYNAPGHL RALMQIYKEIHVVFVPVNIPSILQPIVQ NVISTFKS
15	13916	A	16	375	38	HQQNGFLKKTDPTLLCLQETHFR/CKDT KRLKVRRY/QPNSNQKRAR/VPILIEDK IDFKTKKIFMMIKDLTIINI*ASNTRVP KSMKQKLAGLKEEMDNSVIMVGGFSYPV SIRK
16	13917	A	17	448	189	NRDRVSLCCPGWS*TPGLKRSFHLGLPK CWDYRRDIY*LL\FARHTQMISTHS*QT TNTCSYPAF*KSRP*EPGYNTTHTPHSS DML
17	13918	A	18	1	426	GMSHHARSLIINQLFKKCSTLFVL/REM QIKSLLASSSSSSSRNSVSGQGFETVGT HCGQKCKLVQPF\WKAVW*YLLKLNVFI LFLIYNRNAHLEDTCENVDRALFVIVKN WKLSKYPPGVKWRIKLWYSHSVESSTAV LPKV
18	13919	A	19	2	423	YFETFQPLLRRLGYQGTFFFP\KPWSSC LGIEYNSGPDSCA*FFLQNQIRLVNSAN IRLMAMTLKTNQVAIAQFLECKESDQQF CIGVTHVKARTGWA*F*SAQGCDLLQNL QNVTQ/GAKIPLVV*GDFNAEPTQEA*K HF
19	13920	A	20	10	443	LKVDSGDSEVRYVFILQHITLLMCSAYM NQLLNIFVRPSLLAVALHMTPGFTKEDV YSCFRFLRDVFADEFIFLPGNTL*DFEE SCYLLCKSEAIQVTTKDILFTEKGNTVL *FLVGLFKPF/VESYHIICKSLLDEK*A PFIEEP
20	13921	A	21	11	426	VLVETNNLRMGQVTM*PELPDM/SPDAW TLSDSPSQKIGHAQQ\KYSIIKWKWYTE DWAQACLEDTSKYEQVTQIPMAPNDATL /PSS/AHLAFTAS*GAPSDS*LRNTLGL ICDGST\KPSSTN*KQTVIALQSHAGLN MKEC
21	13922	A	22	1147	1768	QLGMSHGYSSKSMPQKLMCFLFNHHLQK GHECLPKVLNSNPPPIIKYLALQDLMLL SQYSPSRRQEVFSLSQPGGHPHNWTAIS RECLNLLNGMTQKLILYQEAAATNGRVS SSYPVEPKKLNSPEETAFQTPKSSQMPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						PSVPPLVKTSLFSSKLSTPDVVSPFGTP FGSSVMNRMAGIFDVNTCYGS*AT*HSE W\LLNLSLLYHVWLCGVFLLTTWYVSWI LFKIYATKAHVFPVQPPFAEGS*VPSKS VK*QSSP\LIKYLALQDLMLLSQYSPSR RQEVFSLSQPGGHPHNWTAISRECLNLL NGMTQKLILYQEAAATNGRVSSSYPVEP KKLNSPEETAFQTPKSSQMPRPSVPPLV KTSLFSSKLSTPDVVSPFGTPFGSSVMN RMAGIFDVNTCYGSPQSPQLIRRGPRLW TSAS
22	13923	A	23	421	3	KIIFRAFKG*KSPSMPGFKA*KDRLILL LGTNADNDFKRKPM/LLYHSKNPRALKN YIKSIQPLYE*KKA*MTAHLLKVWVTEY FKPIVGTYC*KI/SFKILLLNDDAPG\H PKALIEMYREINIFMSANTLFILQPMEK GVI
23	13924	A	24	226	2	THERTHSKIIHVIIIKITHPLNPSILRP QTTA*IKWRDLGSLQPLP/PG/LKRFSY LILPSSWDYRCPPLRPANFCIF
24	13925	A	25	2	611	FFFFLLLGLLHQIPDVSPTGKYTTLLPL MIILMISGIKEVIY/DHK*HGRQNS/VR NTKLL*QDSWDTFKWKEVNVGDTVKASN GELLPADTVPMC\YIATSNPDRETN/VK TRQALPETASV
25	13926	A	26	1	443	ATQWRPSLVPASAENVNKARSFAAGIHA LGGTNINDAMLMAVQLLDSINQDELVT* GSVLLIILLTDGEPTAWETNLMSIQNNV REAVRGRYSLFCLGLGFDVCYAFLEKLA LDNGGLARRIHEDSDSALHMQDFY\QEV AHPLVTAV
26	13927	A	27	2	359	KAQSKQWLPRGGSGPVK/ARVDEESAKV IVRVYWEAQGILLIDFLKGQRRTIYAYS ENILRKPEL**RNAWGSFSRVLHHDRAP AHFSHQ/TRAIG/REF**KTIRHPHY/S PNLNPLDAFCF
27	13928	A	28	2	427	WRKTVKGHFTDQCRKHKAM/LGN*IHFL EYHIHKHSIQYSGIQATQEKFGGLKTSY CSKD*YITVLDLTLKISNKDVSN*HENP ISMYKN/IPTVIYGSKVIKDRKLKA*I* CP/HRNKKF*YFDYFYVLLNTMTFLKLW RIITEI
28	13929	A	29	47	412	HCDVLLASSRYTCILPYSDRDDGPQDQL KMSVDFRSRRTGS/WFPQNSWGHMGVCG WGGAGRTLDLIHLRIPMRGLRSGGFLCR RKLVSESYG*EPSPL*K*KGGWGSEPS/ LTTVPSQL
29	13930	A	30	336	419	RLECSGMISAYCNLSLPGLSDPSNSASR
30	13931	A	32	1	408	KIALKLRSNYSKISGY/MANIQKLIIFL YTSNEQIEFEIKNTIPFTLAPPKIK*LG TNLTKC\VQELYEKIYKSVMKNIKELNK WRSSYGKGKSKIKIIKINK*MDIACSWL RRLKIVKISVLHNLIYRFNIVPIEIP
31	13932	A	33	412	2	QGHLSLQKFL\LPFVQLCPAPRGGVYRG RQDSLSCGGLHPF*ASGLLCLPTQASAM VGTPPPASLLLCSSILDCCASNERGSVG VEPPEPGTGHNLLVCRLLRPLEKRSIRW KSAVGVARFSRCRPSWLPLARKKNSP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
32	13933	A	35	304	33	KVWGEKVWYWQKMTQIVQWDRTESPQID N*SLTKEIQWRKDSLFNKW*GNNWTAPF SS/RSLNLNKDLTAVTKIKSKWVTDLNV KHKTIKLL
33	13934	A	36	2	424	SKTYSIGHFTYEGKGTITSLWGKVNVED AVGETLGRLLVEYPWTQRFFDSFGKLSS ASAIMGNPFVKAHGLKGLTSLGDALQHL DDLKG\TFAQLTELHCDKLHVDPENFFL LG*VLVTVLALHF/SRRFTP/ELQAS/W PKM
34	13935	A	37	2	433	NKRLPGPGF*KRPNPPGEGGPARYFNPL GGPNREIPLGPEV*THFGPQMRPPVFLK ILKISGAFWGPPVGPPTWGG*EGLNPRG PGYN*P/R/PPAPPPWG*SQAPFPKPAP PP/TGIKPNP
35	13936	A	38	3	425	GAAQLLPVSLPSAQRAIDLQILTTPWEN WTSIASLQHKTTIGRSWLITGPISATSS TPTSCTVASP\TRGHV*RSASWKYDVLQ HSSHMWVVHTAVYLGEAFHQVHATGSCH HRVLSCCPITGRSGRDAL*QLLPL/HAL TEA
36	13937	A	39	2	463	LNEVRDIKLSSDHWPSKTNSFLHSPGFL SRFEPQPASVA/PRP*SQQQSLPGKAST SLWPPNPVPFVTSSLSLSALPGLFLWLP SIPPLPGSPFFSPE*PEVPLFPGPTYHN PSPPD/PTVLEAHPDQAPLP\PGVPTAE QRPTPAP*AHRPS/LPLPP
37	13938	A	40	223	408	RNTV*NIGTDKDFMT*TPQAIATKAQID KWNLIEPMSFC/TYRETIIGVTDRYTRD KIFESGR
38	13939	A	41	3	427	NLKMKSRTSKENIGEHIYDFDIGRFVNT *SKPERKRLSFKTSVQEKTP*L*GKHK* MKLEP\LPYPKINSKWIKDNVRSKAIKL LEENRSESSIWQRML/SIMPKAQAIKEK VDNLDFFKIKNCVSKDTIKKALDRPSER EKI
39	13940	A	42	30	448	FEMREIIVAFHSILIRYHGLINLRKFQ* MDRRYSKEVQDLLETMKLFARIVGPL*H DKFIESHALEFELLREIKRLQEYRTAGI TNFCSARTYDHLKKTR*EERLKRTMLSE VLQYIQDSNACQQWLRRETY\IESGPNP
40	13941	A	43	1	928	LRQRMPPQGLQPCPWPPRYP/PDSPLGC PGGLA\PPNSPSWPKLASLAGSRGSSAP PGVWGLVATGA*PLQRPSAPPPCPR/LC PGREPCMCP
41	13942	A	44	2	409	SKSPDPTQQPLRGGSLTHSAPGPSLSQP LAQLTPPAFGPSTSSLFNLQKSSLSARH PQRKRRGGPSEPTPGSRPQDATVHPACQ IFPHYTP\VWHILGPQRHTP*SVD/HPG LDKRLLPETPGPCYSNSQPVWLCLTP
42	13943	A	45	3	136	LPMTLFTELE*ATLRFIWNHITIQIAKA ILTNQK\NKARGITNIC
43	13944	A	46	365	2	AWGSLRAPRSAVPEPGTPPVMGNALAHR QFSPCLDGLSCPSFLRG*NSPPHPGSPG LPKHA*APAAVSPWVDPDRTVQPPPPAP PST\D*PHCSPPCTPWCPRRLGSAPVMP GCPTASYPRR
44	13945	A	47	1	456	AELSELYEESSDLQMDVMPGEGDLPKW\

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						EEATGTRAAIPWVPPATGAQQLEEEGPM EE\EEAQPMAAPEGKRSLANGPNAGEQP GQPSPGRRTSRAEDEA\EEFDDWEDDYD F\PREEPVKGARLRFLPPS*KTPPSFWE NRNTPLWGGLKIFY
45	13946	A	48	116	442	PQNMGMERKPGPPKGLSWASGDLEDNLG VMSVGFLLSSPDDAVIWRGPRKTGLIKQ FLRNGTGEKVDYFMGDTQLGTSDEHLSS VATWAKAHLGEPGAFTFPQRVSLRE
46	13947	A	49	434	3	FTVPGPLLTVIPIFISKVPFKFSLPQIF NFTPFGFPFQIRV*TIIPISLRFFRKKP LFFFF*NKVPLCSPYWNSIARSWVPAAS VFQV\KESFYLNLLSVPPQVPLNVFLTF FFFFFLGRDR/SLPLLPRMVWNSWAQAI LPLWL
47	13948	A	50	1	482	EKPYQCSDFGKAFNMKTQ\LVVHQGVHT GNNPYQCRECGKAFGRKEQLTAHLIAHA R*KPYGCSECGKAFSSKSYLVIHRRTHT GERPYECSSCDRAFCGKSQLIIHQITHS TENHYECNECENTYPRKASLKIHQKIDL GKKPF/ECNEWGKALLK
48	13949	A	51	1	470	REFLWQEGHRAFATVDEAGEEVLQILDL YADVYEELLAIPVANGTKTDKDKLAGGD YTATIEAFICASGRAIQGGTSHLLGQNF SAMSEIVLEDPEIPGENQPAYANSWGLT TRTTWVMTIGHGDNMGL/LLTPRVA*VQ /MVIIPGGIPKAFLKRQKT
49	13950	A	52	26	448	SPGTEREYRIGQQSVTGVTSVDDSNSYW RIRGKSATVCERGTPIK*GQPIRLTHVN TGRNLHSHHFTSPLYGN/QVAL*GDIVI IL*RRKQRLKGFTEEGIKLRFKEVSAFG DEGEGDYLDDWTVLCNGPYWVRDGEVRF NT
50	13951	A	53	3	495	AMEVKAFAETHIRGFTLNDAANSRLIIT QVRRHYLKEAATTLKTVLDHQHTPSRLA VTRVIQALAMKGDV\DNI*VFHKMLNGL EDSIGLSKMDFINNIALAQI*NSNLDAS V*HIENMLTS*NNVIEPQYFGSAYLFRQ VLEEQLEPTVEKISIMAERLAKPLQ
51	13952	A	55	1	428	QERGTKKEMEDRMTLEETK\EQILKLEE KL*ALQEEKHQLFLQLKKVLHEEERRRR KEQSDLTTLTSAAYQQSLTVHTGTHLLS VQGSPGGHNRPGTLMAADRAKQMYGPQV LTTRRYVGIAAAFAGTPEHGQFQGRPGG VYG
52	13953	A	56	2	453	EDGDLDAFSSDEGLTMAMSYLKDDIFRI YITETQECRRYHRPPCAQEAPCNMVHPI VICYGCYGPEVGTRYTCSVCPDYDLSSS CKGKGLHRGHTKLAFPSPFGHLSEGFSH SRWLRNVKHGLLRWS*WEMGPPGNWSPR TSCA/GEARLGP
53	13954	A	57	3	435	ELNTSIFRSRPIEGLGLNTVLTTDNSNL VI\NRIGIV\PSVTEKEYTDPSSDGTYA WKIFSHETITKAQILKLFLSYDYAVNNP WLAYPHYKSPEKCPSIILHDRLYYLNGL *CAASAMVMIAIVTYNVALLAYHRWNGL TYMID
54	13955	A	59	409	1	LCCEHRGKTVCVPRGKFTTLNASINKER

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						SKISVLSFRLMKLKKEYVK*K*\EKEKI NNRIRIEKINKAKS/WFL*HNKIE*TIR MINHQKRENIQITDFRNERTELPPDSTD IKKAIRKY*K*FYPNIFYNPEEMNKF
55	13956	A	60	1	393	GNVSSCGDHPCEG*LCP\PDKVMS*GI* VPEEACTQCIGEDGVHHQFLESWVPDHQ PCHICTSLNGRKDNCTTQTCPTGKASTC GLCELARLRQNADQCCPENECVCDPESC DLPPVPN*ERGLQSTLTNP
56	13957	A	61	250	1	REDCKRVLYKDKVSLCCAGPCSVA*SCL KAASTFQ\VKHFSLQSSWVYRHAPPGLA NFFHFLQRQVLTTPPGLVLNSWVHAI
57	13958	A	62	365	3	IKKKLIWRLFTFPKPSWGKKTKKGIPFP *GPKKIPGIKFPQGIKKAFKGNR*TLGK GN*KKKKKKKECGPGGDIPCS*IG/RNI VKILIIPKAIYSFNTIHIKIPKTFFTEI ETTILKFL*NH
58	13959	A	63	245	558	FLPTQVISYVKRALAEGAQI*CGEGVDK LSLPARNQAGYFMLPTEITDIKDESCCM TEEIFGPMTCDVPFDSEEDVIERANNVK YGLAATVW/SSNVARV
59	13960	A	64	106	532	ERACQSGTSGQGGVPRRAIGAPR/E/DA FTGAVYIYHGDAGGIVPQYSMHPFA*SL YPSGQ/SVAARGNLSGDSFNCHN*GLQG LLLASSV*RPVMLLNDPIIYTTKN/ISG PKCHE
60	13961	A	65	2	548	VQKYPQQNRSCVPPVAEWAVPQSSRLKY RQLFNSHDKTMSGHLTGPQARTILMQSS LPQAQLASIWNLSDIDQDGKLTAEEFIL AMHLIDVAMSGQPLPPVLPPEYIPPSF/ RRVRSCSGISVISSTSVDQRLPEEPVFR DEQQQLEKKLPGTFEDKKRENS*RGNLE LEKRRQALLEQQRQG
61	13962	A	66	72	952	SSRTYTTSLPLLKKEVTRKIRKYFILNN N*NTTYHNLWDLTKVVFSGKLLF*RSR* EYRKDKISDLCFYIQMLE/QRQVIKPKV STRKEINKSRTQ*SGKETMERPKLEDKF LVNINNINNP**LNL*RKKEGHHCIFYR H*KDNKGYIYANNFNILDQMDKFFERYV TKMD\QEQIVSLNIPIADKSNA*LNNFP SSSSSSSSSSS
62	13963	A	67	139	422	VNGNEPEPL*KGISRHEHRRQPHNGFRP KNKGGAKNQ*ASLGMKTPEAPAHSDKPR RRQHAAYSS*AMPFLGICISFSQCNL/C PPKLNV
63	13964	A	68	274	1	NLKNKAVITKTA*H*QKNTDQWNRIKNP EIN\HPFYGQLIFDKDAKNTM/WKR/DS NFNK*CWEN*ILTCKKMQLHP/SLTTNT KLNSQWIKDL
64	13965	A	69	22	419	KIIGEDGDT/PLSEMAKSQRQIFSKDLV KLDSTINQVDIIDIYKLHHP\KWTVYTF FSSH*GTFSKIDHILLDKTYPNNL*RTG IMQHMLSDIKVFKLEISTRKVTEKS*HT MSLCNKTLEHPSGNEDASAYLK
65	13966	A	70	57	423	KDKNSQVTSEEEEQEGKIKENLNSWRDT R/CH/WIGR\NIVRLSFLPKLIFIFNTV PIKIRTQFFMKLNKPVLKFIY*TKRTRI AKSLLKKK/RQEGKISPTNRRTYYEAYS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						TLESIGASMPSLDLG
66	13967	A	71	394	1	KHFRCMLQEDCRILLLWFFSETGSPCAV SPRIECSSKIIVHSLKLLGSSDPRASLS *VAGTIGVHHHTQP*GI/CNI*GSGRRR SEKQWIKEKNVSSEAKRRRTF*NE*SV* KGDYNKDQGLRLGTVAHAYN
67	13968	A	72	485	1707	SALGLSQPRPPGASDAAPDSTPAGV*TA SSSAPAGEKDANQMEWARRDPGPLHQAA PAPH*SHLVRDKRAQERLRKTSRGPPHS HRSGPVDLSPRSSHSRDSTPVHGPYFRS APDPRGSAPAFRGPIATRGR/RPRAPRA TASHVPLSSSSWKEPEEATAPRF*ASAC MKWRLEAGCPGHRGVWPGPPSRRLFMWA TATGEKSTPSPFTGVWRFGVEACT*AGS PTAHIQHSQRTWQPVPPCTNGSRSPWTS SYPKNQSKVGTVPKRGWACQPIPETAVR QATISQ*ARKGAARPHHQARQVEHSTQ/ QRPSGDSGKFDQRSLCEASTLLQPERPE VQGKICKFRV/GERRRTASPNSAVPEKR TRTQTMVGTAFIGCSGKWRRVYSVRR/R SSPRIPPPGVGSS\PLKTPPPP
68	13969	A	73	1	462	QDHRSKSSHSNKRPSLASSLSENFFQRA AKPLQVNKWKKLYSTPLLAIPTCMGFGV HQDKYRFLVLPSLGRSLQSALDVSPKHV LTKRSVLKVACRLLNALKSSLKMSWVYG RVT*KYLL*F/YRTTNRGLL*SMGFAFR YLPHGDNPAHLERGN
69	13970	A	74	307	436	LP*VGCITEGIPEQDMVRGKHKLLRQEK TRLIGPNCPGVINPGECKIGIMPGHIHK KGRIGIASRSGTLTYEAVHQTTQVGLGQ SLCVGIGGDPFNGTEFIDCLEIFVNDSA TEGIILIGENGA/NAEDNAAECL
70	13971	A	75	1	435	EISDSKAQLAAMALIIDTWERMNCFSE* NHEPLRTHCALAASKLLKKPD\QAE\RE HLCTSL\WSGTNTDKNGEELHGGKRVME RLKKALIIAHQGMDPSLQVRVFIEILNR YIYFYEKENDAVTIQVLNQLIQKILEDL PNLESWK
71	13972	A	76	58	366	EFPDLVKDMNLHIQEAQCIPNKINLNKL MNRHRII/RLLNTTTKKRILKAAKQK*N I/T/IRGSSICMMMDFSSEITEDRRKWH SI*KILK/EKTQNCLPRVFCPVKI
72	13973	A	77	1	445	YHETGCFLMGAIVDITLTFNTYVHFQGK MKGFSLLADPQEFWVDNSTSMSAPMLSG MGTFQHWSDIH\DNLSVTHVPFTDSACL LLIQPHYAFDLDKVEGLTFHQNSLNWMK KLSSRTIHLTMPQLALQGSYDL*DLLDQ A*LSDILTP
73	13974	A	78	53	444	ERGGYGAGPVAWQFLVPSTAPMLQSPPL GFAIDHTPPVPAPAN*APCPLPYAA*RT TGPHHIAHLDTTFGTGDTPHPSSPASPP STPWLPDAFPCPLPTWD/RPPCLQPLLS SLPTPRLPFLCFLLLAPYAP
74	13975	A	79	1	353	HIRTELDYYGLTVVIIYSDT*EAYNYIY IMVT*NVYKPQLWNIFDRATMHSQDVRH HLLCIRLMLKNPKHHAV*/VLNGHYAFV SR/SFKHALVQYVQAFRTHPDEPLYSFC IGLTFIHM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
75	13976	A	80	1	350	LYFYALLFLSSG/CVAYVATRDNCCILD ERFGSYCPTTCGIAYFLSTYHIKVDKDL QTLEDILHQVEDKTS*FKQLIKAIQLTY NPDDSLKPNMIDAATLKSMKML**IMTY EASILT
76	13977	A	81	76	386	PAYPQVRGPASTPASCIRPTNARVLSTT PRGKSVAEAHSVSPSAHRGVTSVIKLWS AKRLH*YGA\KVRPNS\GCTP
77	13978	A	82	1	360	ESILQEDITVLNVGAPNNRASKYMRQ/M LVELQRQIDESIIICEDFNTLISEMDST RPKISKDIVGLNGTIN*LDIIDIYRLL* PTTAEKTFFSSSRGAFT*MDHILCYETH IYKFKLHE
78	13979	A	83	39	344	WGILEGGEYIWHVGGGKSLRASGGLWSQ PPRQPDDSRPLVLVPVCHLLPHWIGPTD LGHKRQW/MGPGAVAHVCNPSTLGG*GE WIT*GREFETSLANMVKPC
79	13980	A	84	1	427	QQAHLAGHHRIHTGEKP*KCEACDKVYR GKSSL/MK/HRRIHTGEKAYKCEECHKV YSR/N/SQTVKDRRIHTGEKP*KCKS\C DKAFGHDSHLAQHARIHTGEKPYQCNGC GKAFSRQSTLVYRQAIHGVGKLY*GNDC HKVFSNAT
80	13981	A	85	88	307	TWTQRRAKLVRRIGWALLPFPRPSGSKP PP*TPPALPPCVP/PQSSPWTPPQPPAP DSREVSKDWTQMRSFKEN
81	13982	A	86	5	375	NSLLNTHSRGPGASHCTFWLHERASSRD LTGAESYGICRLRRLISLSIVFSKSIHG LACISILFLFLFLFLFFVKTGSWLCCPG WPQAPELRQSSLLSLLSSWNYRR*PPHQ LIF\DFFCRN
82	13983	A	87	2	342	VIKNEDHYIMIKCLI*QEDQTILNLHSF NKTNINIYKPHMTNLQKAVDKITITV*T CGTSLSIIAVCRLKLVKL/VEDLSNIIN KLDLM/DNIYKTLHLNIRDYTFLKHTWN IYKN
83	13984	A	88	1	338	CNEPRSHHCTPAWRQSKTPSKKKKQKKK LTTS/CIKASMKSRVQG*LR/CWAQVMG **GGVLWLFVK/REFFTLSINLSKEGHS RRVPCLGCLKKKKKKKKKKKKKKKKKK KKFF
84	13985	A	89	931	2	VASPNALPE*LLPVSGHTHDLERVGVAR LGQPHHTELTACRARMESRDTCPGVTLH P*PPSFPSSSSPSPGGPRTRLTHQGAGL EGSQGPLQSQNPSAA/PLGACRGGWEWP QGPGSGS*GG*LMLRELRE/WQEAAVQL PTPG*PS*ESGRPLPSSASGPTPPGSP/ SP*PGTQGLCGCHPSGLCATAAGPQDGS GPTPTPH\PVQPSCRDSGPGQRLSPTPS LTSWPNTRPSPPTGPGPGPGGRATW/PG S/PSPQRESPSPQLPCCTPGSFAGHPCP AP\AAPSSVACPLP/PDGFPRAPASSGI TTAPSPGPDP
85	13986	A	90	66	464	LWVYSSFPRLPLHSGAESPEGDILWPGL TLFLSPSPSPLS\CHSHLSPTCRRPRES PRFSLCWRPHPPSKPPPG*VKRDCCPSP DPVRLSVSENPSAGPR/VFLRPP
86	13987	A	91	197	2	NAEIIPAPQKVGPFIKIWVINFFFPFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						FFF*DRVLLCHPGWSAVVQS*LTVASNF*F\K*SSCLT
87	13988	A	92	317	2	SRTPDFR*STRLGLPKCWDYRCEPPCPATSSF**HLSLC*QGNL/VVGPPDSIRMGAG\TRKTKCWEGCHFLFFLRRSL/NSVAQAGVQWRDLCPLQSLTPRFKRLS
88	13989	A	93	1163	0	FAFGFEM*YCSVAQAS\VQWYDLTLLQPPLPGVQSDSPASSLPNKLGLQGTSHHAWLNFL
89	13990	A	94	3	363	VLWPCRPAGPSLGLNFPLYSWLRLQTFAAIRPGSTGRRLCLPNWVFTRNSLPFH*LVC/CSSRHNTYLQECTGHREPTYQLNIHDIKLLFLRFAMEQSFSADTGGGGRESNIHLIPYIIHT
90	13991	A	95	17	353	PEPRYVGFISGGKVDIKKTWKTQGRLERTVYYTGMYFINCH\VLKNTDSSWGTSP**IQQHAGKRDNNYQLL\KLQG\QFSEAYTKCYSNPDSTHDVRKVYQDCPLLAPLNDTS
91	13992	A	96	3	355	ANYPRDLCKVTDEGGYTKQQIFNADQTALYWKKMP\SRTLMEREEKSVSGVQASKDRLTLLLGGSVAGDVK/LKPMLIYHSENPRIC*SYSLPVLCKWN/NKTWMTAHLFTTWFTECLNPL
92	13993	A	97	367	2	SLHRARRGKGVGVRMGERLPSFQSWRLRL/RRRKLCRRWGQGPRGN*Q*QKPDGGARASQTDGGGERRRGVQTGSQAERDTSRETYSPRGIQREIVRVSKGGKTGRQWQSQRQIQREKRVGR
93	13994	A	98	115	359	LNFFFYLLNFMLLFHRYYALKVSYFKSSLDRKLLELLWNKYWVNTLSSSSLLTVS/DYTCKECI*ILSKLHSRLISETLFHRK
94	13995	A	99	1	490	CVDPRVRTIFKKDKVGGLPLLNLCIYYKATVT*TVWYWHKD/RTDQWDRIKSLEINPCIYGQLIFFNYYFFSQ*CQDSSMEGNSLFNKWC/CRPLTLYTRIGSKWIKYLM*ELKLYRLSLHDPEFGNGFLEITSEVEITKEEIGKLD\LAKLKTFC
95	13996	A	100	195	3	SRCCKQRHLVQWNRTEKPE/YGRLIFNKGVKTN*WGKNNLFNKWYWDN*ISTCKRMNLVPYLSPYT
96	13997	A	101	1	371	FSLIKISMMLLMKMEK*NLQFIWN/HRRLQIAKARLNKKNKTEGITLPDFKIYYKAVVWYWHKKRHIDHWNRLENSNINRHICSQLILTKVPGANTKDHPFNEWSWEN\VCTKMKPDP/YLSSYTK
97	13998	A	102	6	370	KKGTIPNYF*RE*TDRSKPN*NYATKENYI/PIS*NKKIL*KLANKIQQHIKKKPDNSLFYKIQFGSILETFITINQISKPKEKNHIIISTDAENA\FDKIQH
98	13999	A	103	298	24	KCWTSIYLLLFFRDEVSLCCPGCAQTPRLK*SFCLSFPKCWDYRREPLVPGLDQ/LFLESNRSVSVLKKNVP*WFSNSSGSKSGNHDAFCGIS
99	14000	A	104	2	352	GTIADFTQCCQAADKAACLLPKLDELP\QNGRLRSAKHRLKCASLQKSGKRTFRAWT*AGLIHRFPIAEFAEVSNLPTELTTVHTECCHGDLLECADHRADLAKSICENHDS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						ISSKL
100	14001	A	105	139	361	KHTEAF*MPCAKYY\LFGGLNQICALPE KTPVSDRKTKCCTESLVNRRPCFSALEV DETYVPKELNAETFTFHAK
101	14002	A	106	3	350	ELEMIMLSEEVMLKAKIRQKLGLL/QPV S*VVNAKEKFLKEIKSATPVNTQMI\KN SLIAD/MEVVWIDDQTSHNVPLSQSLIQ S/K/ALTLFSSMKAERGEEAREEKLEGS RGWFTRFKER
102	14003	A	107	225	1	QGIMMDTVEYVGKGEPVRCWWKCKLVAL L*KTTWKLLRKLKI*\YDPAVPLLDIHP KEIKSIYQRDSCISMFTA
103	14004	A	108	390	2	LGYSGVRAPLEEAVCRFSDLKLRAGRTT TLFKADRQGHLSLQRFLLTFDSLCP/AP RGGVYRGRQASLSCSGLHPVGASWPRCL PTQASAMAGAPAAASLPPCSLISDCCAS NE*GSVSVGPSEPGTGHN
104	14005	A	109	304	33	KVWGEKVWYWQKMTQIVQWDRTESPQID N*SLTKEIQWRKDSLFNKW*GNNWTAPF SS/RSLNLNKDLTAVTKIKSKWVTDLNV KHKTIKLL
105	14006	A	110	135	1	KQAILWPGAVAHA/WSCNPSTLGGPGGQ IT*GQEFEKSLTNMVKP
106	14007	A	111	140	338	IMSIILYYGSICYCYYWLID*LILRWTL ALVAQAGVQWRELGSLQPLP/PCLSLSS SWDYRPP
107	14008	A	112	26	361	RSFFWVFFFEKKSLLGIPGGKKGPPLN* LEPLAPGPKGFSGLNPLENGNWGPGPPC RGDFGFF*KKTPFPF\GPGGVKTPNPGE TF/EPKPPKGVGFPGETPGPGPGENLYQ WK
108	14009	A	113	11	330	ASIWLHIFLFLSYFLEKGPRYVAQAGLN LLGSTGPLSASRAAGTTGALHCTQL*TY LLLPKHGKAVFF\QETLLLRSTHPFPLK HVYTPTYELLLVWDRDSLSRPR
109	14010	A	114	350	2	GCCPCLLFPGSPTVFGSLYSIRLVAFVR AVPPVWKAVPG*PPVKM*FFHLFIYLFL KQ/VSLWHPGWS*LAQSQVSRFFPRSLP SNWDYRGAPPRLTLFFFFFKQSQGIEAM VLAL
110	14011	A	115	3	341	RMVSIS*PRDPPAFASQRAGITGVSHRA RPVYSFLLLSNVPVMDVPQDIYPFLVDG YLSLPLVCCV*V*VLLCYPTWPPGLKRS SCLSLPSSWDYRHEPLKPA/SCCVLLSS G
111	14012	A	116	1	384	PSYPGDLTEIMDEGGYPNQQIFSIDDTT FYWKKMPSRTFLTTEKSIS/GF*ASKNK LTFLLEANVAGDFKLKPVFTYHALRNPR TLKKYATSTLPVLCKWNNKA*VT/AHVF TTWFTEYFKLSVETCCSE
112	14013	A	117	43	347	CAAGFGLL*TPPRT*TRKPRRNGTYKPI SLMNINAKILKK/ILANRIQQHIKTK\L LQSDQVGFI
113	14014	A	118	351	23	FNK*CWHNWIFTCKGMNLEPYFTPNTKI NAIKAIQLLEENKEVNLC*LGLGNGF/S RLPKAQMAKETIDKLDFIKLKALCSK\N TIKKVKKSEELEKIFANHIHGTSIQNI
114	14015	A	119	123	340	AADSSTHSLTKPAYLEKQNFFFFQMEYC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						LIPLAEGPWPNLA*MQPPPTGFKQSSCL SLPSTWD*R/HWSPRLAN
115	14016	A	120	1	371	PSYP*DLTEIMDEGGYPNQQIFSIHDTT FYWKKMPSTTFLTTEKSIS/GF*ASKNK LTFLL*ANVAGDFKLKPVFTYHALRNPR TLTKYATSTLPVLCKWNNKA*VT/AHVF TTWLTEYFKLSVET
116	14017	A	121	82	367	YSKRSNTIVAGD/FTPLSALDSSSRHRI NKKTSNCTIDPMDVIGIYTVFHTVSTEY TFFSSANGPFSKTDHLLGYKTSLKTF*T KLK*HQ/CIFSDHN
117	14018	A	122	27	253	MKTENILGENIGEVFGVGKDSLDMSPKA *TIKEKNDKLFFIKVKNFSYSKHTI*KI KNQATVWQ/KLLTVHKSDR
118	14019	A	123	3	305	GTRQGCPLSPL*FNTVLEILVR*ISQNK *INKT/SLTADP/MVLHIENPKGSIK*V LELINEFSQVAGYKINM/QKTVAFLYTN N*LSKKEIKKTIQFIIASKRT
119	14020	A	124	1	327	QVIFCLGLPKCWDYRHEP/RMPGLRGAD FFSLI*ILWEHMF*VMCILPHPCGDFWA MLNF*EREGMFF/CLKRWKSHNVSQA/G PQTPRFKRFSRLTLLSSWDHRHAPPHLA K
120	14021	A	125	74	334	IFEFGVLKVITCLSVSSHEVGKLCPFFF FFKNGV*FCCPGLQGYNGS*L\TLELLK QSSCLSL*CTQDHRCLPPCLANFNLINS SIH
121	14022	A	126	381	60	TVSQVLAHTCSPSYLKAKAGGSLEPGSC YPGCSEL*SCHCTPAWIT\SQTPSL*KI H*KKIIVKRAIVECVCVYVYTYIWLLIL KFSDSIPFAQIWGFHEEFPYWNQC
122	14023	A	127	323	2	RGFLGLSDEVSGQQLFSILSEIENQFKN NLEGCGGSCL/SIPKCWDYRCQPSRLAY A*LIFVFLVE\TKNTGFRHVGQAGLELL TSSDLP\ALASQNAWLTGISHHAEPY
123	14024	A	128	2	354	ENCQINNLRFHLRKPKKEEYTKPTASRR K*IVNIRIERNGIEQK\TIEKINELKSW LFENINKIDSHSGKWMVGEE*CVFVCVC VRERQSDRERETRLIKI*NERGDITADL TEIK*LLILQKLNNY
124	14025	A	129	74	327	GELAMLPRLILNS*\PCNPPA\SASLVT GTTDTPLYPAHYYY\IIIIIIIIEMEFH S\VAQAAMQWCDLGSLEPL\PPGFRRFS CLSL
125	14026	A	130	83	382	YEFHASDGGSRLSSQHFGRPRWKDYLSL EVEGQPGQHSETPSLSLSLSF/CFLEME SCSIAQAGVVQWPYLGSLQPLPPRFRRF *CLSLPKCWNYGHEPQL
126	14027	A	131	749	2	RQSLALSPRLECSSTISAHHNFCLQGSS DSPASASRVAGITGVHCHAKLIFVFLVE TRF\THVGQ\AGLELLTSSDLPALASQS SGITGMSHHVQARCVIF/CGPTFKNQDM KY*NKKEKNQSTFLEHLQNQQENRHAAH TLRHHTAS/LKSSEFLFAIRTSFLIS*K RSGTTGMF*YN/WTIGNGVEDRFVLGPP FGLGVQWYHHSLLQPQSPGLKQSSLFSL PSS*DYRHVPTPSFLKFLRRWGLAILLR L

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of *peptide* sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible *nucleotide deletion*, \=*possible* nucleotide insertion
127	14028	A	132	371	1	KKNLNLNLTL*VKINTNWIMDLTIKYKI IT*KKQEKVGNLEQGKEFSDLTPKV*SI KGNTDK*DV*KPFSL*KPM*GNYRQATD *KKMSAKHVSNKYP\LSRIYKFNDKAKN KPIRKWAKQMN
128	14029	A	133	2	318	NHKIILKDAKKAFDKM*HPFTMKILNK* GIEQYAT/DIIKAMCDRPTADIILNGEK LKAFPLRSGRRPLL\FH*IW*VLARTVR PRKRNKGSQEWWLMALIPSTLGG
129	14030	A	134	3	362	WSELLGSSDPPALASQIAGIIDMKHYAQ PGTDF/STSVYFTLPTQIRL*ALKRKFL L/EFK*IFASI*QFAKCSCMSRNFLPAQ PYHHWHFPNEETEAQGNFSLLWAC/LRE DWIPTD
130	14031	A	135	12	398	KCSTSIVIREIQVKTREIYHYTPTKMAK IKKPDNAKC/WSGCGATKTLIHCW*NN\ SLEIWLFLMKFNICLPCDPEIVPLDLYL REMKTYIHENTYTKVSIAPLFK\QPKSP STGESINCSIIIPRMECII
131	14032	A	136	309	1	QSEAPSQKNTKKQKTKVGGLTS*FQTYH NATVIKTVWH/W/YIGIDIDQWNSIQSP EINFHIHGK/LISNKAAKTNEWGKNSLF NK*HKDNRIFTCKRMKVDSQPHI
132	14033	A	137	2	251	QCGKAFRAASVLRMHGRTHPEDKPYECK Q*GKAFRSASHL*MHGRTHNQEK/P/HE CKECGKPFRSAQNLRIQ*RTQAHIRMHS G
133	14034	A	138	396	3	LELLTS*SACLGLPKCWDYRREPPHPAK MIL*SKSS\LPFLCSKCLNTIWALLLLL CSLVPLLTLPLKEFYAAH*SPDSLKYPV LQKLSKLEMLVLHETVQRKEQLTYSLYK PIFGFLVGYSFPLFCSYKTS
134	14035	A	139	3	384	LDFIKMKNCCSSKELCGKYEKP*T/MEK MFAKHISNK*FIFRI*K*LSKLTKKK*A KDLNRYSLKEDIQMANKCM/KKCSI*LV IREKQTKNTMRYY*NGLS*RS/GQTK** QGWGGTGPLIHCWWEYPMI
135	14036	A	140	63	388	FMYLFIY*LER/CLTLAQTKVQWCDHSS LQPQTPGLKH\PPASASGVATTTIMPG* FLFFF*KRGPCWVAHARTT/WLNLGSF
136	14037	A	141	370	3	GPGHFPALFFKGPGLGPWVPPIIPALLE G*GGGFPGP/RGSGPPGQPCFFLKFQNF PGFV\GAPVVPGFPGNLGRGTALNPEAE GSINLKGPPGLQPGGKTKLFFQKKKKKY QHFQKTQLILCF
137	14038	A	142	363	2	REKATEENFATS*DWLMMFKEGSHFHSI KVLGETPSADVETVVSCPEDLAKIMDED GYTKQIFNVGET\PSRTLITRKEKSVPG FKASKLQRIG*LLLGVNAAGDFKLQSVL MDYSENHAE
138	14039	A	143	99	375	KNKNQNISPPLVRYTLLSPLLLPFIINS FFFFFFSF/CFF*KKSRFEPKVAFQGGN LS*LNPRPKGSKEFSCLSLQSTWITGGP PPHWADFDF
139	14040	A	144	39	399	LQIIYNYIWLYIWLYIFWLVSKIYKELL QINNKETNKNGQKT*IDVSSNNMYMNG* *LHEKIHDIVIR*MRIKTTVTYHVMSTR MVIIKETENKYW*GYGE\KILIYCWWEN

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						FEK/SVWPFL
140	14041	A	145	358	3	REHTAEDKYEASRSWFPRFKEK\SPLRN IIVQGEAATTNGEVAVSY/PEDLAKNID EGGYTQQIF\NADETF*YWKMLFRTFIA REKS\RLPSRDRLTLLLGANAAGDFKLK PMFIYHSDSC
141	14042	A	146	3	376	AVMGMYKINVVFVPTNTSILQPID*GVI LTFRSY*LINT\FCNTIGAIGSDSSDGS GQSKLKTFWKGFTIPKS\IKNTCDLWEE VKISTLMGVWKNVIPALIDLFERLKTLL EEVTAYMVNIGRRL
142	14043	A	147	374	161	EFHRVSQDGLDLLTS*STCLSLPKCWDY SKWQRRI*TQ/DLCDSED*SSIKPIQLC QELMS*MAEMAHGQP
143	14044	A	148	373	2	FFFFFFFCDLLLFPKQPRSHASFSLPSV VPFPEMPSSSLTLFYLFVYNLLR*YL/N SVTQAGVQWHDHGSLQPRP\SLLSSWDH WCTTPCPAN*IFFL*RVGLAMLPRLLLN SWAQAILPLWSPK
144	14045	A	149	3	282	ILKRIIHPDQVFFIPAMQGWFNI*K*IN TV\NHIIRIKGK\NRMIISLDTVKAFGK IQQPFMI*KLGIKGNFLNLIKGTYENP QLAGHSGLCL
145	14046	A	150	3	360	DII*ESKFQGHHTTGVQKGLQYGIILFI I*EVFFFAGFFWAFYHSSLAPMPELGGH \YPPTGIFPLKRLEVP/LLNTSVLFASG VSVTSAHHSLIEGNRKQIILALSITITL GIYFTLLQI
146	14047	A	151	349	3	KKSSGSHLETKSNRLPGPSQGPWCKEIR KGSLAWQEKSWPFYKPFLLEVGGGRVIR GSRMTRHGHLIRSSKTLIKHHVPK*TVQ FNFCLFIFLEMESRS\VAQAGVQWCNIG SLQP
147	14048	A	152	500	0	MPSRLECSGA/ISDAQCNLQNSGAPSEP SSALSNPCG*DYRDTLPLPGYFLKFFVK TRSRYVTPAGL*LLASS\IPPTSA/FSK HWDYRHE
148	14049	A	153	373	2	QAGFTLLTSSDPPASAS\QSAGITGMNH RTWPGNF*PQKSCDSFVTKLMCTCHKNH IYAQSLVT*LGHSYIFF*DSLQPSPPRF KQFSCHSLPSSWDHRHTPPCPARTQLHF GYEYFSRHFLRRR
149	14050	A	154	332	3	THKFQRLTSKSKKLKRKLIFHQGAQKSN SLNPDIKKNLKRSQRNME*EKIFTDHLS SRIYRELLKLKAK/INLIKMGKGYFYEG DT*MADKHIKRCSISPIIREMQIKTTIR
150	14051	A	155	337	21	LGLLPFFQRCPAKRGGI*RGSLAAVALL NCGELHPV*ASWWLCL\PVRGKLPTEAS VMGDAPPPTKLECPRSTSDCCDGSKNFE SVDLSLLGSVGVGSVDLDPVAP
151	14052	A	156	21	491	HPGSRGCSEPRSGHCTPAWGTKVKTPAS TKTKQNKKKK*RTVCLTPWHTLL/RVWC DGGDYSSSLL
152	14053	A	157	3	394	REDLLSPGFQGCCEL*LCHCIPAWVT/S ETLSQKKKK
153	14054	A	158	36	354	LSAAFTSQLLGRLRQENGVN\CSEPRLH HCTPAWATE*DSVSKKKKGKPFWIPNPL SSLSPAFISGQGPWESHLKNPGRALQGG

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						GFQPLICPRPGRTHMSLKSPWRP
154	14055	A	159	78	340	VVFHKAQRGILLAELYPSGSAGHSIEPK TITLFFLGNKVLLCCPGWSAVA*S*STV ASN\FGPK*LLCLSPPSSSDSRYARPHM ANFK
155	14056	A	160	2	362	HLSPLSIPQNRHCHHGPFSVSCWAHLPD GVVAGQRGSSLP/M*GRPGRGAPSPPRR GGWPGGGLTPHLPSGRGGWPGRGTP\PS Q*GRPGRGAPSPPGRGGWPGGGLTPPPP SQTGRLAGRR
156	14057	A	161	293	2	PHLAIRPPTTVDKSALYWKKMPSRTYKV RQKSMPGFKSSKDRLTLFLGAK\AAANF KLKPMLID\HSKNTKALKNYAKSILPVL CKWR\HKA*MSPHLF
157	14058	A	162	2	136	LIVPILIAMAFLRLTERKILGYIQLRTG PNVWTPPTGATYRLLS/P*QP**LFTKE P\LEPVTCTITLYITDPTLALTIALVL* TPLPIPNPVGNLNLGLLFILATCSLAVY SIL*SNRNGIPKTYRTKNSRLYTTTHRP QRLDAAYWCYVQTPIA
158	14059	A	163	1	464	RQGL/DSVTQAGVQGRNLSS\LQPL/PP GLK*SSRFSVSNSWDYRCAPPHLANFFN LFFVQRG\FTMLPKL*TRS\GPGD
159	14060	A	164	1	353	FNYSSSLGNKSETPPQKKKKKKGRGPG ENPGTPTFGGAKGGGNPGIKILKTTGPK GGNPCFKKKPK*PHRGGRP/HGNPVYRG GPGKKNFWPPGGGGSKG*KSPIKPPPGG KKGDFF
160	14061	A	165	45	389	FFVCTFCRERSLLCCRSWSGTPGLK*PS CLSLPKFSDYRHKWPCSARNFLPACLPA CLPPSLPSFFPPS/SPSSSPRQGVTVIQ VRVQWRDYGSLQP*PPKTKRSFTLAFQD LGPQ
161	14062	A	166	330	2	WDYRCAPPHPVLYLKM/STFNIFFL*RG VTMLSRLVSSDPPISASQVARIIDVSHW AQL*RSV/CYVFETGSGSLTQAGVQRYN HGSVQPQHSRLS*SSHPSLWNYRYPPPC
162	14063	A	167	2	396	YSNVLLGIYPKELKTLVHWMFICV*NTC IWMFITALFLA\ES*CSSVGE*IGKTWY IPTMKYYSVMKRNAISSHEKTWTRLKCI LPSERSRCDRLQTV
163	14064	A	168	486	2	LIFGKIYKINNSSKTDNKRGKTQIQILG MKTGDIMTY\QQTSKEYYAHEFNNLEEM DQLFKKHKRP/RIHQYEKHHLTGPMTIN EFEFINVKTPKNQSPGWDDFIGKFYQMF EEFLSENKTGELIL*S*YYSLTNSFYEA SITY*PKPDRQ*KKQSCGPISFM
164	14065	A	169	200	3	GRVDLPPTQESRPPGPPPSDPGVQAPRP SIVRNCGILTRGSPGPD\PSPLSS*AQL CGSPPPPSFS
165	14066	A	170	2	327	PGGIGCGELR*HHCTPTCATERDSV/WN KIIHYIIMLASPNELILPLLNICLEIL* AGPLTAICISMFMATL\FTIAQMGKQPK CPSTNEWIRKMWYIHIMEYYLHFKMK
166	14067	A	171	2	343	PGWSQTPDFR*STCLGLPKCWDYRR/AA TVPGLFLFLTALC
167	14068	A	172	367	3	FIRDVQFISALRYLLTPERMA/MIKKSK NNRYRCGCGK/RG/TLLHCW*KCKLVQP

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						L**SVWRFLKELPLNSVIPLLGIYPK/DKEVIYEKDSCILVFIAVQFAIA/RNIHPTYCPINE*IKKMWYIY
168	14069	A	173	102	345	YQLQNIPRWVYSKLQNLSFAFVLL*RDRVFLCHLGWSSLL/QLKRSFHLYLASSWDYRQVTPRPAN*ILFRD/RGLALLPR
169	14070	A	174	22	401	STRLGLPECWDYRCESSCPATYLPF*HSIPFLSQLKVQVHHRRYFHLFPELSNLPLLSKNVS*TY*KSFLS/WPSLRVLFCFVLFCFVTGFHSVQARVQWGNHGSLQPQPPSLK*SIHLSLPSS*DCR
170	14071	A	175	2	388	SDLQLRAGRTTALFKAVRQGHLTLQRFLLSF\V*LCPAPRGGAYRGRQASLSCGGLHPGRAYRLSCLPKQAWAMVGAPTPASLSSCSLISDCCASNHRDSVGVGPFEPCAGCNLTEHRFLSPSGAVVSC
171	14072	A	176	334	1	KLLELIN*FNKVAVYKINTQNQLHCYTLIRTTQKGSLKTILLTIAPKRIKYLGI/Q/LTKEVKDLHSESYTLLKEIK*DINK*KDIPCS*MGMVFFGVCLFVYFCFEMAFRS
172	14073	A	177	339	2	KNSPYNFPKGKNPGNL*SLKSRIF/CWGSTFAHIGELFFFKMGKKFPAI/RPFFFFEDRVLLCRPGCSGVVRSWLIAAST/CLGWDYRCTPPCLANFL*RQGLTMLPRLLSNSGLQ
173	14074	A	178	3	303	DLRRAACLILPKCWDYRHVPPRPADNSGFLHLIII*VCLPLLCHAQLVFIFFIETGFCHVAWAGLKFLGSSSPLTLA/FSKCWDYR
174	14075	A	179	342	1	INRLNIFTMAIFSTLIYRFNTIPIKIPAGFVEMDKLILKLVWKFKAHGIGKTTLKKNRVPNSKAYYNATVSKT\YWNEDRNINQWN*IDNLKINPCVCGQLIFNKDAKTNEER
175	14076	A	180	2	323	STSYPITGSHAFL*PQNVVDAETNS*HINNVNLRLKIIKLLEENTEKNCHDLGLATDYY/SVTPKA*ATTTKIDKLELIKIKNFCTSKDIT*KVKRQLIGENSCKSFM
176	14077	A	181	326	3	RKRKKKRREREPKKDEERKRLYGKDIIKKRRKDTM/DWEKILQKGVRQRMCI*KI*RGVTQELKANPIRKGGNNLNKVHQRI*MANKHMKRCPKS*VIREI*IPTIMRYH
177	14078	A	182	5	326	TKTIEKAAN*IRRSRRKKIKFKPEIKNRKTTTKINESKSCFYKKTNKTDKLLVKLIRKKKTKKIITKDEKNHTI*DCTEVKGMTECYEQVYANKFDNS\EKMDNFLER
178	14079	A	183	3	378	TVLCSFIVWGLDFFG*IHTIYS*VFCYKWNCVHNFLFRFFSAYI*YLLIFVY*S*IMHLCLICY*LLL/CSCIFFWIFYMLYFSFWL/CFLYFYFYILCPFIFF/CIFICLLFFVYLFLLFIFFFIFLF
179	14080	A	184	365	3	MQLKCIMKSISVQAGVQWHNFGSMQGPPPW\LHHFPASASLVTGTTWARHQGRVIF/IFFFFLMRRSL/DSVDQAGAQWHDPGSLQPLLPGFK*FA/CPCWDDRRAPQCPANFVFLA\RHGFTILAR
180	14081	A	185	51	293	PYVNQEASVLTNSFYQAS/I*KKSNYRPISLMNIDAKILNKTQQIKLNKVNDSRQT

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						GEDQIPKYCTVSDGRMMRDYFPLFSS
181	14082	A	186	326	3	TKICQWILNLGKKREFGFKKKKKIKCPN KRHRLANGIKK*DPTTGCLQDICFRSKD AQRLQIKGWKKIFQKTGI*R/GVAVLTS DNIEFKIKIVTRDRVANYIIKGSIHQ
182	14083	A	187	17	330	KDNEM*IKRTMRCYYTSFTMAKINLKIN NIKC*QG*GTTGT/L/LYC*WKHKIVQP FSKTV*QFLMRSNKYLRYNPAILLLGIY SN*VKI/C*KTYMRMFIVFLITKDWKQP NYSS
183	14084	A	188	124	357	SLWGGDLEGGGEKKERGENPGGPKKPGK KKKKGGNLGARG/VFKKRGRPQKEKPGK KGEKGGP*GAGI*GGGGNGVKKK
184	14085	A	189	333	124	RLRQENRLNP/GSRGCREPRSRHCTPGW ATE*DSVSKTNKKMYKSIIARDCHAENS IVSFLSKRGCVFLF
185	14086	A	190	1	327	KSWLIGDNIPSSQSLIQKKGVNPSFKSM KADRGKEAAEEKSEASRSWFMREKERSH LHN/IK*VQGKAASYPEDLASIIDEGGY TKQ*IFNEDY/MWKKM*FRSFLTREKL
186	14087	A	191	53	400	VNILGPFHLFFTFVQNALSPNIYMTHML TSLGPLHMSSLQTGFPKPSYLKFQPSPH SVPVGF/IPGMQR*FSIHKSVNVIYHVI RMNDISHMIISKDT*KAFDKIQHIGSLF PALSL
187	14088	A	192	65	321	RARTEIYLIHTLLGVYAGETKTGPYTDC M*MFTTAPTTLVKTWI*PKSLSIGERIN KL/WILICTYMEYYSAIKSVLTHLTTWV NPH
188	14089	A	193	127	241	IIKNDSRRICNLTEKLPLRKINS/WPGA VAHACNPSTLGG*GGESRITYNESRNKG EQTQNNK
189	14090	A	194	1	337	DLPASASQSAGIIG*ESIRN*NKLVKKT LKCSQKDPKEDLNK/WKDIVCSWLGRLS LTKVSILPKLIYKFAKIPTKLYYD*KKN RPGAVAQAYNSSTLGGRGGQI
190	14091	A	195	2	333	NFNSLFFFVEIEKLILKFILNCK\VARR ILQRKNKVGRLTLPNFNTDYKATVIKTA WH*HKDTHMDQRNRTESTKINTYKGAKT I*WRKNSLFNK*CWDK/WITTCKRKKVD P
191	14092	A	196	299	2	PHPQRDVVQPSPPSICRIFSPSSIPGIQ SWFNIQKSINVFYHIVILNTQHRSSSSS SSSSSSSSSY*LMIKF/LNKLGIEGNF LILIKAIHGKPTVNH
192	14093	A	197	2	199	LALSPKLECTGAITAYCSLELLGSNDPP TLASKVF/GITGMSH*AQPQVVFLLLYY FIFFFSSSSVL
193	14094	A	198	226	2	KKFFFPNPNLKNFPLGRVFF/CSPG*KF FAPLGFFLVSFLRQKVPHLGSPGKTFFF FFFFGDRVWTCHPCWSAVA
194	14095	A	199	338	93	PQHNGSCL*SQLFERLRAEDPLNLRVQG CNEL*LYLCTPSWVNPVSEKKSIQEKNA NLDFREY/RDKRRENWTCV*NSIERSSE
195	14096	A	200	1	361	PRSHLSQLRVRLSQ/IKKNQKTIGKGFR AIG/MGKKF*GKTLKVPFTRGKVNQWKF LKLKSFLPRKKKTEITL*TLGKHFRKWE KFFATYPSTRE*ISKICRDLNHFTGKKI

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						IIPIFQRAKGL
196	14097	A	201	2	358	ENKTTMRYH*IPIRMAEN*VLAVGTL/LQPWWEYKRV*PLWKTNSLAVTLLNINLPCNPTILLVGIYPRERKTYVYTVACTQMFLTVLFTVAPNWKQSQGPSTGE*KNK*WHIHIMGHYS
197	14098	A	202	110	357	IWVFIWCHFLLPEKTSFFPGFPQCLDIS*KTLFVHSVLFFFKDRVLLCHPGWSAVAQ**FTAASD/FQESSCFSLPGSWDYKRM
198	14099	A	203	2	374	ILKLHAFFMAETPGACKTPCDLRQVFIFIFIYLF/MRLSLTLVAQAGVQWRNLGSLQPPPPGFKRF*GRCLFYPKDGLVCPGLAGS*TGQIGKGIRTLSPDLCLSDGFCGSK*PKS/ASASQGHVG
199	14100	A	204	375	3	LSSILIRGSFNLSTLITTQEHL*LLLPSW\PLAII*FISPLAETNRTPFDHTEGESELVSGFNIEYAAGPFAILFIAEYTNIIIINTLTTTIFLGTTYDALSHELYTTYFVTKTIPLTSPALMNS
200	14101	A	205	393	3	SARLGLPKCWDYRR/ASTVPGL\SLMLLLKSYVSKMKKCE*LVKPLKAKL*DSCKEL*VGNNLIMPSTYDQENDRVDSSLTWLCVLLLLLLLLLLLFWRQSFALVARAGMRWRDLSSL*PLPPGFRQFSCI
201	14102	A	206	2	377	FRAVLQGRWSLQKFLLPFVQLCPAPKGGVYM*RQRS/SLSCGGLRPVRASWLLCLPTQASAMVNAPPPARLLPPRSISDCYTSSEQGSVSMGPAEPGVGYDLLVCCLLRPLEKHSIWVRVSCFSRY
202	14103	A	207	327	1	ILTGNFKQIRMLIYHSVNPRALKNYAKSTLPVNYKWNNKA*MTAHLFIAWPTGCFKPTVEPYCSKKKK\IPFKVLLLIDNAPGHPRALMKMPEEISIVFMPANPASIL
203	14104	A	208	310	2	FCWWAPGMGFPLGEWGLILGPGSPFFLKEGFPGVGQPGPPKRWGLKG*PPGAHWKGF/IFFFADRVSLCHPCWSAVAQSQLTANPASQVQAILLPQPPDYRIR
204	14105	A	209	374	3	GVRDP/LEEVVCPF*DLKLVARRT/SLFFKAVRQGHLSLQRFLLPFVWLCPAPRGGVCRGTQASLSCSGLHPVRASWPLCLPTQASAMVGAPSPASLPPCSSISDCCASNERGSVGMGHSETDVGY
205	14106	A	210	3	196	LENLKF/LDKFLETYNLTRLNQEETEILNRPMTSSKI*SVIKNLARAMAHAYNPSTLGGKGRRIA
206	14107	A	211	34	339	IIKSKRINYMSCELYFNINIDNFFFFETVFRSVI\KLKCYGAFMVHCTLNLPGSTNLSTSASQVSGAINRGYPGQF/IGLEK*FLVKTGFCHVA*AGLEPLGSG
207	14108	A	212	200	312	HYGQFHVLFCSLF*MESHSVT/QAG/VQWP/SLALQTPPPGFKQFSCFCLVSSWDY
208	14109	A	213	300	124	NHIFFYFQIHRVCVCVCVCVCVCLCVCVYRYIYCVSPW/RN**SL*KECLSLVLLTPTC
209	14110	A	214	1	357	QVDHTSDRKANLNMF*KIKVIQTMFSDYNGVKSENNRRKTGKLTNIQKLNST/L*ISNETNEKPQEIRKYFEVNINENTTYQDLWDEVSIVAQAHNPSTLEAEAGRLLEPRS

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						LRSAWTTE
210	14111	A	215	360	1	LTIETYCSE\KKTPFKILLFIDNLAGHP RALMEM*KEMNVFMPAKTTSIMLPLI\S SFNSYYLRTRIHRTFVVVAQSWLQCPTT AISDIQIGPVAMGLLLIPSAFVLCWLSI QQVSKLKH
211	14112	A	216	3	347	SSRSRADGLFFYQCK*QTLYW*HLWYKT QKEKKKTQMKEKKQRINKAR\GDKLPEC EAVCGKPKNPANPVQRILVGHLDAKGSF PWQAKMGSHHNLTTGATLINEQWLLTTG KNLL
212	14113	A	217	75	347	PPIFKRTARGKVTPGWEYPAKG/CGGTF LGNRGLFPNPGFSGPFPKKQVWEGALCA PG*KVCTLKF*FI\SLAIPGNGSKNFFT LFEGPSPIL
213	14114	A	218	3	397	GGQGYSGTGHHGGIWHKMEH*R*PLPPK KKKKKKKKKKKKKKKKKKKGGPPKKKPR GGQNLKGGGKEKPPPQKGVKKKTLSGRI IKKDGREKHTRGELWKKTFIW/EGEKIG EKPPKKI*DHEGKKKVLRGKG
214	14115	A	219	3	401	DSWATLHGNIMK*SAAVL*ALGLV\FGF TVSGPTGIVLSNS*LDIELHDTYYVVAH FHYVLSIGAVFAIIGGLIH*IPLFSGYT LDQTYAKIHFTIIFIGVNLTFFPQHFLD LSGMPRRYSDYPDAYTT*NIL
215	14116	A	220	162	3	KPAQRNL*SNPEKEDINILKRNQS/WPG TVAHACNPSTLGGQGKQIIRSGV*EQP
216	14117	A	221	374	2	WCRDRERERERATERERERERERQTDRQ TDRRREEA/EGWAAWAIN*GRAPGTSLE AALECSCPRRPPQPAPPEQGPFPRTTAR GQPRPPKLLQPEAPSQTRPHGYPWPLRV LPQSGPEVRPRE
217	14118	A	222	3	264	DHMRPKVRGCSEL*SCHCTPAWAT\SES LSQKKKKKKKKRKKIGEKI*GAFFKVAP PFFFFKKKMNLKSPVGIAGVAKNTRWIL KHRG
218	14119	A	223	2	410	ATSPIIEELIT*HDHALINILLM*FLGL HALFVALTTTLTNTNI*HAEETQT**TI LPAIILVLIRLPSLR\ILYISDEVNDPS ITIESMGHQWY*TYEY\TDYSGLILNCY ILPPLFLEPGDLRLLDGDDQVALPI
219	14120	A	224	399	3	GVGKPGFPWAKKWALPPYSKGYPK*VQN LILKVKLLLLKKNPGENSLEATGTWGLP PKARAPKLKPNW/DSPKRKNPGAFKKKK KRQPTEWEKIFANHASDKRLTSRIYKEL QQ*KSKQPIFLIPIYHLNHFKG
220	14121	A	225	360	71	NRTTWVPFKTPPLLYHINTKKK*HTGNK KHKTKRAKKRKKTKNAKK/EKEKNPHPQ RPQKRKK/EEQKPKRGKKKRGKKKKPFK EYSYL*K\YIHTNLQ
221	14122	A	226	3	386	PSTHVSINLAMGIPL*ADAVIIGFHSKI KDALAHFLPQGTPTPLIPILAIIETISL LIQPIALSVRLTANITAGHLLMHLIGST TLTVSTINLSSTLIIFTILILLTIL*IA VALIQAY/VCPLLVGAY
222	14123	A	227	3	372	YSLDSPSLTRFFTFHFMLPFISAALAAL HLLFLHETGSNNPLGITSHSDKSTFHPY YTIRDALGLLLFLLSLMTLTLFSPDLLG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						DPDNYTGSRNAPVKQPRPHI\KPE*YFL FA/YTILDPPYKL
223	14124	A	228	2	263	PRVRSRWEDCLRPGA*DQ/LCAP*RDCF FKKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKGGPFKKKPR GGQNLKGGKKKKFFPKRGE
224	14125	A	229	314	1	LIKTIFLYQVSLCCPG*SQTPGLKQSSC LSLPKCWDHRHKPPCPAQSFYFTFTERA LRVIY*FI*RQS/LRSVAQAGVRWCGPG SLHPPPPRFKQLSCLSLLSSW
225	14126	A	230	86	405	VSYMSIQDHENGHVSGYFELVGQFCLRV GIVGGSTFESSNSHSYIYFFSFYLFIFF EMGLSVTQAGVQWHKHGLLQPQPPG\LT *SSHLSFPRSWDHRPVSPWPA
226	14127	A	231	386	98	FFPQRR*FPFGNFPPFFPPPKLG\PSQK SPIGDFPPPPFFNPGPGPPFFFPPPFGK GFSFPPPL*FGPPQGFF*RAPPFFFFFF FFFFFFFFIRLLV
227	14128	A	232	2	362	TYVLFVIPYVETDLVQ*AG*SYSMDYSN LTRLQTLNLNVPFNIAALATLRLLYLHE TGSNNPIRITCHSDEVTFHPYYTIKDAL G*L\LFLLSLMTLTLFSPDLLRDPDNYT LANPLNTPG
228	14129	A	233	5	365	KNVTPPVNSSQHDLTDIYRNLYLMATEY TFFSN/AHGTYTKIDHNLSHKRNLNKF* RLKF*RLKLNSKGVLWPKWNQTTNQ*QK DNRKLSKHLKTKNTLLNNP*IKEEVSWE ILKMYLREG
229	14130	A	234	3	367	NRIVPNHDIPYFSLCVCVLFFFDRVS\T LSL*GWSAGAGSLLTAAPTSCVQAILCL *SLLSTWNYRRNPLR*PAYL/SYFKSSKSF* TL/LPKGIL
230	14131	A	235	107	2	QEAYE*DKERSSRIYMELK/SIQPKPPN NRVKKWTKEINR/HFSKEDTQTDKRHMK KC*SLICISLVISD*QRNAN*TPNEIRL IP
231	14132	A	236	349	0	NNL*IFLIFLFTSVFLSLISYLFYYIFI RSLPICGLFTYFFSFSYIFLKYLMTLAI YYSF*\FFSLIQVILFALIFI
232	14133	A	237	3	317	TRMHISDKKTYNTNIKRIFRIHLMRQTT QLKIGKRYEQTLYKSIFEWTINTYKEVK QLNSKRKPTNTVIKK*SKDLYKHFSEED IQITTRY\LKKC*ASLIIKEM
233	14134	A	238	346	1	AAAQMPAYQELVEEAIAYGRKLGGSQED QTMNANDQRFVMSAADILS*IPDVVSTE VHARLSFDKYAMSARA\RRLIELSKEYG LSKGRIVI\KLSSTWEGLQAAKELDEQR GIGC
234	14135	A	239	1	279	LLLPPLPSLLLPPSPSSCLPPSPSS/SP PSP/S/PPPSLLHPPPPSLLLPHLPSLL DPPPTSHLLPSIP*LDIPNAPT\NSSNP SCPCRPRSTEYFK
235	14136	A	240	98	2	RPRRPRLVLNS*\LKLSAHISLPKCWDY RREPP
236	14137	A	241	342	1	DTASLLQPMDQGAISTFNVYYL/RNIFH EAIAAIDSDSPDGTGHSKLKTF*KGFTI LDAIKNICDSW/EEGVKISTLTGVWKKL ILTLMDDFEGFKTIVGGVTADVVETARE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						LEL
237	14138	A	242	3	339	RKDSRKRERKNKEKRKGRKEGRKKPIRM TVHFSSKTMVAK/ARRQ*NPVFRMLEE* KN\FPPRILYSEIIFFGSESQIKKFSGD GNPKGSFPELFFLRIPMEVFNLKEAYLR KS
238	14139	A	243	216	3	NSTGTQTQSQKFMLSLVKKLISFIYL*D GVLLFAQDGVKWRDLGSLQPPPP/GPTL FKQFSCLSLPSS*GSRI
239	14140	A	244	408	2	VLTS*SNIAST\WYGLYQ/TQLR/KILA YSSI/THIG/WNNPVLQYNHNITILNLT IYIILTLNA/FLVLNFNSSIGTILLSRT *NEIT*LPSLIPSTLLSLGGLPPLTGFL PKWAIIEEFTKINSLIIPTIIATITLLN LY
240	14141	A	245	3	243	IIMLKAGQMTVFPNEDVWMAYKHTDRYS TSLVMNEM\QIKTTMGYHYAPITVAKLL N/SNTRYWP*RG/CSRVIHCWRKCR
241	14142	A	246	2	337	FLIMDLQKYINPKIKEPQGETNHKTVSF MNINAKILNKILVIQI**FPKKNNVSKF G/FIP*/SQGCFNINQCYSLDERRKYMI ISKNIEKAFNKIQHSSFMIKTKNRKKLP EL
242	14143	A	247	347	1	HYTPIRMTKIQNTDNIKCW*GCGNP/GT LLHCW*ECKMVQAL/WL*TVWQLFTKLN LLLPYNPITFFGIYPNEGRTHVHTKTCT LIFIIAALFIIARTQKQ/PRCSSVDEWI NKLWYIQ
243	14144	A	248	319	2	KKIILFIICTERVFLCCPGWSQTPRLKQ SSSLGLPKC*DYRRESS\PGLNVIL*CL KFHLRVAMLFYVFEV*\IVIFFFLRQSL /DSVTRAGVQWYNLSSLQLPPPGFK
244	14145	A	249	329	3	KFPFFHTGEAKNYAVFVINKRIKKKQHI HIIYNYGGHQKAECKEIEAHVHCWWEYK MMQ/SL*KTAW*FLKK*TMELPYDPVIL LLRIYSKELKAGTRTDVCTSMCSFLFL
245	14146	A	250	316	3	KTHKTIMGTNHIPNEKIDST*LKNLNIR AITIKLL\KNNRVSLHDLRIGHGLLDMT PRAQAAKKKIKR*IDEFIETKNFCASKD NIKRV/NRQHKE*DTMFANHIS
246	14147	A	251	152	364	QLTLSNHINNQIKYK*TRHS\NHHHHHH HHHHHHHHQ*KRLPE*SYKSKSQEHYTY GMDITGPKNLRTIPL
247	14148	A	252	230	1	PCWICEFIVSSNFCWFVLETGSCYVAHA RVQWCDNRSL*PQTPGLKRYSCLSFRSG WD*RH/VPIANF*TLPRGGVL
248	14149	A	253	3	345	DVGLAGLELLTSGDPPALASQIAGITGV SHHSWPLLFFFFFFF/CFFEGGFFFFLP V*SQGGDLGSREPWPYGFKGISRLRFPN EGKIGPQPLAPDMFCFFDKTWLSTVVPG WFH
249	14150	A	254	194	1	GRVDTKWANTHERFSKCS/TTVD*WIFK SWYLCTMEYYSTINKKEILSFVTTWMHL EDIMLSEVS
250	14151	A	255	327	3	VKTAEFVNKWQKNSTKLWNSQAQIDKKK IVNQINDLRQTEIWMGDRIMNLESRIQM QCDWNTSDFCVTPQ\YNETEH*WKKVKR HLEGREENLTL*IVKLKEQDFEASQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
251	14152	A	256	314	3	KNFPSLINFLRQSFAFNGQGGVQRVDLG SPQPLDSRVSDRIRLCFKTQKKKRFSP* QTILKLSKV/E/MTERVLKTAREKHLVT YK/GKPIRLTMDFSAETLQARRE
252	14153	A	257	2	308	RWWWW\EEEEEEVDCGGEV*FFFFCFFF FFFCFYVFFFYLFFFCFFFFIFFYFLFF LFLFIFFFFFFVFFIFFFFFDCFFFFFF FFFFFFFFFFFFFFFFVFF
253	14154	A	258	52	186	CFGKLGWDDCLRSGVQGCSET*ACHCTP AWAT\NETLSLKKRRRG
254	14155	A	259	1	269	LKRSSHLSLPRSWNYRCMPPCPANF*TF FVETGSHHIAQAHLKL\PPASA/FPKCW DYRHESLCPALDSPFTNINSATIITILQ GKCWHYC
255	14156	A	260	387	3	PLLQVAKINPKRILDLNVKPKTIKCLQE NTGENCWDFGSGKDFLDMTPKMQSTK*Q ISKLIKIYNFSSKTQ/SFCTTDHENFLE DIVKRIKIQSHKLEKRFVNHIPDKRLIS RIYQELFRTQHEKPHTIK
256	14157	A	261	62	72	LRIIKFSEESMLKAEMG*KLGLFHQAVN KCNSLTVNEVVNAKKRFLKKMKSATPVK THMIRK\DMEKVLEVWIDQISHNISLSQ SLIQRKVLILFSSMKPARGEEAV**KNY
257	14158	A	262	2	193	GGRGCSELRSCHCIPAWVTRAKLSLKKK KKKNSKF/RELGNKGQFMGP*LRKGFTC YKKRSPLIF
258	14159	A	263	3	330	QLKKKYYEELYANKLGNPDEMDKFLEIC ILQKLTQHKN*KFFKDSRRKSKMNRPIT NRLIQ*PKELPKRKTLRPDGFTGELYHK HFFFKLTKPLHKFF/AKIKEEEPFPNS
259	14160	A	264	326	43	TQETEAGESL\DPGGRGCN*LGSCPCTP AWATGMKLPFKKKKKKITSLPELRFLSY TCSSSQNFLYLNDDTIIHPVAQAKNLGD LDSSPTDPIQ
260	14161	A	265	311	1	FPPFP/SFPLERKEKFKGRKKRGGTKRG PFPPFFPFSSLPLGFP/SPQRA*FLLFR FREFLKFFFPFYLPPKPGLGKFFFFFFF FWDGVSLCRPGWSAVARSRLTV
261	14162	A	266	5	323	DSTKAQKNTVVSIEPGEVGTLIHC/WVQ PL*KTVWWFLK/DVK/LELRYDPAIAHL GI/YPKKNKT*TCTQVNITALFIMTKM* K*PKD/PINNEWVT/KLWYMHTMEY*ST IN
262	14163	A	267	3	293	GSLQPLAPRFK*FSCLSLL/SAGEWHEP WRRSLQRSCHCTPSSLGYRAGLHLKKNN NNNNKSEVSRICTIGIFLLFIY/CIYET ESHSVT*AGVHWLDF
263	14164	A	268	3	332	HLSIINLNVNQLNSPLKAYTLPVWI*KK KWPNY\CCLQEIHFASKNTYKLKVKELK KKFQANEKEKHADKTGFKSKTVK\KKNG HYIMIKRSVQKENIYIYMFLIADPDIC
264	14165	A	269	3	326	KVLERHDVLKLTQ/DKICNLNM/PYTKE MESIVNNLPKKKTPGLHSFTGEFYQTFK NEMILTSYNFSQKFEAEEILNSFYEASI LL\IPKLDKDIIRKEN*R/PNAKILNKI L
265	14166	A	270	1	318	PYPAKLSSLSKGEIGTF\LDKQMLKEFV TTRPALQEILKGALNVLI*/LERKDHYQ

SEQ ID NO: of *nucleotide* sequence	SEQ ID NO: of *peptide* sequence	Method	SEQ ID NO: in *USSN* 09/515,126	Predicted beginning *nucleotide* location corresponding to first amino acid residue of peptide sequence	Predicted end *nucleotide* location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, *E=Glutamic Acid, F=Phenylalanine,* G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						QMQKH
266	14167	A	271	1	318	LKLLTSGNLPASASQTAGITGINHRAQP HLSFSL*LWNET/CVPG
267	14168	A	272	108	322	DSHVIFLLCGNLTVFVCLFLRWGL/DSI THPGVQWHHHNSL*P*TPGLK*SYHLSL SSIWNYRRTPLRLAFFL
268	14169	A	273	341	3	GFFFPFPFFRQGFPLLAQVK/VPWGNFR SLQPLPPGVKQFSCLNLPKN/WGFSLKG FFKKGCHFPF*Y*IFFNGVKKPDIKFSI FTNPFFFFFETESCSVVQAGVQ*HDLGS TRP
269	14170	A	274	41	328	FWLLTPGQETERERESETERESEREREA GEAERGRETDGIDSLIYSKLYSKTIHLK *ILEYI\ATYFKRLFYNWEL*T*AK/TRI* IEKPSVRHQCQQRS
270	14171	A	275	3	322	EAQELL\DPGSGGCSELRSHHCTSAWAT KAKLRFKKKKKKKCPGRYLGNIVLQ*FN IIAKCDKYHIVKLIF/CFSSAYTASIQK LIQVSRTVTHRKNKKTRQYVYILD
271	14172	A	276	175	313	STLISYFRDRVLLCYPGWSAVGQSQFTA A*NFW\VK*SSSLSS\PSSW
272	14173	A	277	254	3	RPRRQFGIEGSFLNQIKNIYKKSTANVI LYVDRLNAFSLISGTRQGCPLSRLPFNI VL*LPVNIIRQ/EKVI*GMQIVKEELNL SL
273	14174	A	278	186	1	PETMQARRQ*SEIFKVLKEKN/LQHRIL YPEKLSFQSEREIKTF\QRLKKFITSRP ALQRMLKE
274	14175	A	279	288	3	GRLRGKKGFNPEGENSKEFFKPLPSGLG AKTQPVFKKKKKKKKTRNPIKK/WAKDP NRYLTKEAI*MASRHMKRCSTSCVIREL *IKTTMRYDYVLI
275	14176	A	280	3	329	LKESSRLSLLCSWDHRFALPPMLSGLVW NSCPQ/CDPSASASLSIGITGMSHHTWL *WLF/C*ETGSHPVTQAGMQWYDPSPLH PTKKGVYLT/RRFWRLGSPSAW
276	14177	A	281	233	3	*IITKDKEEHFIMIKRSIHQQGITITNIC* VPYNRGSK*MK*KLTKLMGENR*/HSII IAGDFNTTFSIMDRAIRKSAKNG
277	14178	A	282	32	309	LPDITPRDHLSPGTMDFIQETGCSKCWR GCGTPVCC*WECKL/VIVQSLSRTVWRF LKKLKIGQVRWLMPVISALWDVEVGGSP EARSSRPAWP
278	14179	A	283	1	302	CKRNNKAWMTVHLFTAWLSEYFTPTVET YCS*KTIPFTIL/LLDDNAPGQPGVLVE MHKDMNVAFRPANTASILQPMNQGGIST FNSYYLRNTFPKAIVAIE
279	14180	A	284	155	1	PRRFFFFFF*DRVLLCHPG*STAT*SCL TTKSASQV\RQFSCLEPPSSWDY
280	14181	A	285	131	15	DRSNPGRFLWTSNSSLYERPREIRPSSQ APPPVNDPI*T
281	14182	A	286	1	359	FFFFFFSVVFWCFSFFFFKKKGGAPGGG GPPPPKKTPLFSPQKKNFFLQKKPPGKG FKGPGLPPPNFGPG/RNGGPLKPGDPHP PDFTPPRWLFKPPF*KRGEPFFPPPGFP KNLFLKKVP
282	14183	A	287	52	419	LEERAGTSWPKKENKKQHFCMKKKKKKK KKKKKKKKKKKKKFFKKGAQIFSF*GGV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						NL/H/SGPGPVLKTGGGGRHSPPPPPSP PSSLFFPSSSLPSLPFLSLPLPSFLPSS PPLLSS/CPPPLFSS
283	14184	A	288	236	325	LNIRTPGSWLXAVAHACNPSTLGGRGRR IT
284	14185	A	289	218	409	KVKGNKADLIRSANGS*N/VKGVLCHQY LEKSFCLETEFHSCLPQLVHWPDLGLLQ PMPPGIARF
285	14186	A	290	3	426	HEETGSPRLECSGMITAHCSLDLPKLK* SSHLSLGS/RHVPPCLAHFLY
286	14187	A	291	382	1	ANFYVTLVQ\QGFTMLRSWRPA*PCDPP TWASQSAGITGVSHHAWPKMSTITLGVY SFGESEVFSIFKFYFLETGSSFLPQAGA **CNHSSLYP*TPGLKQSFHLSLLSTSV YRYLPPCPLCPVLV
287	14188	A	292	3	309	HEVPYFTLNQQLEMIKLSKGGLVKAKMG \ISQIVNAKEKFLKEIKSVIPVNTRMIK QNSLIA\ETQEVSLVWIEDQTSHNIPLS *YLIQSKFLTLFNSPKADM
288	14189	A	293	2	415	ARDQYKKSTKK*AKDLYRHFKNEAI/HM ASNYK/KRCSIS*VIRKIEIKSSMTSCY THLQN/ALKLKSDNFKC*QKCTAMGIIL SWWECNLVQSLWTW\QNLLMLNTHKPY* SAI/PTSGLYPTEMYRNIEQASLRMFWA WRGG
289	14190	A	294	335	108	IPTPK*PLSSPPIHTPYTTIPKP/RPPP P*HPPHIHPPPPPLTP\PLPTHTLPTPT PTNLPHIPPLYSIPPSSPKIS
290	14191	A	295	266	2	GFPKKVFSFPIGPPKLGFPNSVFS/LFT FFNPGLCLKFFQFFPFSAFLPLGFSFPF FFFFFFFF*DRAVLCHPGWSAVVRSWLT ATLV
291	14192	A	296	347	1	DSLQP*TRGLN*FFHLSFLTRWEYRCAP QCPANFC/VFL*RWGFAMLPKLVSSDLP ALASQSAGITGVSHCAWLVFLLFSLYFI HFSKASETPWAQNQSQTPSEYPATYNFK IYSC
292	14193	A	297	284	2	CRQGFVLCRLVSNSCDQVLCVRLCV*VL GLQACAT*LGAEGVSIEFSCFHKGRGCL CRHRSS/HSMFSAWC*PHTHTHTHTHTH THTPSPMQLV
293	14194	A	298	1	96	GTRLCLGAITTLFAAVCALTQKDLTKIV DFST*SQLGLILVTIGINQPHLSFLHIC THALFKAILSMCYITIIHILNNDQDSQT IRRLLNTMHINSTS\LTIDSLS*L/GKP FLN/GYY*QKDLTKIVDFST
294	14195	A	299	3	134	HEGRD*PGNHGDTLSLLKIQKLAGSGGV CL\KLRKLMCENHLNP
295	14196	A	300	2	333	GVGREGGSREGGEEESGWNGGIRERRSG KREEEGKEYRDEVDRKERGEEGGRERER GRGWEEEQKGAS*C/EEGRVK
296	14197	A	301	354	1	TENELLSRIYKNFYQIN/RYKQKNSIKK *RK*QAI/TTETIQTVNKHLKKCSISLI IRELQTKTR*ILYT*LVEKKLKTNGIYC WECCRELGSC
297	14198	A	302	1	282	GTRGMVAGAYNLGLPSSWDYR/*CLPPC LANFFVSLVERGFTRLTTLVLLS*LYDS PASRSETAGIPLIHTSCIVYWSLRNNAD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						IAILCKAQAV
298	14199	A	303	361	3	LPKWWDYRHEPLCLATFFFF*AFPPVPL CMYVPPN/RYVAFFFSLSSF*ICCTFTL YIFPQLMDG*AVSSFLFLQPVGVKFKKK FFLSFFK\KRRSLGMLPRLILNSWAQVI HPPWPRPRA
299	14200	A	304	2	352	ARMVSVS*PCDPPA*ASQSAEITGMSHH AQPIIIS*TIAYVSFSLSSLGT*ISSVR SFTKSMSQLLYFYYFVSL/PSFW
300	14201	A	305	334	1	KNSFFFFFKRSLGLLAQI*/VQWGDFKT LQPLPPGVKQISRLNLLKKWDY*RGPSG LGKFW/IFL*KQGFPQLFQVVLNFFFF/ CFFETESRSVAQAGVQWHDLCSLQAPPP SSC
301	14202	A	306	270	2	DWCAGGGGDGVPRRQVIFVILVETGFWR VGQAGFQLLASSYLPALA/FPKCLDFRH *PPHSALKALFFF*DGVSLLLPRLECNG ASSPRA
302	14203	A	307	306	2	HIFQCVCVCVCVCCVVCVCVVWCVCVCV KLVISQT*LSPLCSGP*A/CTFFSVCVC VCVCCVVCV\CVCVCVCVCKVSDLTNLS TLCSGP*A*HFFSVCVCSC
303	14204	A	308	117	332	SPPVLLRCSLSLSVQLNGKTIRFLK*LK MEL*FHSAIPLLGIYPKGKKFLYQKDT/ CHSIFITALFIIAK
304	14205	A	309	1	351	GTRKTNN*KWAKDLSRHFSKEDIRNGQ* V*/HMKRCSASLIIRIM*ISITV\RYNL TCIIM
305	14206	A	310	1	352	PSPPNSPPSPLPSRPPQPPPYPPPPPRP PRSPL*YTPPAPPYW/PSPILTPSP/PS DPPEPRSSRP
306	14207	A	311	1	405	FKPSP*PLTGALLGLLMTSGLAM*FHLH SIT\LLILC\LLTNT\LTIYQ*WRDVTR ERTYQGHHTPPDQKGLRYGIILFITSEV FFFAGYF*AFYHSSLAPTPQLGGHWPPT GMTPLNPLEVLLLNTSVILAS*VSI
307	14208	A	312	3	176	HEILGSNF/CGETQVSIHCPG*S*TREL KQSSHLNLPKCWHLRA*TTVPGLTTIFH LGKPKHKRVR
308	14209	A	313	298	327	SLTLSPRL*KIKK*RKK*NKCWQGCKEI GAFTHCWWGCKMVQPLWKS\W*LPKKVK *KLSYDPAIPLV
309	14210	A	314	344	3	HSTSLVIREM*IKTRMTYPFTTTKMAII *KNRS*\WLGCGKTGSLIHSW*KC*MVQ SLWNTFGQFFIKLI*ELTIPLLDLYLRE MKTYDHTKTCI*MFIVALFIIAQNVKMS LV
310	14211	A	315	18	321	WALFVYCLEKKEFGQPPRLACFFFWDRV SLCLPGWRAVMGSWVT/VRPKLLAFN*S SHLSLPSSWDYRLIPPCSAKDSICEKNR VSTVDGADKKVRRGKEGD
311	14212	A	316	289	52	ETSCDVPSKGILHFGKRNTHIMPEKWAK GMR*YFH\KEDK*MAHIHVKRC*TSLVI MKMQIKSSTPYHFIPPRLTKPLKSANTK CW*TCIWAIYLSSSMKILSHALCPFFWH DVCISLTEVKNAFTGHITRRFS
312	14213	A	317	57	324	YCVTFFFFGKQSFVLSPRLNCMGPFWVN CSLSLLSTWNYGLVPGTQPFF\EFLVQR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						GFHYVAQVGLKLLTSGDLLP*GSKGAGF TGLTHC
313	14214	A	318	65	341	QWLLKSRSCYFFFL*DRSWAVAQA*VQW R/NPPPPGFKQF/SCVSLLSSWDYRCLP PHLADFWIFSRDQPDQHSGTSSLLKKKK KREIPNLPGLG
314	14215	A	319	2	182	ARGDYRHMPPYT\H*LETGSCFVIQAGL ELLDSSHPPALTSQCWDCTCEPQSWSAP CVSI
315	14216	A	320	345	3	MPPRQAHF\VFFIEMGFHHVARAGLELL GSINPPTSASQSSWDHR*SQSAWITGVS HHAQLGTITSYHILLFLKKGRAHAC*SQ HDPTTCLHVNLCCSLLLAISRPPTTTNL PRA
316	14217	A	321	122	466	QSFSTYC*KNWVTI/CFLKSIDSYLVPY TKIDSKWIIDLNVKPKTIKLLGGNMGEN LCHLMLSKDSSDVTQKA*SIEKQINKFN SHGGTRLRSQPLKRAEVGRVRLSPGGRS YSDL
317	14218	A	322	3	345	HEDAVSAPCNLHLPGSSNCPASASRVAE MTVPA\PCPANFFFFFLEREFGFCCPG /CK*K*VFQKKPKGKKKGRIEGKKGVWG PKLKERERKKRKKERRKRGKERKEVRTE MNGG
318	14219	A	323	206	446	GNLHQCPYKWTHLAKYMCEKQDSIC*IL KECYQKPLLEKSHLIAQVENDEKPADW/ PLLRGEYVEWND
319	14220	A	324	62	327	VERLLRDLRENFCRNPDGSEAPWCFTLR PGMRAAFCYQIRRCTDDVRPQGEAQAWG LQSRAGSLEPEGRGEVSA*W/SARTRHR
320	14221	A	325	441	1	RKKK*ILQGL/EFRLEHVVASPHRDHRV WPRQEGKLFSEGKNKATRMTVLYPEE/S SKKLGSRS*GSE/CTSVFRITLSVGYVA YTGAPVSISERPSAAIYHRMNKW*HQHR RHLLGFSEQEPVQGVEPLQGSSQGPKEP QPSPSNPAPRA
321	14222	A	326	2	358	ARARTLRIMVNLNYAKSTLPVLCKGKNK VWVTAHLFTASFAEYFKPAVETYCLEKI FFKILQLIGDAPCHPRPLMDMHKEVNVF VPAKTSIQQPMD\ISPFKSYY*EITFQA GCCGSCL
322	14223	A	327	1	430	ARENMPGHLHRCIIEQDWRIHMLIPKLN TQMIKIV*YWYKDRYVDTE/YNNIESTE VNLYICGELIFSRSAKIIQWWGKRIVLN KWCWDD/WNL/SCKSM*MDSYLTLCT\K ITPWIINPTGRAKTMRLLP/EKTGVSFC DFG
323	14224	A	328	146	374	KCLMLTKPYNIMRLT*PYEIR*/CGDTF P*SYYA*TGTAVRTWGLTPVIPALWEAE AGGSRGQEMETILANTEKPRL
324	14225	A	329	2	322	ARASRTFIVRKTQCLASKDKLTLVRG*C SCDFQLKSMLIDYSENPRALK/NMLYKR NNKAWMTLGLFTAWSTE\KPTVETYCSQ *\KITLKIWL
325	14226	A	330	350	47	EMGFLHAGQAGLELLTSGDPPASAFQSA GTTGVSHRARPAN*KKKF/CLKT/RVFL CCPGWS*TPGLK*SSCFGLSSHWNYRHE PPRPAQFLLIDFYLRHYRES

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326	14227	A	331	753	458	FFFVE*GVL\HVAQAGLKLLTSRDLPTS AS*VAETTSTHHHA*LHLFNFEKYFCKE QILLCCPGWSRTPALKRYSHLCLPNSWD YRHEHCNEPEEISLI
327	14228	A	332	256	3	TLVLMQSCLSLLSSWDYRHKPP/*LSNI FNLPMGLSGHNPIINGGISVSLDRVVVL FLFC/LCFETGSHSVAQAGVQWHDHGSL HSC
328	14229	A	333	25	358	TPDLR*STCLSLPKCWDYKHVPPHPANI FI*QKLFFISDGQYANVLTWFEGGTFHT *A*RPNHHSYKLRKDQTIIFIYLFF/LR WSL/NSVAQAGVQ/WHNLGSLQSLPPEF K
329	14230	A	334	3	329	HEDVVSPFWPGWSQTPDLR*SACLGLPK CWDYRREPPHLALNAFLT*NIFNL*W/C LSGSNPIIRSICIRFLGKGG*LLFIFIF VWFLTQSLTHSVTQAAMQWHDLGSLQ
330	14231	A	335	26	330	SQLLGRPRQENHLNTGGEGCSL/CKIIL VCFWLGHLLPVWFRC/ILYLF/CVVSLG FNFCFSLVL/CWFLLCFFCAFMFCLFY* WFVICHFLFFFFLFYFFVMFLFF
331	14232	A	336	3	348	DEVFKS/YH*HPMLKC*GDYSLLFHGES DLDTTQILTHPSTTAMYFVHYCQSP*IL YGTIDT*PPVIHRNPIHIRTPYPCLQAS TAINLQLSHMNCNSKATPHSLGYHQTYP PLTV
332	14233	A	337	2	329	ARAARAARVTGIAWAYHLIGKGLEPFFF MALLFLR*GL/NSVTLARVHWYNHGSM* A*PPGLRCMSLCPA/NFLYFLVE/IGFA TLPRLQAICLGSSDLPTSTSGSAEITGV S
333	14234	A	338	60	354	NGKECKKLIYLSIYLSIYLSIYLSIYHL C*YL/SCLSI*LSN*LAVYYLSVCLSVS VCL\VASCL*ISIYLSIHLSFYSIDRIL AHHCVPPTCSLPHATH
334	14235	A	339	1	351	RDADVMLLQILVIFQALALGVQTEGMAG VTHHDRVLVNWVRFPQCL/HRV*SNGT\ P*VGTSASERPGLKQSSHPSLPSSWDYR CEPPCPVNF/CFFV
335	14236	A	340	190	358	FGSWLVFFF/CFLETDSRFAP*AEMQGP NFG*LNPPPPGLRGFFGLSLPGTGDYGP V
336	14237	A	341	306	119	LRWENHLSLGN*GCSEP*FRHCTPTWTT E*DSVSKQKQKQNNLELKKPGSS\CVVF LPETLFT
337	14238	A	342	1	122	GTRGCGEPRSRHCTLA\W*QSKTPSKKK KKKKKKKTGPFFF
338	14239	A	343	92	316	VCWDIPHRKSRTICILFYPLVIFLFETK ICSSFSF*KGCM/WLGAVAHACNPSTLG GQSGWIT*GHE/FKTSLA
339	14240	A	344	83	329	ATAPAPCYFLILCICMCVCVCMHTSVCT /CVILCMCMGLCHIL*TCVA/CTCLGMR FLLPAHIIICVKRFCLMCGSGNSGSLCL
340	14241	A	345	127	357	YGVLSRGRVLPCWPG*SRTSGF/SSPEA NSWPPCLANILYLVETGFCHVAQAGLEL LDSSHPPTSASQSAEITSMN/HRA
341	14242	A	346	312	1	LMNLNRSVGALLTRGVKCHKAFRSTISL LIGALK**QSKSDLGISLSKVVKDLNND

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						IYRSLLRQSEEDTS\KWKDIPCS*TGTP NIVKMSILTKAIYRFNASC
342	14243	A	347	350	243	FHHVGQDGLNLLTL*ST/PCLGLPKCWD YRCEPPRLAY
343	14244	A	348	165	338	HTLDPASHEGPTFLFSL/PVEQCLK*LT LKVATIVLFCFCF*DRVTLCHPGWSAVM QSQ
344	14245	A	349	328	2	SVCPHGSINLSPAETTGACH/RRLA*NI DSRV*AKTFKGK*TNCSYNNNNNNNNNN NNNKPFLLLRLAGDRHPDQLCPPPRRCH FNGATPAGPPSCLRRSHHSSAVCSC
345	14246	A	350	3	338	HEIEELITFHDRALIGNILICSLVLYAL FLTLTTKLTNTNILHAKEIDTVRTILPA IILILIA\LPSLRILYITDEGNDPSLTI KSIGHQWY*TYEYTDYGGLIFNSYILPP
346	14247	A	351	124	382	NTFKS*NSNKTKNAIRT*AKDTKQHFTG EDIQIANKHMKRCLIPLGKR\SLNQEIS PRVRINKIRPGMVAHTCNPNTLGGWGRQ IT
347	14248	A	352	3	368	RDRASLFCPGWS*HPELK*SSCLGLPKC WDYRR/AATAPGLLCL
348	14249	A	353	390	161	FSRDRISPRWSGWSP/DLRLSP/CLSLP KCWDYR/R*ATMPGTFFHFNLKNQDARN QIITCPNLTNKYIYMTSSFILVHS
349	14250	A	354	123	345	LAPQHFASLRLARP/PAGPPCDRPLAPP RPS*FSPAPLPPGADRSVPLSPSVPP*S LPPPAGAPPR/PPPPRDSPRR
350	14251	A	355	37	393	TKHFVSTCYVPEFIAGTNQRKRNRISVL ANVKDKQIILLRVRTAITEGYRNYHVLF LVFVCFFSPPKQGL/DSAFQAGVWWHNH NSL*P*TPGLKLSSHLDLQSSWDYRRVP /RMSSYF
351	14252	A	356	2	335	ARETSKDRLTLLLGANAGGDF\KLKPVL LYHSENPRPLKNYAWST/LPVL*KWNKA *MT\HVFTEWLAEYFKPTVQTYCLEN\K FSILLINNPLSHPRALMDRFKETIGVLM PA
352	14253	A	357	199	377	VGSSCFLKVCQ/C*AVCVCVCVCVCVCV CVCLRCV/CVCL/CV\CVGFFFLVLCG CGCVCVC
353	14254	A	358	1	335	GTRTTCMYHVPPRSANF*LVLERWGLPM LPRLVANSPPQTILLLQPPTVLPNPERT SALY/YRPLLDLSPTSLSPRIPSSPLTS SLSIPAPPRSHLAPPPPRPPPHPPIRPS A
354	14255	A	359	3	369	KPSP*PLTGALSALLMTSGLA\M*FGFH SITLLILGLLTNTLTIYQ*WRDVTREST YQGHHTPPVQKGLRYGIILFITSEVFFF AGFF*AFYHSSLAPTPQL*GHLPLIVII LLNSL*FPTLY
355	14256	A	361	337	121	LWSQLLGRLRQEDCLSPRSQGQNKP*CH CTPAWVTE*DSVSKKGKVVYIHNKKSSL KKK\NSCNMQQFGGT
356	14257	A	362	256	375	EKKTIVQYPHTYGINV*KNLPAKKTPGP DGFIDKLYNTFRGEITTSPHILFH*FKE VAVLLNSFSK\AASITLTPKPNKDIMRK ENYSPISSYIWNQCSFFLEQIFPLSFKL NCPGLIIPH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
357	14258	A	363	170	1	SQLLRRLRSQGACHHAWLIFVFSVDTGS HHIGQAGLKLLS*AIHPPCPPKILARA
358	14259	A	364	330	3	RIMSASASQSAVISDMSHDVRLIDI*HE P*FYQALYSFRQ*ITSSPSYR*SYLLSY KWQDEARC/AFVTAWQAEAGGMLEPSRL VLDS*PRDLPTSASQSAGITDMSHHSC
359	14260	A	365	1	341	SQYGLDFHDLSDLPTMASQSAGISGVSH RAWPASG*FYVSREVICSYRL*GYTPSL LVLESGSSSVTQAGAQWHNHSILYPHTH GLK*SSCLSITTR/WDYRHESP
360	14261	A	366	2	338	ARMVSIS*PRDLPTMASQSAGITGVSHR AWPATGKFYVSRGVICFII*KDTHLFF/ CFLETGSSSVTQAGAQWHNHSLL*PQTP GLK*SSCLSIPKC/WDYRHESP
361	14262	A	367	2	337	ARAGILKH*QRKCKSIR\PLWNNVGYYI LKLNIGITHDPAIPFLVLYPSEMHTHAY *KTSMRMCITTLFIMAIN*KFKCS*SEE E/IGKFWYFT**LLYSNENEHLQLHTTW IN
362	14263	A	368	59	348	SAFGIQENEMPAGRGGSHL*SQHFGRPR RVDHLRSGVPD*LGDR/GETPSKKKKKK
363	14264	A	369	350	3	GWSQIPDLRWSTHLSLPKC*DYRRGPHA QL*TLMYKYLFEHLLSVLLGICPEVEWC /DHMAILCLISLGTVILSSKALHHYTFS PVTCKCSNFSISLSTLVTFHCFLNACYF PLFSRA
364	14265	A	370	908	30	ECSGTILAHCKLPLPGSCHSPASAS*VA GTTGVCHRARLIFLYFLVETGFHRGLNL LTS*ST/SASASQSAEITSVGHHAQL/C LELELK*STCLNLPKCWDYPA*ATVPSQ FGSVFLRIF*PMFISNIGQLFSCSAFVW P*HQGNAGLIE*VRKYFLLFKFLKEFA\ RTGINFR*MSGRTDW*NHPVRGISLLKG F*LVI*CSY*L*VYPYFLLF*EVSLLSP RLECNGVHSESAGITGGSHHAQLVYPYF FFVCDSVLVGFVFLEICHFIWLFNLLVY LCLWYYLIITLIAVKSQ
365	14266	A	371	164	1	SCRQVESYGIKRITCISLASSWNYRHAP PRPANF*FPAEMG\FLHVDQASLDSC
366	14267	A	372	3	383	MVSTPAEDAVNIVDMTTN/D*EYSLNLV DKAVAGLERIDSNFEISSTVGKMLPNSI ICYKEIFHERKNQLMQQKSLLPYFNKLP QSIQHSAITTLISRQLSTIWQS/PPPTK /RFQLTEGSDD
367	14268	A	373	1	349	TLLGNDHIYNVIVTAHAFVVIFWIVIPI IIGGSGN*LIPLIIGAPVMAFARINKLR LRLLPTS\ILLL\LAYAILEAGARTG*T V*PALTRNY*NPEAYGHLSMFSLHLTGV SSISR
368	14269	A	374	443	2	SSGSRSECRFLPLLFNVVLEILAGAIRQ /EKE/IKGIHIGKVKVSIKLTEVINKFI KVA*YKIN\QKSVVCLYTNNEQLEKKFK IPFKIASKRIKYLEINH*GKDLYNENLK TLLKEMKENKWINIPCSWIRRLNNVNIS ILSKVTYKF
369	14270	A	375	3	201	LWIKKLDIIPIIPS*LFFNTELDKLILK LIWKFRGPR/ITQNSFEKPIVGGLILSD FKTYYKATVLK

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370	14271	A	376	11	324	DKFLEHPPLLVLQAVAGKGSPLHCLSTL PTSLFI*DRVLLCSPAWSAVAQTWFTAT ASWAQ*SSNHSPSD*R/PHTTTGHFFCR DKVL/TMLPRLVSNSWTQAI
371	14272	A	377	85	364	YQHNYSFCFISQYVYRLFFFF*TFFKKK GFWF*RLNFQGGNMG/SMEP*PP*IRQF FCLNPLN/SPDYRGPPRGANF*IFLKKK GFQVFPSLSKIP
372	14273	A	378	1	382	GTSGTSYSTIFAGTLITALSSH*FFT*V GLEINMLAFIPVLHQKYT\P*YTHAAIM HFLTDSGA/SVLLIEILLLYSNSLGE*S SIIELQLISIFLSMMLVIPNKFGAAYYS IHALCLDRPQLLHILLI
373	14274	A	379	24	323	IPGLKRSSRLGLLKCWDYR*DNFQHMCL KNFNNWAAYYFVCKICCAVDPHGCSIKV SFFLSF/CFFFTKSRTVPQAEVQGGDLG *LEPLPPGLMPFSGLSL
374	14275	A	380	2	317	AGWFQTPDLR*SPCLSLPKC*DFRG*PP CQKLFLCPIKIF*TRLK/CYLNTL*QSL PLMHFKKNVIYFILYKAALFFFFLRRSL /HSVAQAGVQWHDLG/S/LQTPSPGFK
375	14276	A	381	1	323	VKRQPTEWEKIFA/TLYPSGKGLITRIY KGLKQLEGKN/KSNNLILKWAKEDIQTA NRYMKRCSTSLIIREI\MQIKTTTRYHL TPVKMAFIKR*/GNNEC**GYSEKRTLI
376	14277	A	382	2	248	TQPLILRCLPPRSIYRFNSIPIKIQVNF F*EKEKSLLKFIQNLKGP*ITKTILRK KKVDGKTFPDFTMYYKATVIKTVSWYQ
377	14278	A	383	178	1	HNPPLAISFCFFPFFFFLRQGL/NSFAQ AIVKWYDHDLLQP*PLGLKRFSHLSLLS *SWDH*
378	14279	A	384	312	26	FLRGVFFFFFLRRSL/DSVAQAGVQWPS FGSLQAPPPGFMPFSCFSLL/SFFFFFL VE/MGFTMLARKVSIS*PFGPPASASMP VEITGMSHCLANMFF
379	14280	A	385	1	849	FFFFKQTKFIKLSKYKNIIKKS/SAFLY ISNYLKMKFKKIPST*L*FEVNLTKKLK HLTFYSKEHYTN*VTHKWNNITHS*TGI FNS*IFVLHKMICRYNATSIKIPVTYFI *DIF/EKAYLKFIWYHKTP*IAKAIKTKE* GI/LPDFEIHYKTVVTKTVWHLNKNRDI GQWSRRKREQKYISVFTAN*F*IQVTFF FKGNNSIFNK*CLENFMSTCR\KKK*DP HLTPYVKINSK*ISHLNVRPKTLKLL\H QKIE*KPHNIGLGSKFFDLT*ISQDTKG RTSQSDHF
380	14281	A	386	3	318	LREMQNALESLSNRTEQVEETTSELKDK AFE*TQLNKDK\KKRI*KNE*RLQEVWD CVK*PDLRIIGVPEEEGKSKYLENMFEE IIEQNFPGLARDLDIQIQVAQR
381	14282	A	387	1	382	FTPTRTAVVKK/SNDWCWRGCGSIGTLR HCSWECKMAQLLW*TV/WTFPRKIRQPS DVCCDMVIGLPYDPAVLLLGICPREMKT YVHTADMSVITSVSLVII\ADSENNLNV PSADEWINEMWYIHTVDY
382	14283	A	388	1	341	HKLENLENIVKFL*TH/TLPRLNQEKIQ TLNRSITSSKIKSLIKNTPTRKEKKK\N PGPKGFPREFFPRA\KKQGVPTLGNPFQ

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						KFRERGSLLNYFYKPGLFRIPKLGKNPR GKKK
383	14284	A	389	168	1	KKFFFFSFFF*GDRVLLCHPGWNAVMQT RLTAAS\TPGLKQSSHFTLPSTAGYTG
384	14285	A	390	337	1	TGITPLNPLEV\PLINTSVLLASGVSIT *AHHSVIESIGNLIIQALLITILLGLYF TLVQASE*FESPFTISDGIYGST*LVAT GFHGLRVIIGSTFLTICSIRQLIFHFT
385	14286	A	391	1	235	LNFSYESSMYFALFTIVF\WVFLNF*KF FMN*IYHLCYVL*YFLLV\FVCLLTWFM VFCFFFFFFFFFFFFFFFCFFFS
386	14287	A	392	1	258	SCDRLFANHLSNKELVSRKYIYIF*KSQ DSTIRKQTDKK*AQELNRRFSTKDLQMG NKHMKRCSTPLAI/REMQIKTMLRYHCI PIG
387	14288	A	393	2	317	LAYCNLCLPGSSDPPTSSSRVAGNYRG\ HHDSVF*RAEDINMHEIQFISFLFLNRD EVSLCCTGWS*TPGLKRASCLDLPKCWN YRHEPLCLAFFFNGSWFQCQI
388	14289	A	394	91	408	LGAEFDVRAYLTSGRLTGPGVPFLTGFY SKDHII\ETANISYTNA*ALSITLIATS LTSAYSTRIILLTLTGQPRFPTLTNINE DNPTLLNPIKRLAAGSLFAGFL
389	14290	A	395	3	165	RNKKLKNNRHWRGC*EKGTLIHCCWWCK LVQPLWKAVW*VLR*/LKTELPFDPAIP
390	14291	A	396	661	1	LCPLSSFYRKCALLGFWFVCLFVFQIRV SLCCPRWLQTPGLKGSSHLSLPISWDYR HLPPRLAIGAVFLIFVLMRTCLR*FADP ISLSFE*QQRN*LHILISLL*MVDICLT QFTKWIFL*PKNS**LKRQCKLPKITEL /PKNRIQIYPTD*MSSIPHSLSFYLVCL FVCLF*MESCFVT/TMAAVQWHDLGS\L QPLPPGFKRFSCLSLLRSWDYRRPSPC
391	14292	A	397	320	1	PDSKQQIFNVDETVFC/WKKMPSRTFLA REEKSMPGLKASKDRLILLVQANPAGGF KLKPVLTYH/SENPRAIKNYAKS\TVL* KWNSKVWMTGHLFTALNVLSPRRAL
392	14293	A	398	1	158	CIGPMWENRLILGGRGCSEL*SCHCTPA WAT\SKTLSQKEKKK*NMRKVMIQC
393	14294	A	399	264	1	LINEFSQVAGYKINKQKSLVFLYTKY\Y SKLSEK*IKKAIPFTIPAKKKEIKYLGI NLTKDVKDLYNENYKILKKIEDT\KKWA DTPC
394	14295	A	400	3	343	HEQKRQSKVREVRELSQGLNMDRKRWSQ DLNPGCRTVALSPYHHTRLALNCPGRQW FVGVNFF*RKKIFFFFKFWDRVLLCHLG WSAVVPSWLTAALISW\VK*SFRLGLLS SW
395	14296	A	401	1	345	GTRKNTDNTKCR*VCEETGYFIHCWWGY KMVYPLGKLVWHFLKKVSIHLPYGTSAL LSLMIEKLTFT/CHTKTCTQM/FHVVLF PIVKKWKQPKCLPVGELLNKLWYISIHT IYSAI
396	14297	A	402	102	355	DRVIRLANFCIFGRDRVSPCCPSWARTP GLKRSTSLSLPKCWDHT*ATAPG/LRAI LLYFWDYRCLSPDLVNFACEHFSVELVA FF
397	14298	A	403	156	3	NNKNGFP*SMLFQPSNGLVSI*NI\PLK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						*QKWFSFFFEERVSLFHPGWSAVV*SWL TACSLDLPAQVILPPLSLPNSSC
398	14299	A	404	1	364	GTRSEVIYKLLLQTPWVI*HMRTRLLLQ ACGAR*MWMIL\MIILGLVTCRLTIYQ* WRDVTRESTYQGHHTPPVQKGLRYGIML /FITS*VVFLSCVI\WVFF
399	14300	A	405	3	365	HEQTSHNIPLSQSPI*SKILMLLNSMKA ERGEEAAEEKLEASRGWFMRFKKRSHVH S\KVQGEAANADVEATASYPEDLVRTID EDGDTNKQIF\NVNKTAFCWKNMPSRTS TAREEKQCLP
400	14301	A	406	3	356	HERSDQLYAN/KLDNLDKRSKFL\EGYK LQKLTQKEIQNTNRPTTRI/EISKKKKK KKKKKKKNFSPGGFTGEIPPTFKGQFKK IFKKFFKNLGGEKTLPI*IYGAG/IKLL PKIKK/DPSKKK
401	14302	A	407	116	362	YKYSLTPQKLYNHSYIKKNHNKQNNRNH STTTTTKQPPPPGFKRYSCLSFPLS*DY RCTPSCPVNLF/CVFLVETGFHHVG
402	14303	A	408	3	360	HEVRLWDFAFERNEGGGENEEKVDWLNY RMWFHLIF*AECYSICRLHAYYSCILGP VLLLLFVLIILLFCCL/SFFDYF/VFMF FIFFYSFFFLLFSLFFSLFL/CFIFLYF FIF/CFFLYFFFF
403	14304	A	409	388	1	ALLKFPFPKVLKKPP*GSFFP*GF*LLS /LIFPPYFGRETLFFFF*NKVPLCPPDW SSMARSRVPAGSVFPVK\ESLSLSLLSV PPQVQVNGFLTFFFFFFSW*RQGLPLLP RMVWNSWAQAILPLWPHAS
404	14305	A	410	1	386	VFNAEESAY/YWEIMPQRKFIR/EEKQA P*FRQERIS*YCANAVVFTIRTTHICKP ANPQALKKKKKKKHQLTVFWLYTKKS*T MRTLFLDWFCQCFVPKVRKYLASKTLPL KVLLILDNAPGHLKPHIFN
405	14306	A	411	2	417	AHHIFTARIDVDALAYFTYVTIIIDIPT GDEPFS*LATLR*INMK*SGAVL*ALRL IFLFTVRGLTGIALPDL*LDIVLHDTYY VGAHFHYGLSVGAVFAILGGFID*WPLF \SCYTLDRPYAKIHFTIIFIG/VDLAFF P
406	14307	A	412	295	397	WQWPGTVAHACNPRTLGS*GGRV/TLRS GVRDQP
407	14308	A	413	437	3	PGFGSLIGNLIPASGNGRKSKSCVCVCV CVSVCFKSCT*SLCEHLFTCLCPQICVR LQLMV/CPQNCVCWCPESGLFLDESVCV RLCVCAWMAVWMGGSGSG*VCGCGC\MC ICVGPLLDSELCLCVC/LLGQSKCDCGL RCRLPAWCV
408	14309	A	414	2	392	HLQFIFFWILKIFHYL/FLWFWFYLTSM ALFYLQ*QKRNCMYEVFNRGLFF/SCGE GVSGSPASSSSSPSCSSSTRGGGAVGGG GLGFVCFLLLFWGFWFVFLFCWFLVCVG WVWCVWWVFFLLGV/CCWCFFF
409	14310	A	415	376	1	GFQASKDRL/LLLG/ATAAGDLKLKPML IYNSKNPRVLKNFAKCTLPVLYRLYR*K NYAWMTAHLLKSWFTEDVKSTIQ*KISF EMLLIINNVPGHPRTPMEMYKELNFF\M PANTSIP*PMDQGIVL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
410	14311	A	416	409	2	FFPIKKKKFAGALVFFFFFRKIFFFFPK GEGKRGVLVSLNLLPLC*KDFFSPPPPG EGVLWPPPPGPIFFFFFLKKGFCLFCQG GFYNPSLYLIPLSPFKIWG*TRGFT/LP PPALFFYFFFF*DRVSLCHPGWNA
411	14312	A	417	425	3	RELLAFWQNFKLRPQGPFFSP\GPGGEK KR*SLPKTPPKGGPPGP/SPNGRLPSGG QLPPPRGG/SPQGPPPLPKGPQGWGPPF P*RSPPCPPHRIGVPQVSSSPTPGLVFP RGPLNPGNLGGTKKKKKISSKAARDLEL VRTRG
412	14313	A	418	1	346	LLPDRNLNTTFFD\PAGGGDLILYRHLF *IFGHPEGYMLMLPGFGIILHIVTYYSG KKEPFGYIGMV*AMISIGFLGFIV*AHH IFTV*IDVYTRAYFTSATIIAIPTGVK VFS
413	14314	A	419	2	382	LFSTNHTDIGTLYLLFGA*AGVLGAALS LLIRAELGQPGNLLGNDHIYNVIGTAHA FVINFFIVIPIII\GGSGN*LLPLIIGA PDMAIARINNISFRLLPPSLLLLLASAI VEV*SRTG*IIYSSL
414	14315	A	420	261	378	KKNFFFF*KLNFF*KFFLIFPPPKKKIF FKKKKKFFFYKIFF/I*KNIFFSPQKNI *PFLFFFI*YPFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFTLN SLYFSGRVGGRV
415	14316	A	421	124	428	KPAATHACATIFMCLDQEAIISN*H*AT TQTTEVSL\SFKLDYFSIIFIPVALFVT WSIIEFSL*YINSDPNINQFFKYLLIFL ITILILVTANNLFQLFIG
416	14317	A	422	8	355	PVFSYNHSTLLTFSLSLSFFFFFFAPGK KGEKNGKPGPFRGGFFPKKIKKPFPPP/ GGPKKPPGPGFPQKPHFPFKGGPWPSKT LFGRGGKPNFGGPQKPPLV*NPPSQGP/ HGPSGGG
417	14318	A	423	356	3	KPLGIDLTKKVKKLSKKNYKTLMKKIED DSN*KDNSCL*IR/MTILPKAIYRFNTI SVNIPMRFLPDAWADAW
418	14319	A	424	2	338	PSVRLGGHWPRSGITPLNPVE/VGLLNT IRLLASGVSITGAHHRLIECNRHQIIQA LLITILLGLY\LTLLQAS*YFQAPFTIS DGIYG*TFFGSTGFQGLHVIIGSTFLTI CF
419	14320	A	425	55	342	GPFTPWSLC*GDLQR*P/RAVKFFLKKK KKKKKGNPIRN*RDISS*FLKNLETAVR NFWTFFSYFKSKKLIQKSDHPLKNVKKI LQNDKRYLKLDWG
420	14321	A	426	2	367	DRRRFCTYHKDIGALYLLLGA*AGVVCT AVSLLIRAELGQPGN\LLGNDHVYNVIV SAHAFVIMFF\MEYPIINGGFGN*LVPL ISGAPDMECSGINNISFWLLPPYVLLLL ASAIVEAGSRT
421	14322	A	427	359	74	ICADYTRKPPYMGAPIEFSCATCVL*LT STQRECVCVCVCVCVCVCVSM*VALIPD SN/CIPLSAYVCVCVCVCVCVCVSI* VALLLDSNSYH
422	14323	A	428	52	361	NYPQLSEI***VS*LHY/LFSFLFFYFF *LVSRFVARLECSGAWH\IIAHCSLDLL

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						GSS/DSSPASASLVAGTTGMCHQNQIIF LFKKVFVGRVQWLTSVIPATWE
423	14324	A	429	105	361	SRLFFFFFFFKTNFGFVPKVGVK/WAFF GLMEPFAFRVK*FSGLTHPRTWNYRNVP HCPVNLEF*VKTGFNLVDKAGPKLLT*K DFP
424	14325	A	430	1	379	HAYHIVKPSP*PLTGALSALLMTCGLAM **RLHSITLLILCLLTNTL\SIYQ*WRD VSRESTYQGHHTPPVQKGL*YWIVLFIT SEGVFFAGIF*AFYHSSLAPTPQLGGHW PTTGITPLNALEGPL
425	14326	A	431	1	390	KKVKKWKNLIFMIGRLNNVNMSVLHKVI YKFRAICLR/TFHFHRKKKNLTWA*KHK KALIPKTILKKNGKSGGITLSDYKM*YK TTITTTIRFWWKF/DINKYNKITTHEIY FHIYGQMYFFKIAKTFQGIK
426	14327	A	432	1	392	TRTRGRTQWD*T*LRPI/WTKKKKKKKK GKKRKKKKGVFFFYFFLGF*FFLWVFFF FFFFLGFFFFFWFFFFFFFFFFFWGIFF FFFLLIIYNFFCKF*FFFFFFGFPNFFF FFFWFFFFLDFFFYFFFPRV
427	14328	A	433	382	1	RGGKFQNQKQKRKVSPPPPKKGFFPPAA PKNIKGGGKK*TPPKKGGVS\PPPPKKR KSPPHKK/IGNFFPPPRGKGGPPKNPKK PGPPFFFFKNPPPFFFFPFFFFLFFFFA HKDGLLAREQTQAEVKT
428	14329	A	434	375	1	KYSQLIFDKTAKAIK*SKDCLLKEWFWN KWTSTHKSLDL/SPFTKINSK*ITGLNL KCRIITLLENNIEENLDRLGFGNDFLTT LPEAQSKTELISY/DFIQTNFCSANATV K*MKRQATEWEKIF
429	14330	A	435	1	459	PTRPPTRPSTRTLGFTMLAKLGSNARPY /DYPSYSASHSAGITCVKHCARAVIHDF NGVHRPLLIW*EFLVEISFIFDFFLETN PGFITKGELQGHNLGSLQVSPPGLTLFS CLSLQKSGFYG/HLAKYLVKF/CFGIFS KRGF*GGYPGGAQSPPP
430	14331	A	436	14	382	MARNTSQKDIRIDPNNKCLWLVKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKRKNYFHVI\LKNKAVNNGSTITS TNVMSPGLHIRLIIILSLMIYKKSTTE* VEKQTCYYILM
431	14332	A	437	3	192	TPGLK*SPCLGLPKCWDYRR/AAAVPGL *DILAIFFHHILSESCLFLLVFIHCFNA NLFLRWSS
432	14333	A	438	1	364	DRIALGTVDDLPGRPTRP\AHPIILKVS LADRDAI*NLWQIPIVAS*YIPLGF/WS KAMPCSVDIYSSFEKKKKTVFFDRGQGP TPEIQVLGKAEGVKPFEPRGSKPSWRIM AKPKFYKRFKL
433	14334	A	439	336	2	GMIPEMKGNAGP/SG/PRKPGFFLG*KG KVKAWLNFKPPFRAFWPKKKILLPLGFS GILGPGPKGNLSRPGPPPQAFPLGFCQV LGP/SGPGVGFPKPGQIGWSNNPCLTLQ KNK
434	14335	A	440	1	333	HKLENLENIVKFL*TH/TLPRLNQEKIQ TLNRSITSSKIKSLVKNTPTRKEK/SKK PLVPKGFTIEFSQLCKKLRVPVFMKPFQ

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						KYGERGLFLNGFYEPGLTLIPKFGKNPG G
435	14336	A	441	320	1	WGINNWLSP*EKKGRPFLL\SHPKINSK WIKDLNVKGKI*KPLEGQIG*YLMIFGV EKGLFKGGPKYTLYKRKY*NRELLFIKR YFSLTEKSPAEICHIKKLAKKK
436	14337	A	442	8	391	ERILRHDQVGIIPGM/QGWVRI*ESVDE I/QHV/NQLPKITHTITSVSVGKARDKF NIYS*FKLGKTEKERNFLHWIKSICTSP AASILLEGKESPF\PFRSGTRKD/CLL* P/LGSGMVLEALGTAERRTRKEK
437	14338	A	443	363	2	HHVGQACLELLTSGDPSNLASQSAEITG MSYRAQLSIVTFSAYFLVV*KLSHARGL ML*QSIII/HVLHFHQVKKAFHVS/PEN SQPLHNVEPEDWIF*EHQRKTVPPIHTA RKLQDLEPCLV
438	14339	A	444	1	900	DSSAGIT/GICHHAQII/LFVFVVETGF HHVGQAGLELLTSGDPPASASHTGGDYR HEPPLLASLSFLNKELCTWPERRRKPIF SLPKLDPNKRKFSFPP*LF/IGS*TLIW SLFCFRNVCTQLADPTKSIAYQSSLMKP FGQKSICFGSEKFPDKVYLFSSDRKAKE QVLVVVVVVEY*I*DMSACFQ*ALGFCY CLSIWN/YELPEKFEVLACSLPSRNNDL ILSLKKKSQNSFFVCVFFFFKTKSNFVP QAEGQGPLFG*LKLPLPGFRNISCLNLP GSC\QTGAVPPPPVNFGFLKKNRVSP
439	14340	A	445	3	346	QIGKVKKLNK*VPHEPSKNKL\FLEASS LILCNNNEPFLSRIVTWDENWILYDNH* QPAQLLD*EAPKPNLHQKKKKKKKGLAP FWGAFSRGNPFYFFNPQQKLHF*KFSSQ KRG
440	14341	A	446	2	246	FKCGKTRALMHCWWEGKMLRQL\RKVWQ LLAMLNMELPREPAAPLLSISPRERK/S TTAKTCA*MCIATVCITVKKWKHRLLG
441	14342	A	447	38	393	VILHRQGLSL/VTQAEVQWYDYNSL*P* TPGLKQSSCLSFLKSYCHG*LFVVVVVF KWM\GFTMLPGLILNSWPQ/CNPPAVDA QIAGIRGFHS/VGQAGVQWHDLSSLQPL PPGFKQFSHLS
442	14343	A	448	54	540	RIPFEHASGFLQSSHQKPHCLLHPLSGQ VSSDGQ\FRKFGISRLGNSGIYKAAFPL HDCKFRRQSEDPSCPNERYLLYREWAHP RSIY*KQPLDLIMKYYGEKIGIYFAWLG YYTQMLLLAAVVGVACFLYGYLNQDNCT WSIEVCHPDIGGMIIMSAQRDRL
443	14344	A	449	2	310	FFFLRQSL/DSVAWAGVQWRDLGSLQPP PPGFK*FSCLSLPSSWNYRHAPARPANF FLYF**RQGVTMLTRMVLIS*PRDLPSS ASQSAGITGVSHHAWAKISL
444	14345	A	450	2	466	KQKIFSVDETAFYWKKMPSKTFHS*REG TASKLHTAG*ILLGPNAAGDLKLKPVFG DDSGNLRALKNYAESPLPVLYKWNNKAW MTAHLFTAWFTEYFKPSLRS\FRKISWK I*LFMDNGPHHPRALMEMCKE/NAVFMP ANTTSILQPMDKGVILI
445	14346	A	451	670	212	SSSSP*GS*YQNRTNTIPSPKKKQTKK\ KNNHYKSIFFTDAEILSNILANAIQQSI

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						KRFIRHEQLGFILVVLGWVNIQTPTNAT CYTNRLKKRNHMTILINAEVLYKIQPSV I*KLFPLRGAF
446	14347	A	452	407	219	PLISLRWENHLGPGVQGCSEP*LCLCTP AWMTE*YPISPSQNKTKKQ\HTRKQNQH KNKCVKN
447	14348	A	453	2	395	WFLWFRERSHLH/RVQNEAASADVEAAA SYPEDLAKIIDAG\AKQIVSVEETAPHW KKVPSRTFITREKTTSALKG/RC*LSLV DNAAGHF*VEA\MLIYHSDNPRTL/KN/ YAESTLPVLYKWNNKAWMTACLFTS
448	14349	A	454	424	38	EETEPL/HRPISSAEVELVIKNLPT/KH KSPRPDGFIAEFYKMQKE*LVPILLKLC QKIKEEGLLPNSFYEASISLIQ\NSGRD TV/RKENFRPIFPMNIFAKILNKILANC IQQHINKLIHHYQVLFSSLHSR
449	14350	A	455	2	309	PRVRSQTPGHKRSTCLGLPKCWDYRHEP LHPATASFLVAAVPGM/FADPP/CNMHL NE*MNE*MNGDDASEILSFEMRSHSVTQ TGGQWCSHSSPQPQPPGPPK
450	14351	A	456	3	441	DAWGLVLDRERPFFIFFFFFFLGNGGYF RGPGGRPGGEGPPMETSVSPVKKILRGP GQGGGKARKPHPLGGPRGPNHKTGG*KR AYPTGENPVLTEKPKFTGPGGNGPETPV IGKAGAGKPLNPG\MGGSRNPKWAHCP* TGGKKGK
451	14352	A	457	1	234	PTRPNHLGLGDRGCREPRSSHCTPAWAT ERDWVSKKKTKG/EKF*KGRTK*MS*VE QGGSGGKGIFTLAISNSPLPFF
452	14353	A	458	42	470	KRIPQLKKSPLPLKNPPGEWVGKINFPP PRERPKNFF*KKKTLKTPPKQKFLRKKS PFKKPHFLLYSKATKKQKRGKKKRAPPP KKKKKKENPKIVIFRTEITVASPVLSWA VKPIIHIFFPREKKPHA\KPPPP
453	14354	A	459	2	393	DRPIEQWNKRERPRINLYIDGQMIFSKG TTAFE/WK*NLCNKYVWNAWIC\NRRKN PYLTSSRKINLR*IIDIKVK/PKAIKLP EQNIRCSL*VLGVGRDFLENMNYTRKK\ IGKLDFIKISQLGMVADTSNPI
454	14355	A	460	338	33	GDEKIEKSFFFPISSLCFVP/AYL*QQI RLLIFTRNSRLLFIY/CLFLEMGSHFVT QTGVQWCHHSTLQPRPLGLKQSSHLSLL SSWDYRHLPVVLKWTEACAV
455	14356	A	461	77	435	AKEVEASLSTLARPISIQQQQQQQQQNEK KNKN*PRIAKAI\LS*KGEITLP/ELQL CYRAMITKTAWY*HKNRHIDQWNRRENP ETNPHTYSELIFDKGPKSI\SLFNK*CW EYWIFICTR
456	14357	A	462	157	3	NGRVDLKIQKLARCGGACLQSQL/RQEN HLNPGEKGCSES*LHHCTPD*VTKQ
457	14358	A	463	363	3	PSVAQAGVQWCHHSSLQPQPPRLR\HPP ASA/SQ*LGLQGQATALYIHKYILFPCN VLISFIFPFFFLEMRSHSV/SQARVQWH DGSPQPPPPELKRFSWEAELAVSRDRAT ALQPRRQ
458	14359	A	464	3	396	LKEIAEKVKKIIKFKKQLRL*MKKIINR YLKEN/LNQLLEIKGTLRELQNAVESFN NRL*QIEEGISKLEDKAF*WTESGKIRK

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						INK*TK*TDYIKEPNLRIIDVPGGEEKA KSLKNLFEVIIEENFPGLAR
459	14360	A	465	399	1	PPGVLLNGPPFFFFFLILGPGWVFGQPL KTPLVFFPNFQYHIFPFKISRIF/LPTR FPFQVPPLCP*PFSSPWGLKVVFILLSF FFFL*DRVSLCHPGWNAVM*SQLTAASN TW\VK*SSHLSLLSS*DYRCVLS
460	14361	A	466	279	1	TTNIFNPRRVGSTDAGPLNMKEKEKENV KRRQATGWEKIVAKDTSDKGLLSKIYEE LLKLKNEKTNK*/ILCLKWSKGFNRYFA KEYIQMANK
461	14362	A	467	2	436	RGELPQLDKYLKKTTAIILNGEEL/E/A CPLRSRTRQGCSLSPLL*KKFFPPKSHI ESLLFFNIILEVLYSAVRQENEIKIVEI GKEEMKMYLFTDGNHLCKNSERIRN/YS KVAGYKVNV*T*ITFLYTSREQVEFEIK KTLSMNRFF
462	14363	A	468	2	420	RTTALF*AVRQGRLSLQRLLLSFC\CLC PAARGEAYIG\RQASMSRCGLQAVQASC LLCLPKQAWAMAGAPPSASLLPCSLISD RCASSQPDSVGVGPSEAGVGYNLVVRGL LSRSEKR\NIRLGVTRFSRCV/LSPLSL TRR
463	14364	A	469	1	416	PSP*PLTGALSALLKTCGLAM*FHFHSI TLGILCLLTNTLTIYQ*WRDVTRESTYQ GHHT\QAVQKG\LRYGIILFITSEGSFF AGLV*AFYDSRLPPTLQLRGHWPSTGIT PLN\HLQVAVLGEPVLLAS*VSIT*ADH
464	14365	A	470	211	398	IFFFPKMGGGLSIILCWRRKRHPQKLK* STCLGLPKWWEYRCEPP/VPGQKKNFRP *KTKESPPLVSGGASSASNIKL*IALPP FLEKKKFKKQGFKDPPFPLFFTQNPGQG NFFFGKI*YCPPIFFFFLRRSFTLVAQA GVQWHDLGSLQPPPTGFKRF
465	14366	A	471	62	424	TLMHCWWKWKMVHLLWKTVLNLLIKIN/ RTLNHT*PCNPAIPLLGVSLREMITYVH KKPCP*MFIVALFMVTKNSKHLKCSLTC KWINKLWSLYTMKYYLATKRKELLNHNR SCRNYSSDMS
466	14367	A	472	427	20	LGLRLPFVEQEENKPYYPLAPFSPPEPP MSLYKNSPIYPGKGFLFPSKNNKIPPLN FLKMSNLF*/FALLLGNKDFHLLLLGGP IGIMGDNMATTSQMFYSRVPIFF/CFFE TGSHSVAQAGVQWCNLSLLQSLPPRLK
467	14368	A	473	424	98	NWYLYYYYYYHLLF*RQGL/DSAAQAGV QWHHHCSLQPRRHRLKQILPPQLL\TSW NYRHKPPRLSPYVAQAGL*LLGSSDLPD SVSQSAGIIGNEPLHLASL*FLFAFP
468	14369	A	474	415	75	NHFLKFFPQTQANGPGGKNKFFFLKTRF CFFPPGKRPWAYYKSLQPPNSGGQQI\S APTP*IKGAPKGGPPTRVKFFFFFLF/L RWSLRSVAQAGVQWHDLGSLQAPPPGFM PFS
469	14370	A	475	3	413	PVQKGLRYGI\ILCITSEV\LFFAGFF* AFYHSSLAPTPQLGGHWPPTSITPLDPL EGPLLITSVLLASGVSIT*AHHSLIEN\ NRDQIIQALLITILLGLYLTLLQA*EYF ESPFTISDGMYGSSFFVATGFHGLHVI

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470	14371	A	476	1	440	ITLTDRELSYY*ANRLL*LAYTITFIV*IPLYGLHL*L\PKAHVEAPIAGSIVLAAVLLKLGGFGVIRLTLILNPLTKHIAYPLLVLSL*GIIITSSICLRHKDLKSLIAYSSISHIALVVTAILIQTP*SFTGAVILIIAHGLTSS
471	14372	A	477	2	397	LFVYNHIDVGALYLLFGA*TGVLGTGLSLLIRAELGHPGNLLGNDHIYNVIVTAHAFVIILFIEIPIIIGGFG\N*LVPLIIGATDMAWPRINNISL*LLPPYLLLLLASAIAEDGAGTGGTDYPPLTGNYS
472	14373	A	478	442	44	SSSSPFTPPRGKFFFKKTPRKKFFS/SPGNKGFFSPLSP*KFFFFFNPFFFFGGFFPNFPPPKKNFFFKNSPGFFFFPPLKKKIFFFPPPLNFAPPKVFFKSPPPFFFFFFFFFFFFFFFLRGHPWGREGI
473	14374	A	479	1	439	PTRSPTRPLVLDRERPPFFFFFFKKGPPSVPPAGGGGANLG*GNPPPL/GVKKFFGPKPPKIGE*RPWPPPPGQPECSFFLKKNGLPHGGQGR*N\PPPRP
474	14375	A	480	420	0	YSPPSPPK/YRAPGKKFF*KKPRKEKF*KKKILGFFFPLSPLKFFFFPKAFKFFGGVGPNCPPPKKRFFSKNSPGGFIKPPLKGKNFFFPAPVKFGPPRGFFKGPPSFFFFF
475	14376	A	481	371	2	NKI*NKFSKLNSKKSSSSSSSSSSSSSSSSSSSSSSSPSVNK*IKKCSTSLTISSSSSSSSSSSPT*IAKIKNIDSPKCWQGCRETGLTV\LVQPLWWQFLLKLSMQII*DSANMILSMHARG
476	14377	A	482	3	335	HASGKDRHTDQRNRIKNPETDT*IYSTF*QKC/RLI*WRKDSLVNKWC*SNWA\SPMKKIKLDLSSSSSSSSSSSSSSSSV*NVKLLGNNVGGNLQYRGLRVHTVDVKAQHI
477	14378	A	483	1	418	GVR*FSPLNPPSRWGPKHGPPNL\LNFFFFFFVFLVETRFHPVGQAGLELLGSRAPPASA/FPK
478	14379	A	484	1	356	FCANAVRSMIKTVLIDKATKP/RAWKGNYKYHLPVFNCKTGRT\DSGNPLNWFYQCFVPEIRKYLARVGLPFNVFLILDNAPGHPEPHEFNTEGFRVVFLTPDMPLIQPLEQGVLRTLTA*YQCFVPEIRKYLARVGLPFNVFLILDNAPGHPEPHEFNTEGFRVVFLTPDMPLIQPLEQGVLRTLTA
479	14380	A	485	166	406	FIFWGSVSSSAEGGGWSVVSSLPRVTVRPDETVDVTIHLLKE*CRPGAVAHACNPSTLGGRGGRI/TLRSGVQDQPSQHG
480	14381	A	486	107	429	FWVTQTFGFFWLNPPGGLELWPPPPCPGNFGGNFKKKGGFPLWPGGVQTPGPRGITPPGPPRGGK*RGGPP/SPGPGFLGKPKGGGP
481	14382	A	487	399	2	GSPAPGLPKGWGFRGGPPGPGKFVFFKLPKGGFPGAEIFLGEFFQRGKKGLGPIFPPVFLKTEEGGTLS/NSFFKGRVFLVFKPKAGPKKKKKKTNYKPIYLNNTDTKFFNNMLANRI*QCIKEVMQYDRTRG
482	14383	A	488	419	2	PPPPPPPREKKGGLYFNPKIFLGKSFPPRNPKDPS*KPRVGIFFEGPKPPKKKKF*FGPWGKPPGDG*RKNPFK\PFFFFFFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						*DGVLLCRPGWIAMAQSRPGLQEWNSIS KKRSGPCVLGISSKEVPDAWADAWADAW
483	14384	A	489	629	0	SSSSR*SLLCKCFKN*GEKIRNPIEKWA KVMHRLFTKRCINI*KDVRSTSLMVRET *ITTTLRYHFSPIRLSKT*KLNRTLYG* DCGETGIFIHCWWECKMF*VL*RE/VWQ YLIKLL/LHIPVDTA
484	14385	A	490	2	351	KNRPEMDPGM*GY*VNDEGDTTYQQGNE ELRS/WCWDDNRLAKVKLDLYFPPHITI EINSKWI*DLNIKNPPIHVLEENMN/I* F*HVGIGKHYLTI*LKI*NP*K**IWLH ENKMYCL
485	14386	A	491	42	507	NLAK*IQ**IQTIMHHDQVSFIPGIQGW LNILKSINIIYYTNRL*DKTHITISIDA EKAFDKI*YLFMKGK\KPLSQLGIEGN/ YLKLIKGIH
486	14387	A	492	18	417	REGKKSRVHHFNIKQGRVMSTKH*KTQL /SHSNAHSNKAQISKSQPHGLHDFFKKK KKKKKKKKKKKKRGEKKKKKRGKKKKK KKKRGGGPP*KGVREALFCFFWRKKFFF VGGGGGKTPLGCLQADTPLWGA
487	14388	A	493	413	82	FFSSPPPPLPFFFPHLFPPPPNFFFFFS PPPFFFF/PPP*KTKFPPPPPLFFPPPP LFFFSPPPPPPFFFFFSPPPPFFFFFFF FFFFFFFFFFFFFFFFFFFFFWL
488	14389	A	494	1	413	PTRPPTRPPTRPPTRPVLDREHSPSNLP KKKKKKKKKKKKKKKKKKGGGPLKKKPG GAKKKG/EKKKKKFF*KKGEKKKPPGKF GKKKKIWGGEKRAKTPQKKKTP*GKKKI LKGEGGKKNPKPRGGKKFFSGEKKKKK
489	14390	A	495	274	1	IYRIDCAYMKKVERSKISILSFHIRKLE N/QLNPK*/RRRREIKIGAEINEIENRK *IEKINETKSYF\WKISKPLAKLIKEKT QITNTRNRAY
490	14391	A	496	336	1	VFQYTYNKLVSMFYYCFFL*RWGLTVLL RLVSNSG\PSD\LPSSAS*VAGTTDAHR HTQLCFTTLSDLLEPYFHLGSFIFSLL* FFFLNTESHSVVQVGV*WHNLGSLQPLP
491	14392	A	497	445	382	PRVLIFFFLTPRGPPPPPPPNKVFFPPP PPQNFFFPPPPPPPSWGGFAPK/PPPPPK SFFPPKPPPVFFSPPPKEKKFSFPPPPH FAPPPVFF*PPPPQ
492	14393	A	498	430	2	SPPPKPTRM*\KVKFGR*KKGGGGGGGS PPLSPPLWGSKPVVP*VPKGR/PLPG*A GKPPFFLKFQPFPRPGGGPRCPPLFGGL GQKNGFTPEVVLLL*PKFSPFPSSLVDR RIYCLLKMLEYKSVMMILLFASCLNLYT FPIV
493	14394	A	499	363	3	KKLVTPARVLGDIIPRNRFLQMPQQREN FLCQVWMTKPPTTIFVKTKTGKWYLISL KRFCPAKKKT/IKILVNRVNRQPPEWEK IFANYASDKGLISSLYKDLKQVYKRKNN PITK*VKGMY
494	14395	A	500	145	435	VFMCINSSFLLFIPWYEYTTVWPVTCRR T*MFIAALFVIARNWN*SRCPSTGNW/L KLWYIHTME
495	14396	A	501	162	1	FYNYTIIFIYLFIFIFLRRNL/DSVVHT GV*WRHLGSLQPLPPKFKPFPRLSLP

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496	14397	A	502	343	2	IKKFRWGPKPPLKEPPGV/SPDFPII/N FGNPGPVPGKDFKFPNFPKKKKWGGRAP PVVPTTPGG*MGRFP*PPAFGVPRGGDG SPPPGAPKEGPLSKKKKKENEKEKERKE KSARL
497	14398	A	503	23	405	KGRNYLWEKKKKNMLVRGKIGGGPPPRI PKF*KVIFKTPPGPPFFFFGPPLNFFFF KTDAPLFF*NHPPKSKIWALAPPKKKIF LNPKKPPPFFFPPHFFKKNFPRAFFKNF \AFSPRGGASPSPPP
498	14399	A	504	418	247	PPKWGF\FPKPPRGFFFPPPKGKKFFFP PPG*FGPPQGFF*RPPPLFFFFFFFFFF
499	14400	A	505	26	426	GCTGLLHS*MYAKVVCCTDHPIT*VLSP AFISRISYSPTHPQLILFF*IFFLFLVE TESCHIAQAGLK/LPASSSLPVWASQSA
500	14401	A	506	337	2	IPNLKESA/CPNLPKGWGFKD*PPPPSQ ISLIFKYPKFLKFEI*KKKPPLKKGLFW WV*RKKAPVGF*G\EMALGEKFFFFFFF FFFFFFFFFPRRSFAFVAQAGVQWRDLG S
501	14402	A	507	454	2	TSKTGQPGRRGSPFPI*WAAGQKRSSPP RRGSRAEALLTSQTGWPGRDTPHFPDDG RPGRGAPLFPDGAAGQRRSSLPRRG/VP GRGAP\QSQMGCQLGRGAPHFPDGVAGQ RCFPFPRWGSQVEALPTSQMGQPDRGTP HIPDGVAAGQRR
502	14403	A	508	390	13	RIPPPKSRWKGKGPF*VS*NPRPQI*KN FLPPPP*K/YGDPRGPPPPPIKFLPLKK KGAPPICPGCFEIPAPRESPPLAPPKS* NSRGNPPPPPFFKKKNPLFWGGKTKKLK IFFFFFEAGSCYVA
503	14404	A	509	2	282	WQFLTKLNILPYEPVIMLCIYPNESKT* IYTKTYA*ILLAALFIMAKTWKQGVLKK V\TDKVWHIHMTEY
504	14405	A	510	400	250	LLSVTQAGVQWHDHSLLQPQTPRLK\HP PTSAS*VAGTIGAYHHAWIIFFF\IFIY CRDAVLLYWLGWFPKGLLKCWDYWCEP/ RMSGLFVFWSDLGFRSEVS*ILSSWDYR CVPPCLDNFFF
505	14406	A	511	99	242	VTKEKEGHFIRIK*LIHQEDTTTINIGV PNNRTLKCMKQKLTELKKEI
506	14407	A	512	139	374	SLWGKRIFFFFGADPHFVPQAGGA\WGN HG*LQPTPVGLKKSSLLTFPISWYYRLG TPPPANFKIFCKNGVKPCCPACF
507	14408	A	513	23	401	STCLRLPKCWDYRRESPLPALCMLFL*M KGKYVYMGFFI\LFFFLFLHKI*LLQEN FVYVCLKKNKTKLKA*TKKQKKNETG*N ILVDLNVLS*KKWKCLLWGFILFYF/NF LRQSL/NSVAQAGVQW
508	14409	A	514	7	386	FFVFSTHITLLFLFLFFFFLFPRPPGFF LAGKKNTPPAPPEKPPPP\PPKKKRGPP FFFFGPPQKKPPNSPRGGRGPPPPRPPR KMEKGGPPPPREIPPPPFFF*PPKTPPP PPGGGGGGKKTPPKR
509	14410	A	515	370	2	FVFFQVVLPE*NSFLFSPF*KGLC*RDL AFKRFFPWPPNKKLWPSLF*GFLKNS*K FNFSLKSLEVPFFF\CFPKFFPWI*AFP RFFPFFPPPP*RG*IFFF*DGVLLCHP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						GWSAVVQFWLT
510	14411	A	516	1	163	NTREKLSGGGGTQLS*/LLGRPRQKNHL NLGGGGCSEPRS\HCIPAWMTE*DPVSK
511	14412	A	517	1	390	RIVRVYYKHLC/Y*GSVNPREKIDNFLD TFNLSRLNQEEIETLSTPISSSIIETVI KSPPT\KQKSPGPE
512	14413	A	518	47	312	EYTGLILRLYIE/LFTTQH*KQKALNQA K*LAKGLNKHFIKRGCMNDPKHMKKSSA SLAIRKM*IKTMMRCHYILT*MAKIENK TESTRP
513	14414	A	519	320	1	QNPINKQ*KKNNKKYRLV*HKKPPPFTT QPHQSNQHQ\PN**PQKHT*TKNHHTPP PPP*SPPPPSLSPSPPPPPSPPSSSHPP LLSPSPPPPSSPPSSPPPRTSP
514	14415	A	520	1	368	LKTQQEANNLILKWAKDLNRYLIQK/VY RNVKHTKRCPTS\RELQIKTRYYYISIR *RVKYKKRDNTKC**GRETTGTLVIHYS *EYKMV*PLWETV*QFLTKL/E*SY/P* DPAITLLGIYSKELK
515	14416	A	521	2	264	GKKIPMLYFAEIEKCILKFV\KRS*KAK *ILPKNNKAGGLKFPDFKTYYKAAASKH QVGGLWKELRSTLQAQQTWVPREELRST SPS
516	14417	A	522	1	408	LEKMSTSLAI/RVMQSKTTMKCHYIPIR KAKI*NNDNIKCWQ*CRETGPLIYCC*E CT/LVQPL*KTV*QFLIKVNM\DPAFVL IFIPKK*KHMFTHKKNCKHTFRAALFVM ANTRIIPNIFQFVEWLNKLSYKHIVDY
517	14418	A	523	320	3	TYIYIKTCPRMFT/AVMLTITKKQKQPK YPPTDE*NV\YIHSNAYYSEMKRNEVLI HATTWMNPKNIMLNKASSRKRPHTI*LH IYEMSRIIQYMVLCNCLLLPSMF
518	14419	A	524	426	9	AELPASPTPGTCTPQPLGSGRDQVP\GA VGGTHPGGSGLAGSPP*GGLGMAGCKS* ALPRGEVTEAWRQFKCGERRQASSTGGP GAPSAAAGPGAKPLTAWGQRHQPAAPSA GPAEPLPTQNWCWPASNPGSRTRLSLHT
519	14420	A	525	13	461	ICIWRKMNILLPYTKLNSRWIADLYVKG TTIMFLEVSVREHLHDSQKKIF**DAKL MNQKE*LDILDSINIKSFVH*KAPLREN KGKLQSAIHIYEKGLVSRIYEELLQ\TY KETLKANKKKIDNPIEKWAKNLNRHFTR GCPSIYKHVK
520	14421	A	526	288	570	ATGSLCCPGWSIVAIHGFNHSAL*LLTP GLKHPPASASQVAGTAGMSDCTQLCKIN FFVFVFL/RRQSLAVTQAEVQ
521	14422	A	527	3	438	AVSHDCTTGLQPG*QREILYQRKKKGTF SPLPPPSPGIGGKPALPFWGPKTWPPPG IPPFLFSPPPPSQSGGGPRPLETLAGSF SQNPWNLRDGAPPPPGGGFFG/CPPFGP PGGLG/PPGAPPPPLKNFPKKKGGGGGF LFPPQAKG
522	14423	A	528	2	616	FFFDTEWRSVAQSGVQWRDLGSLQAPPP GFTPFSCLSLQSTWDYRRPPPRPANFFL YF**RRGFTVLARMVSIS*PRHLPALAS QSAGITDVSHRALQVCFITTLL*LSK/H QFKKAGVTL/PHLQCLHEIGLDCVLHKH /WSVHHSPP/HKTNVC

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523	14424	A	529	57	485	RHSSLGNKSETQSQMKKKKREKKKGKEI SFDPAISLSI*PKENKSLYQKD/TCICM FITALFIIAKTQNQPKCPSTDE*INKRV \IYIYIYIYIYIMKHYSPIKKNEIM/SF AATWMELEAIIISETMQKQKAKYCLFSC I
524	14425	A	530	399	3	FFFFFFFFWENPPPPPK/WRGGGKKKAP FFKFFKYKK*LFFF*GGGGGHQQKKKKK KSSSFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFF F*FKGFLLGTTHASAHASAHAS
525	14426	A	531	491	4	SKWIKDLNLRTK/TTKFVEET*VKIFMN LGLGNDFLSMTPKA/LKIDKSDFMKIKN /FCSSKD/TIKEVKRQHTEWVKIFTSYI FDKGSTSRTCKEL/RKQQQNKPIQKCSK VLNRFFFREDIQLSNKLMKGCSTSLNH
526	14427	A	532	184	509	PQWPAHSFLPALGSSGTGPY*VVRQIFD SKDKESSQ/WSHETSDRPKPADHRRRSR PSLATSP\PRLEPHPSLPNHSGLPILSS LPWGAVALAPTHFSALAWP*RPLPCNSQ GEKFFFWFGFF\ERESHSATQAGVLGHD LGSLKPPPWGSKGFFCPSYSGG/WNQKN HLSP
527	14428	A	533	401	3	VIREMQIKPLHIQ/PGWL*SKSVKKY*Q GCGQS/NVLIHY/WLKT*IMGPFWKIVW QFLIKLPYGTVILLSGIYILWRMEKKPP KFCTQIFIAAFFIIQ*PKSENNPNIHQP KNQ*DVHMYIHTMEYYLAIRMNIH
528	14429	A	534	419	93	SLAIRQM*IKIPPRYTRVAK\IEKSHNT KYWKRHGATGTLIHCWWECKMA*S*KIW *FLIKSNINLPFNPVILL*GIYPREMKT CLYKD\CM*MFMAVSFIEQNGKQPKCL
529	14430	A	535	414	2	NFLARGYINCGPQFFFFPPRKNLKWGVP LSNFPPKL*KGGIFGEGPKKVKKNFFFF FLFFFFF*KKPPCSPRLKAK/WKIFGPL KPPPPGLKKFSFLTPKKNGDKRGGPPRR GNFFFFFFLVFLVKTEFHYVGQAGLK
530	14431	A	536	32	435	DRATALQLG*KSETSSYKKKKKKKKKKK DGGAPLKKNPGGAKKKPGEKKKNFSPKR GGKKNPPGNFEKKTNFGGGKNGAKPPQK KKT/AWGKKKNLKGKRGKKNPKTLGAKK FPPRG*KKKKKPPAARPGKASS
531	14432	A	537	348	1	EYIKSTHQMGKNYPLKNTVSSGQVQWLS PVISAQFAIAKSWSQPKCPSLNEWIKKL WCV/WCVCVCVCVCVCMMEYHSAIKRNE LMAFAVT*MRLETIIISEVTQEWKTKHR MFSL
532	14433	A	538	523	66	TDQTSHNIPLSQSLIQSEVPTLFNSVKA E*CEEA/AEHKFEASRGWPTRLKERSRL RNMSV\GEAAGSPEDPATV/INGGGRTQ PQIFSVAEATLNWKKTPCRPFIGREKSM PGFRASKDSLTLCRDFKTHLCLVFHYWN AKHVQVYILLKVTAKI
533	14434	A	539	413	2	RDKV*PCCRSWSQTPELK*STRLCLPKC *DYR/R*APAPGPFLL*VHRHVSIFKSG PLSCRCSNFQD/HDSIKPSFPTIQYAHG NKFQL*TPDTLIFFLKWSFTFVAQTGVQ WHNLSSLQLLPPGFKRSDAWADAWADAW

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534	14435	A	540	385	2	MASKHIKT/CARQLAIREVQIKTTQYHV IPTRMAKVKKT/DNECWHGC*NTLINCW WDCKMMQLLWKK/SVWHSSRGKMYVQLP CTPAIPLLGIYTELKTCSHKN/T/CT*T FIAALLVIAEKWK\KCPSAEEW
535	14436	A	541	44	398	RPPFFFFFKKRPLWKKKQGFPPPA*RGE IPSAKK\PPLGPVSGPGNPPGP*KP/PQ NPPPLGGSPFGKKPPLDIPFPGGPIKGK KWGGPPLAGGATTKN/PPPGGNFWKGGK APPFPSQKF
536	14437	A	542	370	10	FFLRTKVSLFPRVEG\KVQSQLLAAPPS WGQVIPPLQSPE*LRQKDPFSPGG*GCS EPCSCPCLPAWMTEPNSVSKS*KKKRKK EKN**KKKKSFINTTGKIRFRIIH
537	14438	A	543	1	370	FLLRHILLCHPGFCSVATAYCSRDPGSS D/PLPPQAPLPDQ*PRLQA/WHRLAPPH SANFF**RQGFTVLARMVSISQPCDPPH WASQGATATKADDYQK
538	14439	A	544	50	395	IPGLTRQWLLDPCASPSTPPYT/P*VQP STPQNSSPSPKTHNQKGLPMPLSPTPKP STAWKKAILEHTSSSSSSSSSSTCRNR NGYTYTVPEHRPARGHTASQTRKQVLAA THKP
539	14440	A	545	1	370	LCSVTQAGVQRRKLNSVQPPPPRFKQVS CLSLLFFFFF*KRVFTLFPRLEGRGPII FNGSPTLRG*GDPPV*ASKELRTKGGPH QGQLINLF/CLGATGPTYGAQGGFKSPG LRRWAPLGPPRA
540	14441	A	546	178	365	YKKTDATKTKMDK*DSIKLKSFSTVKET INKGNR\QPTEWEKIFASHTSDMGIISQ ICKELKQ
541	14442	A	547	11	236	KGTTKLVVKLSDFKSYFKAIVIKTVRN/ WHKYK\HIDQWNRIQNPEINPHIYGQMI FKKRAKNKQWKKDGLHKKR*WSNDFQET CQEQTMEKGRSSQEKMM
542	14443	A	548	355	3	IKKKNLGRKRFCFFQEEKTWP*TPKKKP LENPGGVFPNPGFPPPFFKAKIPEGPFPG V/SFF*RGGFKGYPPPLFFFFFFL*DGV SLCHPGCSAVAQSRLTASSASQVHAILL RHVDEGR
543	14444	A	549	1	373	CFLICRHTSHMWRIWFQTTAINQIWQ*K ESQKVVSQ\LYI*KLHLLYEVQ*HFV*K YTQ*LLLENADTK*AHAVGKMVLIDLLK AALSLIFNL*KNK*NLKNWPGMVAHACN PSTLGGQGGWLTS
544	14445	A	550	446	2	NIDKAPTVLGKMVSIFPTSRSPPLGPPK CWGHRREPPRPAYFGI*ILFLTPP*NPL NNSPQHLSGKISGIFSDPSLSVFFSSFF FAPPPKKFMLCF*PFFFFFF*DRVSLCH PGWGAVERSWLTAAPISQ\IR*SFHLSL LSSWDHRHA
545	14446	A	551	342	26	WAPPIFFFPPYKRSPQKPFPPPGENNSR GF*IFG/RGGFFKKEGLSQFFFFFLKKV FFFSPGGEPQGYFPPPKASFLKRIFFPP PPIKKGDPGRGSPPRGNNNPFF
546	14447	A	552	3	167	QPHLQDCL*QQNPVAVG*AFSSHPRDSL NNPW\WPGAVAHACNPSTLGGRGGRII
547	14448	A	553	3	413	TLITALSSH*FFT*VGLEINMLAFIPVL

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						TKKINPRSTEAAIKYFLTQATASIILLI AILFNNILSGQ*TITNTTNQYSSLIIIM AIAIKLGIAPFHF*VPEVTQGTPLTSGL LLLT*QKL\APISFIYQISPSLKKK
548	14449	A	554	441	1	SSPPPQARGEIFF*KNPGEEISQHNKKN EVFPPPPP*KFFFSPKAFIF/RGGGGPK RPPPKKKFFPKKTPRVFYKPPQKKKKFF *FPPPVKFGPPRIFFKSPPPLFFFFFFFF* FFFFFFFFFFFFFFRMGCDRWHGKFWIL RDGF
549	14450	A	555	3	455	NTNSSMYVCIYVFILRQSL/DSVTQAGV QWRDLSSLQPLPP\GSWDHRHLAQQ*YL FNVLLLEV\FVYERGTIMVPIL*DCNVN CRVFGTRSLSVYCVMGIFYRC/HIESML CDRCFIFFDIGSHSVTQAGVHWCNLGL\ MKPLPPG*RNFSGLN
550	14451	A	556	1	299	RRMRQENRWNPGGTGCSEPRSHHCTLAW ATEHDSVSKKKKKIRSSLGKKT*FYHNI LKAMG/CITGIHKGPEGAWQREGHFTPP QGPKKAPQRGQTYPDP
551	14452	A	557	3	391	PVWWNSFEASSGWLIGFKKRSCICNIKV QGETASASVEAGVSYPEDLAKITDEDGY IKQQIFNVDKTT/YY*KKISSRTFIVRE KSMSGFKASEDRLM*FLGANAASNF*LK PILICHSKIPMTFKSRAKS
552	14453	A	558	337	1	TRFPPFLGGFSTKFFYRPLVRFPLL/RE RKIFPLPPVFVGGFPPALGPFWGFLFFN *FSKKRPFGFFWGFFF/CFPKFLPFKPFL GFFPSFRRGFFFFFETVSLCQPS*SAVV Q
553	14454	A	559	117	419	IPPLLLGVGLFFFFFIRKKRGVFSPRWR GGGSNFGLLETPPLGIDPFSGLTPPKSW ELRAPPPPPIKF*KFFLKKNGF*WVSPG GLEISALLVFPA/SASQ
554	14455	A	560	347	1	IYKELKQLCRKKSNYLIKKWAKNPNRHF SEEIQMANRQMKRCS\TTPVIIREMLIK TTLRYPASPVKMAFI*DR***MF/WQRC GEKGT/H/CWWECKSVQPL*RAVWRFLK KLKILLP
555	14456	A	561	2	375	*IPPPLQNGEKIFMII*TGAEKAFYKIPF* PFPIK/TLNKVGIKGNFPHIIRAL*EKP PAYIFHGEAESFPVRSGTRLCPLLLLLF HPVLEVLVRAICPLK/E/IKGTQIGKEE
556	14457	A	562	391	2	ASGSKGKKKYPPFLRGSPPLPGNPLFFL EGGEGKFP*P/RNWGPPPKIFPQKGQGN PFFFFFLKGPKGGGFFPPQGEKGVGFPL PGEKSQRPF*GEKGGVPPP*RKKPPPFF FFFFFSETVLLLPKLECS
557	14458	A	563	384	3	ISDSGVHPLGLPKRILLCQLSYHVWP*P KCFC/PHLCLFMTLFQPP*GLPSVCAPS KQEEHGCFPISVARQEC*PLFPKNLDT* HFVGNFLKFFFFFF*DGVSLGHPGWSAI LTHCNLCLPGSSNSLPQ
558	14459	A	564	522	120	SLFLPTLECNGTISAHYNLHLLGSSDCP ASASLVAGITGMCNLCLPSSIDPSTSAS *VAIDLRK**GARGNCPVS/VLEKGWPE AEMGRGESASWWDPRLGRPGVAKRICRR HCCPVQQPQVSMEPSGPASPN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
559	14460	A	565	73	264	KDRHIDQWNRIESPQIKSMTIHLWSPDF FLQGY**KDRHIDQWNRIESPQI\NL*L YIYGHLIFFYKGTE/IQWRKKTLSSKWF WDNWIFKCKQ
560	14461	A	566	413	1	EKKKKVPSQVLTPKPQVLGNFPRFSEEQ *LSLVPVSSLPLQSLSGKNQGP*ARRVA LCFGKSPGSQQIWF/RLP/EDIVTTVQA SYSKKRLFLSLLDFQYVLQRREGAVNSA NLSLAPW
561	14462	A	567	397	1	FLGQDLTVAWARVQWCSHGSLKPRLPGL KGSSRSATG/SASPYLVPMFLSNLFWHV YIL*LYKTMTGI*MEM*FTPSCPMYSVV RDV*IFFSFETEACPVAQAGLQWRSLGL PQPPPPGPKRFSCLSLLTSWD
562	14463	A	568	437	1	KFSEDPAKLIGEDGYSKQQVLNAN/ETA LYWKNMLSSTFLARKETSMPSKLQGTG* LLLGANAAGDFQLKSMLTCHFKNPRALK NYATSPLPVLHKWNNKAWMTVHLMTALL TEYFKPTIKTYTYHNTTGSLTTPHASAH ASAHAS
563	14464	A	569	234	1	FFPPFPFKASSPPQGTSSSRGVF/PPFF PPPKKGFFPKIPPGSSSPPPF*EKTYFR FPPFFLAPPGVFFR
564	14465	A	570	2	396	FS*AFYHFGLALTPQLGGDWSPAGITQV KSLQVPVVNT\SGLLASGEEIT*ADHNV IQNNRNRRIQALLITVLLGLYFTLLQAS ENFKIPFTISDGIYGSTFFECAGLHGLH VIIGSALLTICFIPQLTFDC
565	14466	A	571	3	403	HASGLPSSWDYRRPPPRPANFFVFLVEM GFHHLNKAIIKSFACNEIQPLSAVSVAG LVGCV*VCKCLFPVL*Q*LFQF*/S/HS IANWMREWPLRLSLF*LIC*GERMSGFA TQSRRDPCSLPGFLYQVLSLAKFR
566	14467	A	572	100	371	YKSNDFYVYGILHFLTTI\FFFFFFKKK KFPPVFQVGGQGGNLS*LNPLFLGLKGF SCLKLPRSWNNRGAPPPPPNFGFFSKNG VSPCNPG
567	14468	A	573	371	1	REGARES/TWSSSHTPVQKGLRYGIILF ITSEVFFFAGFF*AFYHSSLAPTPQLGG HWPPTGITPLNPLEVPLLNTSVLLASGV SIT*AHHSLIEN
568	14469	A	574	353	103	SLQLQPPGLN*SSHLSLLSSWIYRHKFP CPANVRFFVFFCRDGVLLVAQAGLRA/S ASQSAGITGVSHLAQLVNPLLFYFSRAG D
569	14470	A	575	1	206	FCIKKIIGFIPGK*GWFNISQPV*SLTN RIKEKIHISMTAEPIISIITEKVFDKIQ HPLILQKPFGQK*EYKFLNLIKGICEKN /PIPNIIYNGEILKQGCLLSPFLFNIVL EDIVIQSVKIKEGINIETQELR*SLTNR IKEKIHISMTAEPIISIITEKVFDKIQH PLILQKPFGQK
570	14471	A	576	157	255	YISPTPPFPPDLPF*NYLPNPKLTSPAP NFQIY
571	14472	A	577	365	3	PPHPSVFFF*KSPPPPPPLFFFPPPPFL FRGGPLYYSPP/SPPLFFSRRGKDTNPP PYSGLSVAGQTPPPPPRRTPPLVSPPPP PFFFF*RGGPKNKKAKKQTITFKSPPGT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						NKPKHKNDRDI
572	14473	A	578	2	323	VGSWEPDEKVSHRELLLSFLFYPFFSHI SS*ETLIDFALTSTDIWALWHDAENQTV VKYINFE/HVWVT*FCHPTSPQAISC*E DERPGAVSHACNPNTLRGRGRQIT
573	14474	A	579	369	1	AHLKGTLGGFPDFPFINLEFRGGLTSCP NPLNNWE*R/RPPPPPGKIFGAFFFFFF FKVETGFHRVDLLVLIS*PCDLPASASQ SAGITGVSHRARPTPG*FKKKIMTF/CL *KWWSHYVAQIG
574	14475	A	580	394	125	AAEGEQGREGWRNRPRGRERASDRERER VR/ERGEERERGEERAPQ*SERWR/E/R SRERERVRELWSDSDRALEREALLR
575	14476	A	581	416	1	KGQDLYGEV*KVLLKVIKQVLNKWKDMS CS\KINILISFPIRIALKFFF/ELDEI/ CSFV**NKC*RIAKEVLKKKQ*CLGGHL /TSPHIRRSYNTTFSQSIWCCYRTKQID *WTRTQNPEKDLRI*GDLIYDLRCCSSS RA
576	14477	A	582	3	403	NCFSQFNVIIMEIPAKFFIDINKLILKC FCKGRSILKKKR*EDS/QRRNFLVIKTV WYWQRECHIDQWDRINNPEINLHKYSKL ILDKGAKAIR*TKES/I/YSK*C*NWKF CM*EK/IDPKLNPLYK
577	14478	A	583	402	121	QSLIHSKALTLFNSMKAEEAAEGKVEAS RGWFMRF*ERNHLHNIKVQVEATSAGVE AAASSPQD*GKTTDE/GGYTTQQIFNVD ETAFYWKTMPS
578	14479	A	584	255	517	IYIFGFIFRGRVLL/CTHPS*SVVLQS* LTAALNFWAQVS/LPSSWDYRCTPPCLA FFFFFCRKGGSTLCPRLVGNSNPLKFPP LGTPCF
579	14480	A	585	1	414	SSHSCCSKA*SSMGPSPAFYKLVPLFLC LFIWDGVWLCHPGWSAVVQSLLTAASTS Q\VHPSS\CLSLRNSW/EYRYVP
580	14481	A	586	392	43	CWDYRCEPPCLA\TETGSSYISQAGLEL LASSNPPMVCHPKCWDYSHETMHSAQNF FLKGIS*F*LCCSHFIHNHLLWLGKVIH TYTHAHTGLEKYKTQCLDVKCIYSDLLD GAIK
581	14482	A	587	1	394	GTR/YGINLFITSEVFFFAGIF*AFYHS SLAPTPQLGGHWPPTGITPIEPLEGPLL NTSPLLASGVLIT*AHPSLIENNRNQGI QALLITIVLGLYFTLLQASEDFEDPFTI CDGIYG*TFFVVTGLHGLHV
582	14483	A	588	190	3	DGINLKIPGGIFFFLKARSHSVTEAGMR W/P/NYGSLQPRPPGLK*SSHLSLLSSW DHRHAPPSC
583	14484	A	589	157	387	TKKRGRVGGVVWIKILGINLTKEIKDLY SENYKTSLKEIKER/DTNKWKNIPCF*T ERVNTVKMSILPKAIYRFNVIP
584	14485	A	590	891	0	PPPPFFFFLPALIFFFPPPPQ/PKTPKK KKNPPPPPPP\PPPFSHIP*QFLSPPPQ HHHFIHHPPPQPPFHPFYYNPFKFFFF* NINVPPPP*K*IYFF*TKFFFFIPNIFF F\TKKKIFLSPPPKKFPPLLTNLSLPIL IKNLLSKPPPPQI
585	14486	A	591	1	496	GTRAYQIVKPTP*PLTGALSALLMTSGL

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						PMRVHFHSITLLILRLLTNTLTIYQRWR DVSRESTYQGHHTPPGQKGLPYGIMLFI TSKGFFFARFL*AFYH\SSLTPTPQLGG HWPPTGMTPLNTLKDPLLNTCVLLASG/ VSIT*AHHSLIENNRNRIIEALLMTIV
586	14487	A	592	175	2	PFFFFFLLRHSLTLAQAGVQWCDLCSLQ PPSPGFKRFSRLSLP/H*PGMVANFCIF SK
587	14488	A	593	107	733	AAAAASKVLM*REGQLPGAT\GTGGVQA *APGSVA/AEGASVEGPGFGDTAPAHQG LSPTRSHGQGGAGRAS/SSQQGSPGGRG DGASEVWSGAL/SPGGGKDGASASVPRG PYAEAEKGGWALRGLGGVAAPGPPSRAG QAPSGS/YTGPNARPAPWPIPGQGGGLR RDQAG*VSSWTGSTEPGAHTAHRAPGHG GKGGSPQQPHPQGPGQIPT
588	14489	A	594	10	435	FKWLLKSHAICFWTRS*SYCDNVCVPSL WAHHLGIRTEIPEFFLSKFLCTSIIPHF TYRRQLRLIQGSTE*EA*EDKLEQK*AL GAAQFTLPGMDVFVCFVFCF/CLFEMES HSVT*ARVQWCDLGSLQPLPLGFKQFSC LGL
589	14490	A	595	437	3	DEPKKWKTIPCSWIERTNI/VLKMAILP KAIYRINA/VPIKLPTSFFTEVGTFSQN *KTTILKFRWNQ\KRA*IAKATQSRKNK ASSIT/PDVASNYKTTVTKTARHWYNNR HVDQWNTIENTEIKLHTYSQ*ILSKAGT SKQWGKEHV
590	14491	A	596	2	498	FFPFLGKTKPPTHLFFFPPPPFPIFFFK IFFGPLFKKKNPPK/PFFKRPPSFPKNF FFFSPPPPFNPLFSKAPPPIFFFFFKKI FFFPFPPLFKKSPPKTPL*ILGFFPSFP FFPPGFPFFSLF*GGVSLCHPSWNPVVL SRPSSKLASAFRMPPVEG/SPFPPSP
591	14492	A	597	1	311	RRVSSESRWRSLESRGRSLEIQGRMERP RCQRFRENSCVAPRHCKGPGGKGLQALF *VPVAQLGEPGAQLGDPGAHGEATVPEV QGE/PAALLPGTAK\PGGEGSPGFIPPR HCRGTGEEGSPGFTQGRETSKAQQRTGC LLSCRGCLCLSVSGDS
592	14493	A	598	302	2	FLRFFHHKKFTKALNRHFSKDILILLLSS NHMKGCSMSLVIRD/MLLKIT/MKYQFI PTRMA/IIKKTDRYWQKN/CEKI*TFIH CW*\NEKMVQPSWKAVWQFLRK
593	14494	A	599	3	386	HTWPPPPRSPTAPPARTQPPSLQSALPA PQPGKKKKALRNEKG*NGSKKG/RGQPR PPPLRGPNGRTRSPAGICKGGGGFCPGV SKAQGAPRPGGRETVVPGFFGRRPPLPR GPGPPGVLWTSRHCPLR
594	14495	A	600	374	53	EGFFFFFPRWVGGQRALFWSPHFPPPGV KIFFPPPPPGWGGLRGLPPPPFNFFFFL KKKGFSPFCPVFSQLPPAGVPPPPPPP/ TGLDLRG*PPGPPPFFFFFFFFF
595	14496	A	601	393	1	VSPPKGCVSENKIPPPHNYYFAKTFVHV KLFGVAPLFLQILF*GPFLTSIRGLIL\ WIPYSPGY\TLTLLIAPRHFLRTIIPVF RSVLPKTYLGLSGMPRRYSDYPDAYTT* NIGAFRIARESVVGRKLDL

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596	14497	A	602	1	155	FCFVT*SGVQWRNHDSLQPLSPGFK*FS/CSSWDCRHAPPHLASFCIFRSTRP
597	14498	A	603	170	455	KPNASLKRVLILCIQLQSSRQQKNNPT/VKKWAKDLNILFSTEDL*TVNRYIKKYLTSLVIKKYHFIPTRLSKMKKTEHSKCWESCGEIETLTCSW
598	14499	A	604	3	449	TLLSNLEEAKKKKEDALNETRES*TKLKELPGVCNETMMALWEECKPCLKQTCMKIYARVCISGSGLVGRQLEEFLNQSSPFYFWMNGDRIDSLLENDRQQTHMLDVMQDHFSRAFSIIDELF\QDRFFTREPQDTYHYLPFSLPHRRP
599	14500	A	605	169	435	KYENTKINRR/VAPN*ISLSPEKKKKKKKKKKKKKKKKKKKKSASSSKASPSSSRGG
600	14501	A	606	453	29	TSPPPPPGENFF*KKPP*K/HFFPPPQFRFFPPPFPLKIFFFPPSLFFFWGVFPHFPPPPKKVFFPKSPRGFFFPPPLKKKFFFSPPLFFFPPPGFFLSPPPFFFFFFFFFFFFFFFSPFFFFFFFFFTVKNFYLLCYFYKN
601	14502	A	607	170	408	NEYDHFSIIKERRDFIVCVFFFIFSR*SFTVVTQAGLSSLQPPLPGYKRFSCLSFLCSWDY/RVVHPQGSANFFVFLVEMG
602	14503	A	608	2	448	SLHPVIYSEGIKSRQSPCWR**KTVKKKKKNPNQKPKKKKN/RPKNPLGGGKKFF*PEKKPGPGKKILKEKGKKICPFPPQKKNFKILKKKKKGAPLKKNP*GAQNFPGMKKINFFP*REVKKNPIGIFKKKPLFWGGPIGANPPPENL
603	14504	A	609	441	28	GGTFLKGIKSAPKI*KGFPGWGGARFPARDPPQFGG/PKGGGSLSPRGLNPPGPPG*TLFFFKKPKLTGGGGPPPLIPALRGVRP*NSLYPQRGGGAQIPPGPPPPGGKRAPCFQKKKKPRRKEKKK
604	14505	A	610	445	1	LWLKKNTGGGGGSPPLFPPLGEPKRD/GFPRGRGFGPPPPPIKNPPFFLKNQNNPGGGAQPGIPGPWGG*GGEFPLPP\SPGFH*PRFGPFPPPRGTKREPPFQKKKKIANCFLLSDKSLLLEEAWGQVVGPSPLEPTVAPKPNPRGKAQ
605	14506	A	611	253	437	KKKKVQDMFSENFKML/NEIKATLNKWKDISYS*VRRLCVVKMAILPT/IQSYRLNIIPIKI
606	14507	A	612	186	2	KKKKVQDMFSENFKML/NEIKENLNKWKDISYS*VRRLCVVKMAIL\P\KQSYRLNIIPIKIQA
607	14508	A	613	37	453	KTPPPGENFFLKKPQKKNFFPPGNWGVFFPPSPLKFFFFP*TFIFFGGVWPNFPPPKKKFFFKNSPGVFF/SPPP*KKKIFFSPPRYFWPP/HGFFFKGPPP
608	14509	A	614	1234	0	KKPPNTPN**WAKDLNRHFIKDSSIKDDQYY*SLGQCKLISQYNFTCTRIAIIKKTNNNKSW*GCGETGNLIH/WIECKMVQ
609	14510	A	615	327	188	FFSSSLLIISIPKFNHVTSLLRNLK*AMLGSSHL*LQLLRRLRREDHLSPGVSGCSKL*SH\THCTPVWVTE*DGRKGLAGDGSHSVTQTGVQ
610	14511	A	616	103	446	KKKKKKKKKKKKKKKKKKKKKKKKKKKKK

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						DGGGALKKNPGGAQKNRGEKKKFFFF*G G\KKKTPGGFWKKNPFLGGGNFAPPPPK KKKPLEKKKNF*GGRGEKPSPLPCGKEK FSHKKK
611	14512	A	617	3	429	GLLSIIYKELLQINKISNLVGKWTKDK/ NKQFLKKEIHRLAK\YMKRYSTSLVTIE M*LKTRYYFHPLNKIKHDNNIHC**GYK EVGILHILLEA*IGKPFWKAITVTVLNA PVFCL*FCFEMEFHSCCPSLKCRAPTSF IGAS
612	14513	A	618	427	6	WGGPPPPPPIFFFFPPPP\PYFPFFFLQ ALFS*RVFFFLTPPPPKNFPPP*GPPPP PPPPPPFCV\FFFPPPPPPPPPPFFFFP PPPPPFFFFFFFFFFFFFFFFFFFFFF FFFFFFFLVENCVFINSITSDIEQKISI SC
613	14514	A	619	68	434	YSKD*PINTKKKKKKKKKKRGGAFKK KPGGGKNKGGKKKKNFF*KGGGKKNPRG NFGKKTLFGGGKKGEKPPQKKKSLEGKK KI*RGKGGKKT*NP/CGGKKFSFGGFF* KKFPPGGGGKY
614	14515	A	620	454	90	NFPTPEKFGPPQGNL*KAPPFFFF*KGI PFFFPG*KQRGGFKSPQKPPPQGKTIFR PHPPKKGGPQGPPPPGGKIFFFLEF\KK KGGFPG*PRRFFFPGPGKPPPRPPKKAG IQGETPRPGP
615	14516	A	621	432	2	PEAFLSSLLHPAPGEKFFLKKTPEEKFL TAKKYRVFLPPFPLKIFFFP/LRALIFL GRFAQIFPPQKKGFFPKIPRGVFFCPP* KKKNFFFLSG*IFAPPGIFFKGAPPFFF FFFFFLDRVWLCYPGWSAVARSRTS
616	14517	A	622	422	2	GGGPPLPPPRGGLPPPK**KA/VGGGKK PPPPAPL*NPPPPKKKIGGGGGGKNPPP PPLACFFFGFFLPPPPPSFWGGEKFFFF FLSGGPPPPQKKKKKKKKKKKKKKKKK KNKKKNQTKKKKKKKRAAARDPRVRPRV
617	14518	A	623	176	401	KFSMFIILWKAYYTLCVCVCVCVCVCVC VCVIMYLFISSQ/RRLCFLGEGKICSIS LTVLRRGSRVCV*SQDLPVC
618	14519	A	624	1	355	HSSGLDNLTALAHSHLCCGV/CLCFLVL VCVCVCVCVCVCLCVCVCL/CLYPGPQV PK*SKNSSTSCLLFHFTSARTICP/CC/ CVVFCFCFFA/CYQTCL*ILTSCL/AIC TASGVCL*ANKYSM
619	14520	A	625	2	400	HTRLIFCRDGVLLCCPGWLQTPELKSLL FSFGFLSLFFFFLERDPGSHGP\VGGGG PNLG*WKFWPLG*KQFSFLTLWRRGNT\ RGPPPPPPGLVFWF*KKTGFCFVAQAGL EQRPFGDQPVWASQGAGITGVP
620	14521	A	626	307	3	VFFRLPLTQGPGLFACFCPPPPCRFFFS FFPGSNSPFFP/L*KLNFWAFEPPPFFF FFFFFSILFKDRVLLCHPGWNAVV*S** P*TPGLN*SSHLTLPSGRV
621	14522	A	627	1	391	NPPPLGGAKEGGPPRARGSNPPYPYWET PFFF*NPKIFPGGGGHPVIPSFPGG*GR KFPLPREGGVPL/RPNFPP
622	14523	A	628	191	375	LILIFKTIFNFLILNFNF*SGGATQAGG QGRNLG*LQPPPPWLKRFSCLNLLSSW\

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						DYRGWP
623	14524	A	629	3	382	HHCQIRLFILLITASEVLFCFVLFFFET GPCSVTEAGVQ*CN/HLQPLSPG/PPTS AA*VAWTADVHHHAWLFVCLLI*DGSWS VTQAGVQ*RDPSSVQPPTPGLK*ASC\P AFQKCLDYR
624	14525	A	630	396	2	CRIENVLKKKKLEMSNLSEEGMLKANIG QKLSLLAPQQVVNAKESLLKEIRSALPL NTQMIRMQNSLSADMEDIL/VVWIR/DP TNFNIPLSQSIIQSNA/L/TLFNFMKP* RGEEAA*EKFDAISG*FTTFKERS
625	14526	A	631	47	392	LHSFFFLFLGKKIFTPGGGGGGQKPFF* NPPPPG*RNFFFLPP*KTWFMGPAPPPR KIFGFLKKKGFPLGGNL/SIGTPPPRGT PPPLPPRGGCYGGGPPPPPFIFFFRTFK NFSN
626	14527	A	632	39	382	LFFSPFFFKNFFFFFGRFFFWGGVAPIF PPPKKIFFSQFP/LQVFFFSPP*KKKFF FFPP*IFAPPKTFFSIPPPPFFFFFFFF FFFFFF
627	14528	A	633	2	213	LDKPGKHSKISSLQKI/HNGVCLQS*LL GWLRQEDCLSEGS*GCSEL*FYHCTPAW ATK*DPVSKKKKGFLK
628	14529	A	634	2	206	QENGMNPGGRACS*PRLRYCTSSWATER DSVSKKNE/TNKTTLLREI*HFVGGPNG KKGLLKTVKGGLT
629	14530	A	635	205	2	KRSLGLLAQI*/VQWGDFKTLQPLPPGV KQISRLNLLKKWDY*RGPSGLGKFW/IF L*KQGFPQFFRVVFN
630	14531	A	636	3	399	QVQQTPASCPLDSDLSEDEDLQLAMASM TFPKKKKKKKKKKKKRGGAP*KKTRGG PKK/IRGKKK
631	14532	A	637	122	373	VSNILWTQSLLFFFFFLKGSSLFVPQPG GQGLDLG*TKFPPRGLKEFSCLTLRISG NYGLAPP/HPG*FCFFIKKGVFPCCPGW F
632	14533	A	638	390	3	LLVLFLPQDGWSPFAFPHEQKLPEVSPK ANAAMLPVQPAKP*AHPTFFFY*FPSFR FFFARMG*SS\YFVPNLTKLSEILKGPI NDMREVFFPIFRLLILFFFGDRVLLCGP GWSSVVQ*L*LIAASA
633	14534	A	639	392	42	PSGPGKPGGKTFLRKPPFQEACKRQGFY PLFPPKPLKNPKAPQNRKNLGPICPPPK P/QGPLRISPQNSQSGSL*GPNKGNCFP A*TWGPPGAP*RGPPKGPPFFFFEKVME AMGLA
634	14535	A	640	390	1	LSFSEEGMSTAEAGQKLGPLCQ/TSQVI NAKETFLKEIKSVIPVNIQMIRK*NSFI ADKEKILVV*I*DQTSPN/IPL/SQCLI QSNVLTLFSSKKAERGEEAAEEKFINFS *RLRKEAASADREAAESYPEDL
635	14536	A	641	368	3	KKGGYGVPPPFSPPPGFLGEGSFLPPKI KVQKTL/SWPPPPPPGGKKKTPFFKKKK RKNFLTGFFFFP*KKGPFFFFF*CPVV* KFWGGGFKPIFFFFFF/RDRLSLCCPGW SAVV*SQFTPRV
636	14537	A	642	134	413	QKDQRNRIESLE/IR/PHTHNTLIFDKG VTGFQYGKDSLFNKWCWDN*RE/ITQNL

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						SLDPAHTTTNVNLKWTRCLKARP/VKTL VENMGENLRD
637	14538	A	643	2	436	GRVESINLPLGCRLFKKRDNIKCGQ\G* RAGGSLIHCW*EC/EVVQPLWKRIQQFL IKLNIHLPRDSTILLLDIDLDGHPKTSA LFIITHNCCFIHNHP*LEQPKCPSTDVW MHKPWPIHSMEHYSAIKSAAVWDNFKGI LL
638	14539	A	644	446	75	LDLLTS*SACLGLPKCWDYRSEPPRPAF NF*/STTK*SLWSSHKQDYICRFLLSYT ATQKFSTLTTY*SHLKTF*NAQMPRLYL QSLILGSIF*KSNLPR*FQCAAKAENH* *SDLYCQIMLFSFM
639	14540	A	645	318	1	KGVPRKCKNSYVGPPSGPPIK*ILFF*I F*DRISLCSPGWNARVFS*LPV\T*TTG VKKWWPLSLLNI*GYKGVPPRPGIFFFF FFFRDR/SLTMLPRLVTWVQVIFQ
640	14541	A	646	3	348	QFSSFFVLIYFTLPFMVSFCF/WCFSNL VLFCEIIFFLIFY\YYSLVLSFFYCLLV LFLSKLSFF/C*YLNITVFICSMTSFF* RIL/CCLNFIKTSFNFLL**FGMVLESC FFFFFFWP
641	14542	A	647	2	553	AILIPDKIDLKK\VTGDKE*NVTMIKGS IHQEDVTTINIYASNSR/APKYMKQKLK GKEKQISP*K/VVGIFNTPFSI/DRAPR QKINQEIEDLNNIIRQIDLKDIYRTFHP TSEYIFFSSAYET/FSKIGHKLKHKTSL NKYK*TEIMQSMPSD/HHGMKLENNE/N VGKLTNMWKSDTLVSDWLGAVAHA
642	14543	A	648	388	1	GPPR*SPPFGKPRGAVPQ/GGGGLKPPG PQGENPFFFKKPKITLGPGWGP/RNPPP LGG*KGKIP*/PPGGGGSNKPNFSPSGP PGKQKQNFFSQKKKKKKEKKKEKPES*C PGTSPQPVTDGSQAINASISS
643	14544	A	649	387	25	PGMRGGFPPFPLKNFFFPPGP*/MSGGG GGPNGPPPKKGFFPKNPPGVFFSPPKKK KIFFSPPPENLGPPRDFLKGPPLFFFFL QKNPGVFFRAGQGNPPQKLAKIFPLPPG GGGGAVRHI
644	14545	A	650	918	2	LGLKGLTIYKILHSTIADHTFFSSSHGT FAMTDHILGHKIHLSTFSKE*EIIPSTS FQ/HHSRNLN*K*INNKVNWKIPK\FWR LNKTLLNNT*TKE/GLKRHKNILS*TKN ITYQILWDAGKAVLRGKFIVLTT*IRKE ERSK\TTSFNIRKRNKKLIINIRTEINE IENRKSEKILN\TKSWFFEKKKSIKSIK TLARLNKRKRKETQIPKHQK*RRGITTG NMANKKIKRNIHEQPYTHKLGNLDNIGQ FLEKRYLPKLKQGEI*SGWAYIN/SKEM ESIINTLPKRKAQDLKMFSQSE*YQTFK EKK
645	14546	A	651	282	265	GVFFLKKRPTVF*KKKI*LGPHPQLKGP PGVFQ/HFPI*NFGISGRGDLFFFFFFF FFFFFFLFLRQGQVSVAQTGAQWHNQGS LQPPGLK*FS
646	14547	A	652	6	223	LYAHKFNNLDEMDQFLQRHNTPKLIQEE /HRLTVIK*IKSIVINLPKQKA*GPDGF SGEMYQLLKEEIIYNVF

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647	14548	A	653	128	337	FXFFFXXFFFXFFXXXFFFXXFFXFXFFFXXXFFFFFFFXXFFFFFFFFXFFXLIFFXFFLFFFFFLFF
648	14549	A	654	238	2	MAAASTTLLALVIISTTF*LPQVNGYIEKSTPEECGFDP\SPARVPFSIKFLLVGSPIQTHALDIALFLSHTRALPHTHT
649	14550	A	655	325	3	CSEHKKNVF*LRAKKTNNPNLKWAKDLNRHFSRENIQVAEKHI*ICSASLGLREMQIQTTKC/WHPVWKTV/WTILQN/LHTRLPYD/PAILLLGIYQRELKTCSHKNMYTSV
650	14551	A	656	3	1655	FFLGMESPSVAQAGVQRCDLCSLQALPPEFK*FSWLTLLSWDYRRLPPCLANFVFLVETGF\TMLSRMVLIS*PCDPPTSASQSGGITGVSHRVQPALLFFLSCLCVKMIVHAPLVKTCRPSTVGSCL/SVPAFWE
651	14552	A	657	519	84	SRVRCQSA\QMGGASHLGYSGVRDPLEEAVFPFSDLKLHAGITTTLFKAVRQGHLSGFAKDF*RPAEQ/GT*YTSKLA/STKQNILHEE*ITFVLLLPKHEGIWMPSVPPKPFLFFS*GMTNSGSAGILDFVPNHPSKDG*HYVLITSH
652	14553	A	658	38	383	EKCIFFFFFLERGFTFGGPPGGRAQFWFNKTPPP/HKKREFPALPPPGGGNNGLGPPARENLVF*KKRGFPLGGKRGLNPRPQGNPPP*PPKGG/GNNGGGPPPRQKK
653	14554	A	659	98	394	KPPGKKRETPSQ/NKKKKKKKKKKKPFFPPRGGKKNPFKKKRGG*KNPPPRGGGKGNFPPVMG*RGKNLPPPRKPLFPPPQGGGKN*KK/RA*KNSPQNFF
654	14555	A	660	214	567	GFSVINIGLKMMMMIIIILRDSLTVTQIGVQWHNLSSLQPPPPGFK*FSCLHLLSSRDY*HAPPCPVNFCILS/ERQFHHVGQAGLKLSASSDPPTLAPQRAGITVPSHQ
655	14556	A	661	463	392	S*HFHPSSSSSSSSSSVINYY*/FGLLLC/QVAHFYNSIDQQMIQSQRPMMLQSALAFEQIIKVNGLLILL
656	14557	A	662	205	242	GTGWQGGGLDG*QMTLGWPGSGVGGSAAP*GI/GPGLPGLPAPPAPSP
657	14558	A	663	63	351	QSETPSQFKKKTQIELLYEPAVSLLGIYQKERKSVLKKHYTPMFTAALFTI\VWDQPR/CPKYMKR*NVMY/HVYTHTHTMEYYSATEKNEILF\FATTW
658	14559	A	664	1	358	FFLRQGL/DSAAQAGVQWCNHSSQRAPPLGLGRSSH\PASLAGWSAVA*SRLAATSTFRVQVILLSQPPE*LGLQSCSITQVGVQQWRDLGSLQPPLPGFKRLSCLSLPSN*DYKRLAPPP
659	14560	A	665	10	257	GMNERGNITKEIKKIIWEYYE*LGTSQLDTL/ELNKFPERYKL/PRTNSQSIENMNRTITSDYISNFKRLPKKSPGLDGFTGEFI
660	14561	A	666	360	2	ENKKIFNSAPPPGSPFLFPPLWEIRPEGFLKPRVLNPPWPPN*APPFKPPMGPPFFPLFRGVRVGDPLSPPGLRLP*PGLPP\GPPG*PWGQNPTFFSKKKKKSWLDSSGFLEPNISVNF
661	14562	A	667	328	1	NLFAENYECPENKKKNFQKKKIHQIWQN

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						SEFMKVTEYKLNYQN/SQLYLYMPEKNT *KV/ILEKHPL*PQITKYFGEILKKDVL NLYTDKYKISLREVKGEQNKWNNVSS
662	14563	A	668	405	566	IHCQWECKTEQILWKTVWWFFTKLNILL PGDSAIMLLGIYPKELKMYIHTETCT
663	14564	A	669	218	2	LLMLESLMFVPPFPSFEKWAKL*IY/CH GAHANFLPSFFPSPPFFSLSFFFFYNRV FLCCPGWSAVVRSQLT
664	14565	A	670	2	210	NFGQEENSEMNSLCSYLHNLEKGEQTRP KASRRKEIIKI*AEI*K\VQRSNRENK* KKWFFEKINKIDKPLARLTKKWRT*ITI VRKETGTITKDPADTKRIMKEY/YKLLY MHSF*NLSRNLKRYREVIEKINERSGSL KRSIKLTNL
665	14566	A	671	200	3	SLCHLPHVASKATLET\GLVEHMW*DFF CFFETESHCIAQSGVQWCNLGSLQPLPP RFKLFSCLSL
666	14567	A	672	94	374	PKFRPQETTEQTSQFLQQINCKGRKRQG KRTYRLGEIQKQSQPMATFELYLD/H*F *LAKETL*LGAVAHTCNPSTLGGQAGWI TRSGVQDQPGQ
667	14568	A	673	312	3	WKMGQLPGRPQLPQLSQEKILSLNSPNV FKKKKLK***NILPKKKRPDCFTHKFYQ TFKEEIIPF/L/HKLT*EFEKKEILLKS F\YEGSVV*AAKLNADINKKTTH
668	14569	A	674	34	438	QLT*PD*HFIKYSTQQQKTFFSSTHRVF AKLGHNLVY\KANLNKFKWLQVISNMFL DRDRIALKINNKK/PSSPLKYLQTHLLL NDPRIKEGSKREIIKDFALNDNATY*NL WCL*NGTLRKVYTTKCLFRKEGPQM
669	14570	A	675	3	349	QKDRKSVRPSS*NPPLAVEKIPI/LKQN PERFNGPAFFKIAHGLTSSLVFCLANSN YERTHSRIIILSQGLQTGFAIKTFRKLL ASLANLALPPTINLLGELSI
670	14571	A	676	346	1	KMVKLL*NIVWKLLK\GLTEVPHGSAIF PFFIPIFPKEMETNVHIKTCTWAFPAAF FPMAKKKKQSGNNPTTDE*IQKK\W*TH IIDYYSAIKRNELLTHATSCNITLSKRS QTKK
671	14572	A	677	357	6	AAGDSELKPMFIYCFQKPMPL*IMLKST LLVLYKWNHKAWMTACLFTAWFTE/HCK PKLETYFSEKRFLSNIT*LMKASGHPRA LTEMYKEINVVFKPSNTTCTLHPMDQEV ISTFNSY
672	14573	A	678	401	155	YYSVAQAVVQWRDLSSLQAPPPGFE*FS C\PASWDYRHKLLTSGDLPASASQSAGI TGVSHCAQPLSLFVFFLTNQRFVAALS
673	14574	A	679	292	395	Q*KISFEMLLIITNVPGHPRTPMEMYKE LNFF\MPANTSIP*PMDQGIVLTFKSYY A/RNVFCKAIAV/DSDSFDGFGQSKLET FWKGFTI*DVIKNIDDL/WRGVKIPILT GVWEKLIPTLINNFEVFKASLEEI
674	14575	A	680	275	3	WPRQASLALNT*SIHIYIHTDMRTHAHT YIFGMKSVTQAGVQWHNHGSLEP*SPGL RRSSHPSLPTSGEHRRTPPR/LADFLHC L*R*GFTML
675	14576	A	681	330	507	GSV*PVNLIRNCQPFVQSGCA/SLHSHQ E\WYMCSPHPRHYLVASVIFILAILFFF

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						LRRSL
676	14577	A	682	390	43	HHLPIRYICLSISSILCLSFIMYLS/IY LSIYLSIYLSIYLCQRCQIPLVFLCLLL S*LS*IILILNFSCFFVGRTIVLS
677	14578	A	683	396	63	ADPTEIQRIISDYYDQRHTNKLENL*KM DKFLKTYNLPRLN*EEVETLIRFIANHE IALIIKSLPIKRSPVLGGFSVGF*HIDK EELTPVLGLFQK\IKKEEILANSFYESR
678	14579	A	684	1	396	EETLPLFADDMILYIIKKKQKTKKTTKE STKRY*N**M\NVFGKVAGYKVNTQKSI N*QYTI*KVKLAS\FSSSPQKNKIGINL TKEIQNVYSENYKTLKEIKDLNK*ESIP CSQIRRFNIVKMTVLLKLIYR
679	14580	A	685	283	3	NCVESSNTHLWEPSQKPLSSVSLTDVCP PMLSAALFAIA\RSYTLPTRSSIDE*IK KMWYIHTMEYYSAFKKKRIMSFLMPRME LKIFRVNKIR
680	14581	A	686	53	324	HCFCDRIRAAFCFYILDCPFFISITHKL I*IFFFFFLERESIFVPGVGGGGPNFGS LNPLPPRLRRFSCLTLPRGGDYGLGPPC PT/NFCVF
681	14582	A	687	39	208	NIFFCREGFAMLARLVSNS*NWPGKVTH IHNP/STLGGLGGRITQTQEFETSLVDA GA
682	14583	A	688	47	341	SSGRVFVLFCFFETGSHS/VLFRLAYSG GISAYCSCHLLSSGDSPISATR/GTTGM CCSAQLGFCVCVCVCF/IFVF*VKIGFC HVAQAGLELLDSSNPPTS
683	14584	A	689	229	1	GRVDGRQIACQEFKARLASQSAGITGVS HRAQPFFCFC/LLFVVFEMGSHSVTQAG VQWCAPGSLQPLPLRFK*FSC
684	14585	A	690	339	1	KKGPPGGPTKPEGGRFPRGPPGGGKEVF PPPPPGGKGEKKRGGAPPPFFFLKKKRK SGKGG\N*FFPPGGGKKGGQKKKKRVFF PKKKKKKKKKALSLSLSLSLSLSLLG
685	14586	A	691	372	0	YDYLYIKKL*N/LREKIDKFLDTYNLSR LNQEEIENLNTPITSNKIETVIKSPPT\ KQKSPGPE
686	14587	A	692	117	297	APLLESSSASYLHFSN*DLQMAH/KHTK RCSTSLAFREM*IKTTRRHHFTPTKMAT SKRHT
687	14588	A	693	122	322	EQTNSWSIDFFFQRCHSNAMGEKNCLFN KW*WDNYVAI\AKKMKLSLFKPYIKTNS K/WIKDLNIRAKT
688	14589	A	694	21	342	RSHFRHLNEYYATQQGNSDVHPLLIHSN ISTAIIWQLQRQERRKEKRLKEVKNEKA LKEIFFLRGWVLLCHLGWSPVVGS*FIV TLN\FGLRQSSHLSLPSSWDYRPV
689	14590	A	695	2	343	KFVPLHSGLGNRSQKQTLSQRKKKKGGV FVAWAKVQWHNHG*QGP*TGLRQSSCLS L*GGWVKL/PGGRHHAWGFHHVKKVGLE LLTSDDAPSSASQKAGITGMSHTAPGPK NLV
690	14591	A	696	336	3	IPPVKSPKFPILLKKKKFSLFCFSGAPF PCYSPPRAQKKGW*KIFSPPPK\QKKPG ALFFSPKPAFFPPPFKKKKKKKKAKEGH YLMIKGLIQQEKIILNIYASNIGARRRG
691	14592	A	697	374	2	AFY*KKMVSRTFIAREKSMPRFKASKDR

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						LTFLLGAGNFKLKPVLVYHSENTRALKN YAKSTLSVLYQRTTKAWMTSHLFTEWFT EFFEP\TVETYCSEKKIPSKILLLTDYA PRHPRTLMEMYSC
692	14593	A	698	361	3	PQMCPPPPR*QGIIFL*L*THCFFCTVK ARLFLFPPF/S*RKGGFFFFE*RKFFKY FGWELFQIRFKVFFFCDRVSLCCSGWSA GART*LTAASTSPAQASLLPLTLPSSWD YSHVLPRLV
693	14594	A	699	75	362	KDCAYGICSKKQKGFCLTQTGAWQQYEE I*GLET/GFSRSVHSMGQRRYWDYRHAL THPANFVFLVETRFLHVRQAGIELPP/S SSQSGGITGVSQ
694	14595	A	700	2	277	FFLYTSNEQSEKKI/RETNWFIITSK** NRNVNKEI*DLYNENSKTFLKEIKEDLN KWKGILSS*TEKLNIIK/PTAI**FNAI LIK/IPMVFDK
695	14596	A	701	1	407	GTRKHFSKEDRQYHKSLRKQIKT/TVSY CFTPTKLTTVGKTANSK/CWAGCKVIGT LIHCQ*ECEMVWLLWT/SVQQFL/RNVK LYETAISLLGICTREIKTPLHIII\IIA KKWQQLRCLSTDEWINNM*YIHTMEYYS A
696	14597	A	702	209	3	SLNRRLSFFFY*RQGLALLI/EPGWGAV ARSWLTPASN\FELQRSSCLSLRSSWDY RRVPLHRVSLRFSC
697	14598	A	703	308	3	TTGLKRFARVGPPKCWDYRCEPPGLATS SVLKAFQPIGSVPPRLSRILSFM*NQ* YRMLITSTKYFPRMVSISRPCDLPALAS QSAGITGMSHHAELVPLV
698	14599	A	704	603	2	PLPP\GLQVESP/CVSLPSSWDYRHAPP RPANFSVF**RRGFTMLAKM/VLIS*PC DPLASASQSAGISGVSHHAWPKQT*LLD TDKTEGIFLTNHLLRIPPPMFYQYILIK VLESVKETKDKRKSVSSCTLYRCL*ILF IS*AYIKFTTFFFF\ETDSRSATQAGVQ WHGLSSLQPPPPGFK*FSCLSLLSSWDY RSMPPRPA
699	14600	A	705	3	366	ARVTYYSGKKEPFGYLGMA*AMISIGFL GVIV*AHHIFTVGIDADTRAYFTSATII MAIPTGVKIFS*LATLHGSNMK*SAAVL *ALRFIFLFTVGGLTGICLSNSSLDIVL H/DTYYVGAHF
700	14601	A	706	358	3	GFHHVGQAGLKLLTS*SARLRLPKCWDY KREPPHLAPDRKYFSPLVFARDNFVPQG P*\HVWINICLSQVKAATGIYPGEAGAL RNRLHPH*RIFWPQRPRVPIKSPWTLRV ISTLCSC
701	14602	A	707	358	67	QLSSTIWY**KN/RIDQWNKIAQNTSVH RKLISDKVTKPIQWSKDSLFNKECWNN* TSICKK/LSLDSALTLFTKTNSK*ITEP GSVAHTCNPTTLGG
702	14603	A	708	34	363	RTVFFFFFFFFFFFPKKTPFFFPGPRGG *IPPPEKKIFPPVFRGKFKKPPHLDPGG GNFPRKPPFFFLGP\SFFFLGKTLGGGG WIPFPPPWPNLFFKKIFWGAGGPSPF
703	14604	A	709	1	380	STCKRMTLDSYFTPYTKINSKWNKDLTV RGRTIKLIEENIGVNLHDLGFGSGFSDM

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						TPKAQAKRKIN/WDFIKYLKFCA*EDSI ERV/N/RRSTEWEKIFANHIQ*GN*NIQ RILKLSKL*ARLKWAEDL
704	14605	A	710	382	30	PGTTGVHHHTRLTFVF/CGRAKISICWL VWNS*AQSACLSLPKCWD*EPQHPARFV SFNTRSGIPIISTNPSLSLSAFPSQGFV FLFPHFPASHPETALAEFFLGTFSLSPP GPFTPAS
705	14606	A	711	1	377	LLVICGMQMKITVRCN*TLNKIAIIEKK TAKCC*HYGGLKTLIHQWCKSNMVQPLC KTV*QF*KKLNIQLLYLLK*KKAYIHPS NCTQMFIA/ALFSVLAPNWKQSAY
706	14607	A	712	1	390	LKYKIMLGMAAWACNPNYSGGPGNITA* TW*AYMALTRLEPGRGDHTAALQPGRQS TTPF*KKKAVPFRA/RPVKMREREI*KP FSPE\RTYSCAQEGPGRTFGSAQDLEAA GGRGHHRMGAVWQEPHRLLG
707	14608	A	713	2	393	KVRRQIINVDTATDSIGIKWIIWKHYV* LYANKFNYLAEMDTYVERYKLP\KEIDV MNSLVPAKEIIVVVKILLTKTPDPHIFT NEVYQTFKEYY/PVLYKLFQKIEDERTF LSSFCEAGINLISICKRFFF
708	14609	A	714	219	1	PRPGAVAHACNPSTLGGQGGRI*TQSSI IKACCLIHDLAIQTQKQMT\WPGAVAHA CNPSTLGGQGGRITRSGARDQPSQHSKT PSLLKIQKKLASVVAGACNPGYFENYIQ KLLRGPGT
709	14610	A	715	381	126	IIAGGGGVCT*SQLFKRLRQEDHLSPGV RGYKEL*SYPCTLAWVTE*DPVF*KKNY /TLNTSPKETNKK*GVRCIKTGKVLIFV AAG
710	14611	A	716	417	1	CYCCWGATNKILLLTDNASGRQIVLMDM YKKNNVVFVPVNTRSFVQLMDQGIILNF KSYLRN/TF/HKCIAVINSNSS*ESGQS KLKALWKGFTVLYAIQNICDSGQVKMPT LTEV/WKEVILPLMGDFVRNRTSEKQNY KLS
711	14612	A	717	406	122	MFSRDAVSLCCLGWS*TPELKLSSSLSL PKCWDYRGEPPCSAAKDF*IIRKR/HSC RNIIRNSDAWQR*TTLVSYDRNPP*FPS PPPNSPLCPAA
712	14613	A	718	535	1	HNLNKIV*NLHVENYKMLVKDKKT*ISC LWVRR\LVKIPVLPKLFYSVIVFPIRSL VRYFIEVCTFTLKCIPKEKDLKQPNRF* KKKKKVHLPFIKVYY\KLQ*YIATVIKT VWY/W/YSKIDKAKWYKTEKAEV*PHEY DQLILAEVQINH\NLFNKCY*SN*TTIG KNMNLNLSFTSYT
713	14614	A	719	255	1	GKLQPNKGLISLIY\NL*KLVRKSNPKE KWAKGMNR*LTEKGIQIAFRHMKRCSPR FIMKAMHIITTWSYHFSSKRKTRIQRLT
714	14615	A	720	381	0	KFIAVNEYIIKEIDLPINNLTLYLKEL/ EREELTLCKASRAEVI\KIRAKIIRELT PIRKTDNQSWFFLKIHKIGQ/PFKLD*L QKKKRVREKVPITKLRYENRVITTNFTE /IKRIIREYYDH
715	14616	A	721	3	381	IYREWRDLTRDGTYQGHHAPPGEKG/VC RYGIILFITSEGFFFAGFF*PFNHCSLA

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						PTPQLGGPWPPTGITPLNPLKVPLLDTS VLLASGESIT*AHHS\LIENNRNQLIQA LLITILLGLYFTLLQA
716	14617	A	722	56	455	KTIINIKPPAIIQYQTPLFV*SVLITAE \LVLLSLPGLAVGITILLTDRNLNTTFL DPAGGGDPILYQHLF*FFGHPEVYILIL PGFGIISHIVAYYSGKKEPFGYIGMV*A MISIGFLGFIG*AHHIFTGGIA
717	14618	A	723	398	3	HQLPVFWQYNKKAWTTRPLFVDWLH*CL VFEVSKYPASKGLPFKVVLMLDNAPD/H PTQNSMSS/DSKGIEVIYLPPNTMSLI* FLDQGVIRTYR/RHYPQYSMQRSIRPMQ EISNKENIIKVWKNSTTDDAIVA
718	14619	A	724	318	14	TPPFFLNIPNLFFLKFPSPPPPWFLTKS LFFPLKLKPKVFGK*SLSKF/CPFPKFN PKPQKKNFFFPPPPFFFFFFFLRHNL/ VCHPAWSALAPSQLTATSAS
719	14620	A	725	2	371	APRCKRFSCLSLPSGWDYRCMPPRPVNF F/SIFSRAGGLES*PPMIPPA*A/FPK/ CWDYRHE
720	14621	A	726	430	97	PKKNPFWKRA*NGGAQKDVPLSLP/SGW AGGSPWGPGF*PPLGPKGGPPFSKKPPG GVGPFLMPPTPEGGGGKLA*PWPPGFNP PVSIFLPRPPRAGGKKGTPFPKKKKKEK
721	14622	A	727	406	1	GGAPPPPFFFFFFFIKKGVFPF*QEGFFF PGLKN/LPP*PPKKVGVKGGSPPPGGFF FFFKKKVFFFFPGLRTRAQIKVPSTLVG QG*KILPPQVSQEGGVKREGPQAQLFFF FFFFEMESHFVTQAGLQWRDIGSP
722	14623	A	728	98	368	KPHKNAKCPIRVAIVADMENNKYW*GYG EMGTL/LHY*WEGNIEQPWE/T/VWQLL EKLNTELPCDPATPLLGIYPKTLESRDS NRFFIFFFSF
723	14624	A	729	19	404	VCVISICLATEILFFLHTRPCVCIYCVC VCVCLAVWGTLCVYVCIESCVCVCFHLT GVLC/V*VCVISICLATEILFFLHTRPC VCIYCVCVCVCLAVWGTLCVYVCIESCV CVCFHLTGV\CVCVCVCIESSVCVCPPT CGTVCVCVRPPGVLCVCVCVCQAAWVAV SMCLTP/CPC/VCVCVCVCV
724	14625	A	730	432	12	FFHKPNFPAARKGRLFFFIYPSKCLISP KAL*F\FGGVGPFFPPPKEGFFPKVPR* CFFRPLIRKKQILFLPPLNLAPPGVI*M /PPPPIVFFFFFFKRDRVSLYCPGWSAV A*S*L/TAVRTRGLK*SSCLSLPKCWEY KCEP
725	14626	A	731	332	7	NKTRKEKFLTRSISRF/CFPPFPLKIFF FPLRA*FFWGGLPQIFPPPKKVFF/PKI PKVFFKWPPLRKKIFFFFSPLILGPPRV LLKGPPLFFFW*VFFF*DRALLCHPY
726	14627	A	732	70	294	FLRFCVETAINKIAIILANF*NFL*RWG \FTMFPRLVSKL*DSSDPPTSVSQSVGI TVVSHHARLNFFYYQNSRR
727	14628	A	733	1	355	FLLRHILLCHPGFCSVATAYCSRDPGSS D/PLPPQAPLPDQ*PRLQA/WHRLAPPH SANFF**RQGFTVLARMVSISQPCDPPH SGPQGA
728	14629	A	734	50	395	IPGLTRQWLLDPCASPSTPPYT/P*VQP

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						STPQNSSPSPKTHNQKGLPMPLSPTPKP STAWKKAILEHTSSSSSSSSSSTCRNR NGYTYTVPEHRPARGHTASQTRKQVLAA THKP
729	14630	A	735	451	0	GPSSSPTNIPTPVSWNSFK*SSQVAGAT GTCYHAWLIFVFSVEMDFY/HPVA*ASQ SAQLCQYFMIFLRQGVSLCPPGWSAVAW SKLTT/CLCLPGSWDHRCALAHPANFLY FWWR/HSC
730	14631	A	736	2	477	PSHVSNKRLISKIYKELIHLNSKKVSNP I*K*GQSLNRDFSKASFLPP*KC\QMVN RYIKRCSTSLIIKEMQIKTTMRCHLTPV RLAIMKKSKDNKPSLVWDC*IRVLHLF/ CK/WICQYVQL/FWLLLSNFLVKQPF\Q LPAPPNSPTLG
731	14632	A	737	3	2344	AAGGPTAQSPAQLAGRALRLARWRAVAV GACRPGAGSPCSVQGGAASELSPRPQTW IGSLKP*TFGAAAG*AHRGCGGSALLN* ATPRPAPGLPASPTSSQALPAPLGAWGH SDHQPRAFP*SPQASTAIRKEKKQRAQP GRASVCPASNPFISSRALPVLQHGPPAI SGAGSAVASQAPGSS/GSHAESGSPALA HTP*GS*EPHSLIVESTRKS\ELPSSSQ GRLLLPLLTPGVAS/PVGTKLPGATAAT AGALHQPGLRLSSLQGVGGAKNKQTGCC CLQLPTTGLPQAPGALRPLGRLGPAAAP GEHRQRTSPQGTVPYGGIRQGWEQPQRL RAYGTALPPPHTPPGSSGP/RQAPGCRG SGAGEAAGIRDTGGGGPGRRAPCSQASP GRGGWQAQVGCETCRGCAQSS/GGGAVQ PGLPRKPYPHS/AR*ENLVVPFPCSPRT RAQEPQTQGEE/GVEGPQGSPCAPGAVR GRGIQLSSEPGKLARQG/PASGDGP*EG TGQEPSQAFSSARHPWPSEARMPDTAIC RNQAQ*LQLTSSQPSMGPQLRKSLPATP QPNSYWDGGNSATLGRTTNTRRHCGMSN FGARGDLLGTVPT*QPLMQRRKEKPRVG GEPVQSHTVCG*\PAGVSRGWPLRPMLP ERWRPLSASSGSQGRPGLHPPSLA\CGP SSSPHRTCSP/GLDPGLPDAGSIKPPSL VGAGQGAGST/GLD/GPGLSLLSPGKSL LPPSSPATGLSGLGWAQSAF*SLLTVA* WLNPVPNGPSDTADCTPAQAPTAPAMLE NQANKSDFFFH
732	14633	A	738	37	450	NQKKWPPPRSSKPARPLFFFL*QKYIKD P*KTYQGCFFFSPPPKKKNPPPPKGGGF FFFF*KKKGGGPPP/QAKKRGGGGPPQK GGAKKNPPRGFTRVFKGPFKKRGPP
733	14634	A	739	2	426	QEFVLGSAPGCGCWVGGEGRVSSPWGDR KVGGPSNSRHWNKGAGPSCPPGPSLAAG LPGRRAGSWAPVLW\PGPP*GLAQLPSP LW/PPSPPQEREPPLPD
734	14635	A	740	21	392	AQEFKSSLGNMERPLPYQKKKKKKRPGG GA/RPLETQPFGGPGGGEKKGGKKKTSR P/IRGKPPFL*KKKN\CLAWGGGPAL*P QFFCGVGEKKTFNPGGGGLGKPKPPPFT PTRGKNQTPQKKKKK
735	14636	A	741	1	408	PSSQGG*EAGG*LEPRSSRPAWAI*RDP

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						/GSPEKGKKKKKKKKKKKKKGGGGFKK TPGGAKIKGGGEKKNFFFKGGEKKNLGG ILEKKLFFGGGKNGEKPPKKKKGLREKK KF*RGKGGKKAENPGGKKIFQKKKK
736	14637	A	742	394	1	RDPLEEAVCPFSDLQLRAGRTTALFKAV RQGHLSLQRLLRLFVCLCPAPRGGAYRS RQASLNRGGFHPVRAYLLLCLPKQASEM AGAPSPA*LPPCSLISDCCASNQ*DSVG /VGPSEPGEGYNLVVRRFLS
737	14638	A	743	384	1	FTGPYLKNNGYSFLFLYPPPSVLGNWQP PHPGRVFPP*DVNFNQWIFVSL/ISSLK DEPAFSSTLYSF*QHFFFITYLPPP/CF FLIESCSVAQGGVQWCNFGSLQPPPPGY KRFSCVGLPSSWDYRCV
738	14639	A	744	2	410	TPLNPLEVPLLNTSVLLASGVSMA*ADH SLIENNRNQIIQALVITILLGLYFTLLQ ASEYFESPFTISDGIYGSTFFVATGFHG LHVIIGSTFLTICFIRQLIFHFTSKHHF GFEAAV*YWHFVN/VRGLFLYGSIYW
739	14640	A	745	393	1	PPPPPRGRGSPPPPFSRKGGPKGKPPPP GNFFFFFKKRVFPF\CPGGFKS*V*GVP PPFPPKIFKFKGGTPFPGLWSPLKSKKS QFFWVPKPGERKKLFPPFFFFFFLRPCL SLSPRLECSGAISAHRNL
740	14641	A	746	2	290	KNLCRENYKYE*KKLKTMKDLCKEYYKV *MKKIKENM*KDKLMNFK\NNIKISTLI KVIYKFNAIPIKIPMTFFAE\LK*ILKC V*NYKRP*IVKAI
741	14642	A	747	59	364	CRFFFFFGLGGGGGGGGGPPPFF*KNP PNPPKKIPNWGFFFRGPGFAPKKKKGPF LGEPPPWGAPLYNPPPPFGGGGAKFPPI FFPRAGGPQKRVG/RPPPPPPPPPPRPK KKKNLH*LECVEGTEEPPTRPPTRP
742	14643	A	748	2	371	SSCLDLPKCWDYRHELLHLAHWLVLGIF LLLLFCFVLRW/RSCSVVQTGV*WSDLT SLQSLLP
743	14644	A	749	339	198	IADMEKV*AF*TEHKTNHISLNQN*I*S KVLTLFNSMKAERD*EGPEEKFGASTGW FMRFQEISQLYN/IDV*GEAASADGEAA ATCAEDPAKIPDEGGSPK*YIFNVD*AT FIRDLSWIFCTSCCSFSISTCCFTLHVM L
744	14645	A	750	249	2	KIFKPPAFPVSFPPFPL*DSSSPPEP*I SGGRVGPI\FPPPKKGFFPKNPPGVFFS PPLRKKILLVPPPLNLGPPKGPLKRPP
745	14646	A	751	1	288	VVNHMTDEGLVSRIY*QPLQL\KRKTEN PVQKWTKCPNRRFSEEDEQMARKHKQGW PASRAIRGTQSKIIMRCHFTHTRMARIK KEKEAGPGGSCL
746	14647	A	752	494	2	ETGSWFGPQRLEVQVVWIKSSLQP*PPW APVILPPQ/LSSG*DHRHVPSRPG*LKK KFFL*RWGLTMLPRLLLNNLPTSASQNA AITGVSHCARSASVFLILRQGLWVWEE/ GAQW*SALSHLPV*/LSR*WCQP*PLG* DSGSGSPLWRRLAYLPLCALWKEVTMCS
747	14648	A	753	1	533	YLSPRLECSGGITAHCN/LRPPGLK*SS QLSLQ\SSWDCRPAPPRPAARLIFFCRF EEGRRSHYVAQACLKLPGS\SNPPTVA/

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						FPKCWGYRCEPPHTGLCS/GLSEFGFCL WWGACSRSSHKNPGCGTA/CPAVFLHSV GYASHPSSTSRTAFTLGWVLVFVFRDKG LTVFSQAGSTVGVILG
748	14649	A	754	1	346	ELSKSTLPALCGGNDKAWMTAHRFIAWF TDYLKPTVENYW*EKKIRLKVLLLIDNA PGHPKALLEMYTEIHVVFMPADTTSIL* PTHQGVISTLKFCYL*NTFHKVQ\CYID SDSS
749	14650	A	755	1	323	EDQTSHNVLLSLNLIQSKALMLFNSMEA E/R/SEEAVEEKFEASRE*FMRLKERSC LQNIKVQGEEASADGEPPACDPEDLAEI TDEGDCIK*QIFIVDKTAFYSKKMPS
750	14651	A	756	1	344	ARQQPGDPARGGGRGRRL\QPRQAASFC TGTLARARHTCEGAGVLRRPADKLASLN *HFSQKKKKKKKKKKKKKKKKASSSSS KKKKDSSYSSSSSRGGSSSSSSSSPPPP PPP
751	14652	A	757	119	317	NRYFPFLRVKKFPWVEGPFFFLR*SLTL LTLVAQAGLQWRNLSSLKSPLPGFKPFS /PSA/LSRWDYRR
752	14653	A	758	2	363	CILAIVKSAINRIAN*YI*KCSMSIITK RQA/IKRKNKTRRYQLIPVRMTLIKKKK RW*RCEEKGRLAHCWF\ECK*RQPL*KT K*RFLKKLKLP\FITAIALLDIYPKQIK SE/CKKH/CAILFIALFTIAK
753	14654	A	759	358	1	KADFCFPPTFSPRVKKIFPPPFPKKWG* KGP/LPPPGENCVFFFFKKKRGFSPLGG GFFYFFPPGFPPPWPFKKLGFKGLTPPP GPPQKILVFFFFFFFFFFE/DGVLLCRP GWSAVAQS
754	14655	A	760	316	2	KATRSQDIRRIQVKLKEIEPQKPLQKTN KSRSYFF*KH**NRTLTRVMENKREK/N EIDPIQNHKEDITTDPTEIQTIRKYYKH LYAHKLKKLEEVDKLLDTNTL
755	14656	A	761	3	321	FPLGLWGSLGAKPEGQAPLYPPTLSKRV VPLC/DKGRSAVTFNTVYSSGSSRVVFP PPCM*IYRLCIKGRSSDPEQKKKKKKKK KKKKKKASKKKKAPKDSSSPKT
756	14657	A	762	315	2	KTERW/VFEKINKMGQS*DGLTKKNREN /V/QINKIQNERGGLSTGSTEIQRVIRG FCEPL*AQILDNLEKMD*FLQPFHLPRQ NYKKKKII*KKPISKVIELVIKNL
757	14658	A	763	226	329	NPTTLEGQGGRISKGPEF/CSRDEVSPC WPGWFQTPDLWRSVRLGLPKWWDF/RR* APPPGLNLFFRMLSTHGSW/CQHPCFKF PTSAFQYIYIYIF/SFLSRSFTFVAQAV VQWHDLGSPQPPPPGFKQ
758	14659	A	764	335	1	QSQERPDSFQVMNLTLPRAPSMFLVSPR TELSKSP*\PPAFLCPCVWPHSTLLSQT LKY*IKYP*SPTPFPSFVLF*RDRVLLF HPGWSTLAGS*LTAASNSWAQVTLL
759	14660	A	765	100	310	HFGRPKRENCLSP*V*DQTLHTHTHTHT HTHTHTHSRSENGGMRLTPHIPERVRW\ GIIC
760	14661	A	766	315	3	IFPNPPRIFIQNPHPFLFGFFPKKKEGE KNWAMETPRFSPPPLGGKKAPTGFPPPP IGF*GPKPLIKGRGP*/PP*KNTKIFFF

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						FFFFF*DRVLLCHPG*SAVARW
761	14662	A	767	1	309	KEPYKLTELHNEIRVACGHLSKKKKITW VSDS*ASCPSKTRGNFIGPSAGSRAPSE KLEAHFHGCGSVNRVHLT/CK*HKRRPL GVAHLEVSDQKSGRTSLALD
762	14663	A	769	1	316	GRAPPPPPPPPPTPRVHTSSKSESEPER /DGRE*EPTRSLERL/LFFASYFCLEAR QSTSALPPLPLSPRSGPT\VLLCPSPPL PGERPPNPTKLSREKQTKQTHRAR
763	14664	A	770	2	366	AREIIILTF*QMITFLNTKGRT*SLILA SLIIFIATTN\LLGLLPYSFTPTTQLFI NLTMAIPL*AGAVVIGFRSKIKNALGHF LPQGTPTPLKPILPIIETIILLIQPIAL AVRLTANITA
764	14665	A	771	2	364	NAFPVISGAWTEYPLSHFIQRCRQKKE/ LNGLQIGKEEEIFLFKDAML*IESPKES VQKRLDVIYKFSRIAVCKINIQKSNIVV YVWNTQFENEVKTI*DPQ/DIKHWGIIL SQRKKE
765	14666	A	772	3	376	HEPLGKLKLSLLFILATYSLTVYSIL*S G*ATNSNYALIGALRAVAQTISYEVTLA IILLSTLLRRGCFNLSTLMTTQEHL*LL LPS*PLAII*FICTLAETNRTPFDLAER ESELLSC/FNIEYA
766	14667	A	773	3	350	HEFFFFILKMYLGQAQYFICFLFFFLGF HLK/HKSCSVTQAKVQRRHLGSMQPPPP GFMQFSVAEIKDVHHHAQLIFYIFRIFI F*F/NFLRHSLALVAQDGVQWRDLGTLQ PLPPPG
767	14668	A	774	1	359	GTRYAAMLSALGFIFLFTARGLTGIVLA NSSLDIVLHDTDYVGAHFHYVLSIGAVF ALIP\GFIH*FPLFSGYTLDQTYAKIH\ FTIIFIGANLTLLPQHFFGLSGMPRQYS DYPDAYTTW
768	14669	A	775	2	369	ARGSICLRQTELKTVIAYSSIRHIGLVV TAILIQTP*SLTGAVILIIAHGLTYSLL CCLANSNYERTHS\RIIILSQGLETLLP LITF**LLARLANLALPPTINLLGELSV LVTTFS*ANIT
769	14670	A	776	2	353	ARGTGA*VDS*LTTLHGSNMK*CAA\LL \WTLRCKILFTVRGLTGMAITNSTLDIA LHDTYYVVAHFHYVLSIGAGFAIIRGFI H*FPLFSGYTLDQTYAKIHFTIIFIGVK ITFFPQ
770	14671	A	777	3	353	HEGLHL*LPKAHVETPMDG*IALDAGLL RLRGYGIIHVTLILNPLRKHILHPFLVL SI*GIIITSSICLRQTDLKSLIAYSSIS HI\SLEVTAILIRTPL\SFTGADILIIS HGLTCS
771	14672	A	778	367	2	FCPI/CPNQKFMGVGAVGPALYPNPFGG LGGLV/TPGAGVLNPAGPPG*TPPPPKN PNLGGGPALFFPPLKGLGWKIALTPEAK GSINPNSPPALPGGGPNQTFSKKKKRKK LMLVYSIELTSRA
772	14673	A	779	3	432	HEPLHWLSSCVCPACVCVCVCQ/CLWLQ VGVQ*CNYSSWQHEPLH*VHTRVYVCVC LCHSVAQAGVQ*CNYS/CTAACNSW
773	14674	A	780	213	466	DDILPVWNYSISFLFFFENRAFFLPPGW

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						GAGTQL*LPAASN*GPKGPSRLTLL*W\ DNRHGPPC/LDNFIFLQKKNLTLLPRLA LN
774	14675	A	781	304	373	R*VFFFFFLKKEFHFFPQAGGQNQEMG* LHPLPPGAG/RF*CLTPPHSWDNGEGPP RPPNFCFFRGNKVSPCGP
775	14676	A	782	389	1	PFPKN*CRVNSRPNVKHKTI/QLLEGNL GASVDDLEFGDDFLDTIPKVQSMKERS/ WDFIKIKNVCFAKDNVKRRGPATNWKKI SVKDLSNKGLLPKIYEELLKLNNTET*R LT*KWSKVLNRQLTRETRA
776	14677	A	783	1	383	GTSP*PLTGALSYLLMTCGLAM**HFHS ITLLILGLLANTLTIYPGRGDVSRQSAY QGHHTPPVQKGLLYRIILFITSEAFFFA GFF*SF\YHSSLSPTPQLGGHWSPTGIA PLNSL*VPLLNTWRLL
777	14678	A	784	1	389	GTSIVIPTGVKVFN*LATLHGSNMK*SA AEL*ALGFIFLFTGSGLTGIVLANSSLN IVLHDTYYGEAHFHYVLSIGAVFAIIGG FIH*FPLFSGYTLDQTYAKIHLT\IIFI GVNLTFFPQHFLGLSGNA
778	14679	A	785	374	1	ELNAYWNVMNLQNLIWNAQPLSIMQIFQ ILIKSQIQNTLVVSISDTGYLPGIDKWN CI*LKILCIVKVTINRARMPVIDWENTF STYTNDKGLIPKYKELKHS\KQTNNLIK KWAKGLHSHSRA
779	14680	A	786	1	363	GTRLYHANTN*KKLRVAILISEK\TDFT VKKIRNKEGHYIMIKRSIL*EGITILYV GTPSNRVVNYIRQKLIKLPGEIDESTII LRDFNTPLSVIDASTRKKISKNIVESNN IISQLDLID
780	14681	A	787	1	361	GTLFSSERKNPTWVSLNQKLEMIKLIEE GMLKAETGHKLRLLQQ/TSQVVNAKEKF LKEIKSATPVNTRKTRK*DSLLADTGKV LVACIED*TSHNVLFS*SLIQSKALTLL NCMKPERGE
781	14682	A	788	1	352	GTRNYAKSTKSKLYRWNYKAWMTAYLFT AWCTEYFKPTVETYCSEGL/SLKILLLI DNASSH*RALMEMYKQINVVFMLDNRIS LLQPVDQ*VILTFKSYLRNTFHKALAAR DNDSSD
782	14683	A	789	365	128	PLDQHGETPLLLKIQKLARRNGAHLYSQ LLGRLRHENLLHPGGRGC/SHCTPAWVI E*DCLKNQTKTKAPRRVSISHSA
783	14684	A	790	217	257	WSGGVAHPVIPATQEAEAEELSLGGRDC SELRSCHS\CTPA*VTQAGVQ
784	14685	A	791	2	363	LAILHQTVS*FVHAKEKFWKDLL\KSAT PVAI*MIRNLNSLYNLIMETV*VV*KED QTSHLIPLS*SLTQSKALIFFKAMKTDR GKGAVE*KFEATRGWVMRLKEKFCLS/H HIKVQG
785	14686	A	792	2	362	GQKLGLLHQTVSKFVNAKEKFWKELL\K SATPVDI*MIRNRTS\LISDMETV*VV* KEDQTSPLIPIR*SLTQSKAVNLFRAMK PVRGKGAVE*KYEASRGWFMQYKEKSC/ RMCNIKIQG
786	14687	A	793	2	360	ARAGSTMAFKNYAKSTLPVLYKWNKKA* MTAHLFAARVTKYVKS/YCLNKKIPFKI

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						*VFIDIVPSHPRALIGIYKE/INVFMPA NTTSTLHPTDQEVISTFKCYYFKNRFRK AIQLPYSNSY
787	14688	A	794	2	359	AREKLYLSILTPLQRSLVIAFAATELTR YYILFETTLIPSLAISTR*GD\QPERLN AGTYLLFYTLVGSLPLLIALIYTHNTLG SLGILLLTLTGQELSNS*ANNLI*LAYT IAFIVKIP
788	14689	A	795	157	365	GIIEEKGYLPEQIFNAKCSGMISAHCSP RLPGSSYSTSA*TDF*CQVQWYDLSSLQ PPPPRFKLFYLSDPSTWDYILAPP/RPS **FVFFVEMGFRQTPE
789	14690	A	796	224	372	IFFIFIFIYLFTEWRQSFALVA\QAGVQ WRNLGSL*PTHPPPRVKRLSCL
790	14691	A	797	482	1	NSFFFFFFLFPEAKDHKDFPSPPFPVFK KLKGFC*APP*VQKPVFYLKSF/CLKDY MLSFPESKVNFPSPPFL/SPSPLFMVGD PPLPPETYFSFCF*DPHSINFFLPPGPF LFHFFFFLRWVLLCHPG*STAV*SLLTA TS\VK*FFHLSLPSSWVYRCTSC
791	14692	A	798	1	415	NLGGGGCSELRSYHCSPAWATE*DSISK QTKTL/NKDHTRAGWERA
792	14693	A	799	2	401	VQTGFHHVGQAGL*LLTSGNPPASAS/Q SAGITGMSHRARPQ
793	14694	A	800	73	307	PMALEHHGCGMCLDFLPTFGKSHCFVLR CAEMETRSFLPSWSAGA*Y\CLLQPPPP RFS*LRLPSRWDYRHLLPCPAN
794	14695	A	801	87	401	SLIEIWTLKKSTCHNLYNVVLS*HSLKA IVLARHS/VESLTHVLKMCLV*NFVFAF S*RSLCFFLKISRPVVVAHVCNPSTLRG *GGHITRSRDRDHPSQHGEIPS
795	14696	A	802	3	354	LRHYTP\PG*QSETLPFKKKKKKKKKKK KLSFFPPPKFLKKKKGLFKNPFKKKGKI FFNPPPPKKKGFFLIVNPPPKKKNPPPL GGGGPPKKIYF*KTFFFAPPPKFENPFF FFSPRF
796	14697	A	803	1	830	VETGFLHVRQAGLKLLTSGDLPTLAYQS AGITGVSHCAWLFFFF**CLAVTQTEVA PS*LTIASN\PGLKLSSFFTLPHHARLI FKIFSRNEVLLFSR\PSQTPNLMQSSCL SLPKCWDYRCEPLYPAESLSF\FIKLSC MLKCLEVKCNDVCNLL*NTLIKWINEWI EGWIGRLTCVKQIEKNVICRI*VMLKAT QPVGTEPS*ESRSTNSGEAMW*SKDNTP FPVFVSVFVLRQS/LCFVAQAGVQWSHL SSLQPLSPRLK*SSCLSLLSSWDLRARA
797	14698	A	804	389	3	FIWPFKGAPENSFFVFMWIKGHKCPKKG FGRKKNQLGPKIPF*KKKKKGAFPLWLK RFQGPFFFFFEMEFHS\IAQAGVQWCDL SSLQPLPPRFKRFSCLSLPSSWDYRHAP PRPANF\CVFSRDEVSPCW
798	14699	A	805	161	21	RGGGCLQSQFR/RRLRHENRLNPGGGGC TEPRSYRCTPAWARE*DSVSK
799	14700	A	806	405	82	FFLRWTL/DTVTRGGIQWCNLGSPQPP/ PPRFKRFSCLSLSSSWDYRRPPPCPANF LYF**RRGFTMLARLVLNP*PRDPPASA SQSAGITGVGHRAWPMPIFENRFDL
800	14701	A	807	938	2415	KITFWETFWITTVHPHLCKEREAIAGIL

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						RRWS*NNW/MIHTHTKNLNPYLTPDTKA TFK*IIGLT*RAKTMQL/LESFCQKENT GENLSDLGVGKDFLRHKKHGSIKGEKIA KLDFIQVKNF*SLKDTFKKMKKYALGWE KIFAERVSDRGCVSRRYKEL*L/IELKD NPIRKGGNNLNKVHQRI*MANKHMKRCP KS*VIREI*I*TIMRYHCILPRMAVMN/ SD*SHGDKNGGSSGTLIH\CR*ECEMDQ LLWKTIGQFLSK*M*RCHTDSSIPFLII QEK*NCISTKKTCTQTFTAA/MYLLVIA KNWKQLPYPSSVWI/QQIWCIYT\MEYY SAIKRTVDTLNN\QMDLKIIRFNE*S/H NLRRVHCMY
801	14702	A	808	414	1	KPKAKLFVPVRQVVNAKEKFLKEAKSAA PLN\RMIRKQTSLTADTEQV*VIWIEY* TSHSIPLSQSLIQSRVLTL\SMKAETGE KAAEENLEDSRG*FTRLKEKSHLHNIKV QGEAVSADGEAAAGYPEDLAKIIDER
802	14703	A	809	399	1	TGPPPRNQPFNKPAKGNFWLFLFFFL*F /CNFFFFFFFTGAFLSLFGI\LV*CLML VWGNFSP*PFKYCFTFSFFLSFIFLIFL WLLLNTCLYICYTFCSYLTVL*CSFLFS SIFFLLYF*FWRLLLIHPPPTRP
803	14704	A	810	1	392	ILLAGAIEDAEPGSG*TGYPTLTGSYSH PGAYVYLTILSLHLAGDSSILRAINCI\ TTLINIKPPAVARYLTPLFV*PVLDTAM LLILSLPVLADGVTILLTDRNLYSTFFD PAGRGDPILYQHLL*LLRH
804	14705	A	811	66	411	RETRAGAQGLSRFSPPWGNPSQKIFLGP GFKKNPGPQKKGNFFFFF*KKFPLVSPG GRGGGNFRSLQGPPPKVPPFFCFNPPRK GG*/MGAPP
805	14706	A	812	3	392	LSVPQFPPFFLKKTFRNCPPFCFSPPNI LGFPLKGSKK*GSFFPFFPPPNYSFFWF PSYSF*NQPCLTRGPF*NQKFPRL*KGV PILRL*SPLFFGPPPHSF/IFFFFDRVS LCHPGYSAVAQS/LLTAASS
806	14707	A	813	690	153	IISIDAKKAFYEIPPPSVISSSSPTDSL YYNLGFLKNFKKGREVKYLNIIKYIYEK PTANIIFISGKLKAFSLRSGTRQICPLS PLQFNKVLEVLARATWQEKEIRNIHIEK EEVKLSLFVSNILCIENPLKMP*KNSSN **IQRVAGYKTNI*KIS\AFLYTKNKLF CCLSHPIYDIPL
807	14708	A	814	32	376	LFGLARSYITEGGRLPENPTIPHG*REF WELCNKCD\TMRPKPSLHCSRCGHCVTR MDHHCPWINNCVGEDKH*LFLQLCFYTE LLTCYALMISFCHYYYFLPLKKRTLVRN VYI
808	14709	A	815	2	423	YPLYPFKIFIFPKGFNFCREVGPICPPP KIKVLSKNSQVGFYTAPYKEKNNTLPAR VNFGPPKDSLKRPPLFFFFFF*RDGILL CYPSWS*TPGLKQSRCLGLLKHWDYIC* PLHPASF*KKHYSLRILP/SLLADAW
809	14710	A	816	404	54	SLAHFFPPPKKGFFPKIPRGVL*PPP*K KKFLFS/HPPVNLGPPRDFLKGPPPSSS SSSSSSSSSSPGG*MIFY*/P**FGPAL VQPMACYCKASCKVKAPFFSTHSGLMVA

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						PPTTAQS
810	14711	A	817	3	410	DAEVGGSLEPG\SGGCSEP*SCHCTPAW VTG*ETVSKKKKKKKGFFPPFFFKRGP FFREIEKKFGKKFFSKKKKKKKKKRGG PFKKNFWGGKNLRGGKKFFFFLGGEKK KPRGFFEKKTFFWGGKNWATTTQK
811	14712	A	818	1	404	IPINSLTSKINKLLKRHKLP/HLNQEEI DNLTRTIPI*NINF*IYKQNTGPDGSIS KFY*TIRKT*Q*FYTSFQKIKNEEVLPN SFYEASTPLASPKKKKKKKKK
812	14713	A	819	421	2	LPPKRRCFSPKPPRGFFFAPS*GKKNI/ CFPPR*NLAPPGVFLKGPPLFFFFFFFF FRGRVG*SWVPAASPLQGQVFLPPQ/SS *VGGSPGPPEHARVNFFFFFFFFF*F** RQSLTMLPSLVSNSWA*TILTPQPPKVL GLQ
813	14714	A	820	84	418	ILTCHNARLGEKSQIVTMQASQNNPKLV NICEVFLVFFFWKPIFFGTQVGGQYFNL SSL*VRLPGYTHFFCLTLPKSWDYRPIP PS\PIFFCFFNKKGVSPGYPGGCNILVF
814	14715	A	821	290	3	FSPPPENLGPPRNFLKGPPPFFFFFFFF FFFFFFFMFCVLIY\FIFFCTNLLFLDF CIT**T*NWFISSKAVCLFLFLPLQPAS QKTKNRCRKSFF
815	14716	A	822	416	2	ITKLTEEKKIWSGKRKNDYVKYAGASQN YTAVVLRPQSMITLKDSSERKAPHWGEL NVV\HVHHFIWKER*PEV*IYIES*AID GGLASWSGPEKNKIGKLGAKKV*RRDMK TDPLECTQNINIFGFVCLFGDRVSLCW
816	14717	A	823	409	45	PPPPFLFFFF*KKKKAPGGGSQGPKF*P PPPPKGKPPFFKKKKKKPGGGGGPPNPP PPKGGGQK/QFFPPQGGNFNKPKSPPPQ PPRGQKKKPPPQKKKKKKKKKKRLNVTG PQFLQLESGTY
817	14718	A	824	1	408	IFSEHNGIKL*INTKRNFRNCTNIWELS NMLLNNH*VNKEN*NKKFIKTNE/NKN ITCQNL*DTTKVVLREIYSKKCLLQKKK KKKKKKKKKKGGGALKNYLGGGQFYGGE GNFIFFFWGGAKKPCGWIFRRRPFFW
818	14719	A	825	259	274	YL*YLLLYRRYSA*IPL/LGYYLKKRKL LYQRDTYTPMFIAALFTIAKMWSRP*SP VV
819	14720	A	826	422	105	FFFSKIPWGNFFPPPPKRIFFPPFPPKI FFFPPPPFFFWGGFSPFSPPPKKVFFPK SPPVFFFPPP*KKKFFFP/HPPLIFPPP GFFFKPPPPFFFFFFFFFFFFFW
820	14721	A	827	15	402	IKSLGKNIGINLGDLVLNNGF*YTLPKA QATKEKIDN/WDLAKAKNICA*KDTIKE VERQPKK*QQTFVNHLFDKGLVSKHV/N EL*LINKKTNH\HL**WAKD*NRACSKE DVHMTDKLMKDVPSLVIREI
821	14722	A	828	420	3	KDAHTCPPGCKGGFSGHRALKAICRNQG FLLTTTEFLTHKCPLPGQEPWGQHQG*R DSPRRVSPAPGTWQPPCHRERACLAPSA VE/GPS*IQEQEKSLLFFFFSLLRWSL/ NSVAQVGVQWRSLGSLQPPPPRFKQFSC LS
822	14723	A	829	1	269	IKIKNLARHGDSCL*SPLLLEMLRLEEN

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						LSPGSRGCSEL/CQPARQGETLSQTNKQ TNKKPHQVQLPCFEIINFKEFITCLVLR LPGNSW
823	14724	A	830	432	1	GYNNQQIFDVDQTAFY*KKIPSRTSIAR EEKSMLGFKASKDRLILLLLGAKVAGDFK LKPMLVDPSKTPRELNN*ARCTLPVL/V KWN/KAWMTAYLFTV*FIQYFKPTVDTY C/FKILLLIDNAPGLPRAVMDR*EESNV FMPVNTTL
824	14725	A	831	1	233	KKLQIKYLGINLMKYTIHVVSICQKLLM KEINEDLNKWRDVLCLWI*RLNNMSILH KLIN/RINLLQLRI
825	14726	A	832	3	477	YQTCKEDLTQMLLKIFQKIKGEGIIPNS LYDASIAMMPKSDKDRTKKF\NYRPISL MSIDAKILNKILPNQIQQHIQKFIFIPE MKG*FNIRK*INLIHLITKMKTKTPMII SIGTEKVFDKIKY/PFPITTLTKLGIDG RSLDAIMVARE
826	14727	A	833	3	402	RYQTPLLV*TVLITTALLGLSLPVLTG GITIPLTDRRLDTTFFDPAGGGDPILYH HLF*FFGRPEAHILILPGWGIISHIGTY YSGKKEPFGYTGMR*AIISIAFLRVIV* AHHIYTV*IDRDTRAYLPSLHN
827	14728	A	834	7	395	DPQRVSCMALSSNSFFFFFWERKSLFFP GREGRGQIWVNGTPPLQGKRNSPASPPG GGGITKKAPKLHPPKKGWGGGLEKPP*N QRGGFGI*SPGGKKGFAGG*KQGQKSKG GGKKKGRA\DP*AYIPLK
828	14729	A	835	41	444	DPRVRKKERENLYRSVSIKEIESVI*NF PTKKI*GLDGITSEFIQILPKKKPK\IK KERTFSNPFDKTNITLI/SKPETTFTKK EN/VRPVSLMNI/DCKILLKVLANCTL\ HI*REIHHDS/INFIPAIQISFNIQKTN
829	14730	A	836	3	415	HAYYIVKPSP/WIPKGALSALLKTYGLT M*MQFQSIKDLRLGLLTNTLTIYQ*WRD VTRKSTYQGRHTPPVQKGL*YGILFIT SEVFFFAGIF*AFYQSSLAPTPQLGGHW PPTGNTPLNPLEDPILNTSGLLGIGVS
830	14731	A	837	378	0	TPPKGPGGKIFLKK/SPGRKIF*PPGNG /PFFSPLSPLKFFFFPKAFNFWGGGGPQ GPPPKKGVFSQNPPPGKKRPPQKEKKNF FP/PPGKMGPPQGFF*RAPPP
831	14732	A	838	383	38	GPGEKIFLKKPREKKLSPPGEKAKFFPP SPLKNFFFPQGVFFLGGGGPKRPPPKKK GFFQKTPRGF*IAPQKKKKKNFPPRGKF GPPQ/RIF*KGPPPFFFFFFFFFFFFF WSL
832	14733	A	839	59	418	TKISSKDQKQY\TTPGW*MAEISTTFED AEIIDALIFPFNLPIWLHKKPDCSWKVS VYCKLK*VVSLISATGLDIINT\LLEEM KRVSGTWYIATDLAKTFFYI/PDQKEFA FSWYG*KDIF
833	14734	A	840	5	335	IRHLF*INKFENLDKMDTT*KLTYEGIE SLN/RII*NF/PVVKSLGSGSFTSEFYS LFKEEITAIYKPIWRVEKGGI\LPTCFA TRITLIPKPETCIMRKKNCGPVLFMNGH F
834	14735	A	841	1	38	RRLKLEDHLSLY*KINSKWIRELNIR/P

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						ETIKLVKKDKGNV\QDTDPGKDFMVKTT KTKIDKSDYIKLQSFYTANETVNRVKLQ PIE*GKIFKNYSSGKGLLSMIYNELKQQ HRNNNLI*KLEDHLSLY
835	14736	A	842	2	424	GRVGSIPLSQSLIQSKALTLFSFMKAET GQEAAEKKVEANRGWFTRFKERSGLCNI KVQ/GAGGDTAASSPADPAKINDEGGHS /KQQIFSGNETAFY*KKMSSGTSIAREE KSMPIFKASKDRVTLLIGANAAGNF\KL KPMP
836	14737	A	843	281	3	FFFFFFFFFFFFFKTFLFFGYWFSIFFP LLFSISLLLSFSGSFVTFAFQPFF*VSR YHYQHFNSTF*FL\KL*FIF*IFFLISI LFLFHGYNF
837	14738	A	844	409	1	RCGGTCPWSPVLRRLR*KDHLSLRG*GC SEP*LHHCTPAWATE\DSVSKKNKKKGI SCRQHIVGSFFFHLKMCLLNGLLSFFTL NVIIYVVEFKFTILLFLLYSICSLSHLF SFPAKSWINSKFESLFVCFNSFS
838	14739	A	845	63	451	KNQEQESEETLPNLFYKASITLIPKLDT QK*KKRKEKKRKKKK\EN*KPITHRNIY AKILNKILAHQIQQYIGKIIHHDQVGCI P/GAFDKIQYRCMIR/TLQKMGIEGTHL NIIKAIYIRPTDSIIENREKP
839	14740	A	846	60	460	RNNEPFLDQIVTYPEKWILYDNR**/PT QWLDGEEGPKHLPKPNLH/QKKVVVTVW WSASLTHYSFLNP\ETITSENYSQEIDE MH*KLQSLQLASVNRKGQIPLHDNPRLQ VAQPVLQKINELGFEVLPHPPYSPE
840	14741	A	847	344	2	NFLKFHPGGETFLQKGYTGYFSPFTP*K FFFSLKPLNFLGRVGPFFPPPKKGFFSK IPQGGLISPPLRGKVFPPPPRLNLGPPR VFLKAP/HPFFFFGI\PHGLQPRPMI*K PTRP
841	14742	A	848	439	132	RRVAAPPPSKNIFFPPGSYNCGGVWPQK SPPPK*GFFPKP\SGVYKNPPQIEKVFF FPHARIVPPPGDPIKTPPPIFFFCFNSI NFSLRGAQLYVWDFLGSGC
842	14743	A	849	94	470	LNHFLSFFLSFFLSFFLSSGSLSLSLSF FFFWKGSPPPP*GTK/QKPCLKKKKKKK GGGGGQNFFTPPGGKKNPPPQGGGGGGS PAQKKKP/EGGGPPGSKKKNPGGGFKKK KPPKKPRGGGGKPFFP
843	14744	A	850	2	396	FFKKENIQMANKHVKTYTTLLVIREMKI PTSMRYHFTSIRVAKILKTDNTRC*QEG RTIRILMLC*LQNKMVLLL/WKNWQFLT KIKIFLF\FDPTISLLGIYPREMKTYVH SSFIHGNSKNNRTGNNLNVHN
844	14745	A	851	369	36	SKGASDILEKPPLF*EVGLPTPSPPLGE KMP/FNYKGGPGKGISLLIFPKKKFIPP GGHFPFPFP/PFFFMDRVLLCHPGWSAV AVSQLTTTSASRL\K*FSCLSYSEG*DG RIS
845	14746	A	852	1	367	PPPPKIKSPSGPGPPSKRGSPGAPPRGG KFWFLSQKGWGGP*FPPPPGVKPE/NIP *PPRGRVPL/HLNLAPAPPPGPPK/PKP PSP
846	14747	A	853	1	378	AMLATLISNS*PQ/CDPPALAPQSAGIT

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						GMSPCARPTSCSFYP*ILLTVRTFIKIR NFFFFFDTGSNFVAQPGGEGHDHG***P QPPGPNKSFNLSLPSRWDYGGAPPCPVI LCIFCKDEVSSCGSG
847	14748	A	854	369	1	SACFGLPKCWDYR/R*ATTPSLEIIIYI ER*EKTTSPDNANRFDVTKLHHYDCSVM DF*KAL*NGDDFPVLMSKMHMQSLNII\ FVFCFLRQGLALSQ/AGVQWRDHGLPQP QLPRLQPSSHLSL
848	14749	A	855	380	335	NPGGRGCSELRLCHCTPAWAT\SETLSQ TKIQPKKQEV*LL
849	14750	A	856	373	1	LRIKILNKKGLANLIP**R*KIIHSQVE FIPEMQA*FIIRK/TPSIKWPIVRTKKK KKSQMLISIDTEKIFDKIQHLFLVKPVI KLGIEGTFINFIKSIY\KKSTTATIISG LNASPLRLKTRQDF
850	14751	A	857	369	44	KVQNLYFEKKLLNKIKVDLNKW/NSLCT RFRKLNIANIIMFKLIHRYN/SKVKIPI KIPANCFGEIDKLILKFI*KFKRPQIAK IILKKNKDGYILPDFKTYYIYMQYHLC
851	14752	A	858	1	348	QWHAPAS/LARPPPPRFK*FSCLSLPNS WDYRHAPPRLANFVLFCFVG*GGIHL
852	14753	A	859	1	366	CTSPTFNQKLEMIKL/EEGMLKAETG*K LCLLCQKV/QVVNAKEMFLKEI*SASLV NTTMI\RKQSFTADMEKV*VV*IEYQTS HNIPLSQSLIQSKALTLYSSMKAERGEE AAKEK/LEASR
853	14754	A	860	12	366	PSTLGLRRASCLSLLSRWD*RHMPPHPA N*KNFFCRDG/SLTMLLRLVL\NSWPQA IHSPWPPQ
854	14755	A	861	424	78	NPRPLEGQTASFSLAPNF*TTLGKKVNP FF/SLKNPPPPPPPPKIWAPQGPFGPPS PGGLNGGFFLPPRVKAPIIHKGAPPPQF PPQKKKGPRVFPKKKKKKERKKEKGMTR AFCYP
855	14756	A	862	327	3	SHWFFAAV\GREISM*AMAPDQTKKICP RSAEDAIKYFLTQATGSIILIRAILFNN RLSEQ*SITNTTNQYSSLIIIMAIAIKV GMAPFHF*VPEVTQGSPLTSGLLVL
856	14757	A	863	1	341	YDRNKWKDIPGS*IERLNIVKLSMLPTV IYRFNVILIKIPMTFFAETEKSIVKFSR DYE*PKQS*KEQNWKTHTP*FQ/QFFTA TVIKMVWY*NKDRYIY/DQWNRI*SLGI NPCI
857	14758	A	864	32	324	LVWPFFFFFFFF*KKKFFFPPF*RKGK NFFFFTPPPPGLNLFF/CPHPLKKWEKR APPPPPN*FFFFLKKTGFFFFTQKGLNF PPLETPPLTPPKGLN
858	14759	A	865	350	3	RVKNPRPFWGF*MVLKPLSFFSKKTN*I LFPLKIFSPPKTVPWGKIFLGAL*NPFF CFKNPLWFFGF*KL/SFFFPPLYFF*KP LAPLKRRFSFFFFFFL*DGVSLCRPGWS AVARSR
859	14760	A	866	342	118	GSVTQAEVQWCDHGSLQPETPGIK*S/H PPTSSYQVVGTTGVCHPGLAMLSRLVLS SWPQAILSPWPPTVQGLQV
860	14761	A	867	1	354	VKPSP*PLTGALSALLMTFGLTM*IHFH SITLLILGLLSNTLTIY\Q*W\RDVTPE

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						STYHGHHTPPVQKGLRYGIILFITSEGV FWAGSV*TFYRSSLSPTPQLGGHWPPTG ITPLN
861	14762	A	868	3	344	QIKNPDNISC/WIRCGATGMFLHCWWEC KLLQPLWKTT*HQ*SRR*AVPLSGMFP/ NRYSSTCTPASI*KTFLSALFMMTPL/C LSRVEWIK*SWCNQKL*Y*SVMKRSEEF SLKNA
862	14763	A	869	345	1	KQAGLKNVKITG/EGASVNQSR*VS/YL GTIKKITEEKGYLPERVFNAGASAVF*G KKLPQRTFISK/EEKQAP/GSEVGKDRL TLLFCANMSRFMISTALLYKAADLQSLK GKDKHRL
863	14764	A	870	340	45	FCSFCRDRVSLCCLGWSRAPGLK*SSCL SLPKC*DHRC/AA/VPAWFQRCILEKKN QIY*CAERIL*SERPHTRHLDSSTVNIL PCPLSKVIFWKKKNQIY
864	14765	A	871	209	72	KLWDIHTMEYYYSAIKRNKPLKYTTWMD LKDIMLCEKANLKRSHTV
865	14766	A	872	3	353	SFFLGPPPFFFFFFPPPQPLPIFFWRFF FCFSPPKKPPP/PFFL*GGSPPPPF*RG FFFF*KKKGGVFPPPFFFFFSPKVSPPP PKKGGGG/PPPPFFF
866	14767	A	873	3	267	DFTMLARLVSNS/WPGVVAHTCDPSTLG G*GGWITRSGVRDQPGQHGEI
867	14768	A	874	1	346	PRRPFFFFFFFLIVFIYFKCVYLF*DKV LVCHPGWSAVPHHGSLQP*PLRIKQSSH LSLSSS/WDHRHAWLVFVSFYRDEVSPC LANFCIFL*RQDFSMLPRQ/VLKAICLP WPPSL
868	14769	A	875	1	172	KLLSSGSPPASASQSAGITGVSHRARPG LLNFFC*CAFSVPGPCLGYPDTFTH/LC PPSFHQSVIASLDFSCLS*L*MSP
869	14770	A	876	1	348	LLFCFNNYSFFHGVKPKIPAFFVFGPGC LPHFFPPITPAPFFFLDRVLLFPPGWRE MGPF*APPTFSPQG*GVFPPPPPQ*LGP RGPPPQPGVFFFFCIFGRDSA/LAILPR L
870	14771	A	877	1	203	GFHYAGQASLEVLTS*STCLSLPKSWDY RRGPP/*PGLSYFLYPSLRS*FICAMSI HIPFIKKKKASD
871	14772	A	878	343	102	EWEDCPSPGGRGCSEPRSHHCTPAWVRE TLSPKKYLFLQP*KLKNTKIYLSISIP* ELET\ILKILHFKMMNPLHSYNFFF
872	14773	A	879	2	359	RDITKGDMQMETKHM*SFSTSLTSGI\H NSPIRPSKMKNIDSTRYWRGCRAIRALI HCWWRC*MVQPFGE*ISSFSKKLNMYLS YDERPTFRYEK*K/P*VHPKICV*MFMA AFFLISPNW
873	14774	A	880	205	1	FFRGVTEGL*EPPYVESVI/AGGTTARR PLFFFFFFFFFFLRWSFALVAQAGVQWR DLGSPRPPPPGFK
874	14775	A	881	150	2	CRARVDGVPWRNPGSLKPPSP\GSSDPP TSASQECGITGAHHHTRLT*VF
875	14776	A	882	345	1	KGNQPWKTEKRALFC/TLKKKKIFKNSP PRGNF*KFFVKKKIPLKKEKGFSPTWGK KKEFFFKKKKKKKKK**AKDLNRNFSRE DVQMAKKHMKRCSTSLIIREM*IKTTIR

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						YHF
876	14777	A	883	2	355	DRLLFSASHLDLGTLYLLFGA*SGVLGT SF\SLLIRAELGQ\SGCLL*NDHIYNGI ETAHAFVMDLFIVRPIIIGGFGN*LGFP NKKGADMAFPRINNISF*LLPPSLLLLL ASAIVEA
877	14778	A	884	262	2	PTCEQSEREIKKTIQFTTESK*IKFVGI NLAQEAKDLYTETIKYKTLLKEIKDTNK *KNIIYV\SWTRRFNNFKMLGWAQWLMP VIPA
878	14779	A	885	16	318	ILRADCADLFFFFFLGGKKGFCFPRLKG RGETLLN*TLIFR\VKGNF*PKLPKIW/ DFKGWPYHL/AENFVFFLKKGGLTLLPG LVLNS*IKEPFHLWPPKGVA
879	14780	A	886	298	322	KRRTP*YPPGEPHFPPPPPQG*KARGAP PPPPKKGFF\PEKKKKPGVMVQGTTQKP PKKTKVRVD
880	14781	A	887	353	3	FPFWGFLKTLFGKALWLFKGFFFFAHQK FFFLPSLPPPP\LGFFLRGLT*FKIFSP LF*KGAPQKGISHPLFFFLISPKPPPPF FPFFFFPPPPPFFFFFFFFFFS\RDRVLL YCPGWGA
881	14782	A	888	22	341	IPCTCLKLHGKVHDHDQSQLWWPKPQEE MRTLENNLAVLQSILQWLDIELPYDRAI ICAREIKTYV\QQNCT*TFMLALCITAK KW/KQLKCPSTDEWVSRMWYTCTR
882	14783	A	889	51	338	ERSQLQWLMPIIPSLFFFFETQFLFCCP GGRAWAIFKIFEFLA\PK*KQFSCLTLQ TI*VYGLNPPPRKNFVFLKERGLFHVGQ SGRDLPPSGDPP
883	14784	A	890	1	225	GRLRPENHLNPGGRGCGELRLCYCTPAW VTERDTIS/RHTHT*NYFY*GSI*QLAN SCCCNMLNKFNVICILRWC
884	14785	A	891	357	164	GKGCSDSRLCHCTPAWAT\TKTLSQKKL ILKKQNKFRS*LDD*INMRCTVWPCFHV FLFIRAAPLFSDWLYNK*MNRNT
885	14786	A	892	207	302	EPFSGIIINESIHQEGIIVLNVYTSSNR PSKYMKQTLIELKGEKVKSTIIVGD/FY THLLVIDRTSR*KR
886	14787	A	893	86	332	VMRVSCCCLKD*ISLCHPTWSAVVQS*L TVASNSW\VKQSSFLGLPALWEAELGGS LEVRSLRPVWAT*TP\FCKNKKL
887	14788	A	894	2	336	FFFWPPPQTFLKNPGGPGPKREEGPGGS PRGQKQGPPGLHLTGFGGQPGG*KNPEP GPGGRAPKGETRGEGGGPTRPQIP/QLI NGKSGKPPKVTLNGAWGTIKIFLIKTPV G
888	14789	A	895	1	214	ARESLASFLPPSLPPFLLGLRFLPSFLP FYFSFLPSFLGFGSFLPST*VPSFLPSF LLFFPSFLPWLWFLPS/FLPSFLPSFLP SW
889	14790	A	896	131	352	TLHESDSESVPRDFKISDALAVEDDQRS PGTLNAAELS/SSVRERKKKEK/KPEPG L*DQSIKESDSYMVSGGRIQ
890	14791	A	897	3	184	CSVAPAGVQCHDLTSLQSPPP\SSSNPP TSSNPPTSAF*VAGTTGMCHHAWLIFVF LVDAA
891	14792	A	898	327	264	NRAVSLMNLDAKVL\KLISASQIYVYIK

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						KMIH/HNQIRFTMRM*GQFII*TAINIY HKLIK*GRKHMIPLIYAVKIFEKI*YHN IMIKTLHKL*IKEPPGSFIYSL
892	14793	A	899	3	313	TKAASHSQ\RANLQFLVGRIH*HLKSRT ISPGRVGATAAVNSTAILEYLTAEVLEL ARNASKDFTVKHTTPHYLQLAIRGDKEL GSLFKSTIAGKGVIPHIHKS
893	14794	A	900	340	1	HLCPHKEHLY/LLQTSCPLAII*FISTI AEHTKAPFDMAKVESELVSGFNIEYAAG PFALFFIAEYPNIIIINTLTVTIFLGPT YVALSPELNTTYFVPRKIVVVRVFIIIM FV
894	14795	A	901	1	252	LTFFPQHLLGLSGMPRRYSDYPDAYAT* NILSSVG/SSFSLPAVILIIFMI*EAFA SKRKVLIVEDPSINLE*LYGCPPSFPSF
895	14796	A	902	326	1	LGPPPPLKEPPGVFPIFPF*FWNFGPV GPF*KILIGPLILDFPQFFFGGVSQIVF PPF*GKIPFF*KNTPPFF*GIGGSIPHP PLFFFFFFL*DGVLLCHLGWSAVA
896	14797	A	903	1	352	KGIFPVWSCG*KGTQKKGGLSQGGQGNV PPCGIHFVKEFLGFPGAQLLIS*GGRLI F*KGPKKGFLP*TVFG/RRAQFEAPR
897	14798	A	904	325	2	RLEEKLNDYWNEMKVKKNTEYPLNLPVE DIQKRPDQTWVQCDACLKCRK*PYGMDQ HLEK\WYWCNNHDSQFRYCMVPKDPEDM DLVHPNYGKPYKKPSKETYWFSQMP
898	14799	A	905	1	329	IGLAIHGAERIVRGQTAKSLAVHN\VCE QKKIKKKKGGPGREFQNLKWENPKNPGG SF*RGLGPQSNFFYLKQ/RLGFFF*KKP PKI*ILAMEPPNKKIF*KNKNKAHFFF
899	14800	A	906	148	2	DVDKLFLLRSLPTL*RPEYGSYMIEGT\ TGQPYGGTMSEFNTLEANMRIR
900	14801	A	907	384	1	ESKRSIFGPPNPPPPGFKGFSRHAPLWL RSREPPHKAGVKKGFPRFRPGS*MPIP* SFLQNCLPQRVGFPSLPPPGAPFLKISL FLRQESRSVTQAGV*\YGLLQCRPPRLK SFSCLSLPNSWDYNR
901	14802	A	908	3	297	TKIKSL*INHLIRAKTVKLLEENMGINL HDLSSGRQQPFRYDTFQ/SMINTAIKEK IMKLSFVKMGSFISQRTPLRKERQLTK* EKIFADVYLIIGRRG
902	14803	A	909	169	373	ASNILSATDISNTFGPPGSQGFSGREAY VEAGTYYTNFSCLGQVKVF*YWMQLIVS IVLL*LL*VTQKL*L/GPRQEKFV*YVP AST*ASLPLKPCDPGGPKVFEMSVADS/ DV*SLWLALIGESKFRCLVF*SKFLPSS AYTYSPLEKKLFILLGCFVMICFCFCFL RRVL
903	14804	A	910	132	368	GRIFLFVGQEKGARVSFLFLF*DRVSLC HPGWSAVAQSQLTTS/TWTQNNSSHLTP P*VAENHRCA/PHTPNVLFLC
904	14805	A	911	2	339	NSWAQE*AGITGSCHHTQLTLEF*AHDR QMMFFLFFLKTNFTFCPPA*RPWPGLGL TE\PLLPGLKHFF/CLTLPSNWDKGHLP P/HPYQI/CGFLRKNGASLISG
905	14806	A	912	3	381	LNFCDTHPLTPRPVSIQRQCLPLVEAGI RWRALISPQLHPPT/YSLLSSWDYKHAA PHPANFFFFFFKKGSLTMFPRPGGS*IF

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						IYLLIYLERESY/AVAQAGGQGPNFNSG QPLSPRFKQFSYLSLLR
906	14807	A	913	394	1	MSKGKIG*KLG*KFAQKVSQFVNAKEKL LKEIKHFTLMNT*MI*KRNS/LIADLEK ILVVWIENKTGYSIP*TQNRIQSKALIL FYSMMTERGEEA\KKFEARRDYFMRFKE RSRLQNMKV*DEAANADGEAA
907	14808	A	914	326	200	HNWLSIWKKVKSNCFLMPHTKINSRWIK DIKI/R/LHRIKILQENVGNHIYKI*RQ KRS*PRHNFLHKNCKCLVWHKTNK*NH* KIYL*CI*KTFAVFM
908	14809	A	915	3	334	LVVRVKGPKFKFWLHHQLGLYC*VISFF INKMKEYVLIHRIK*DHKNIF*MGYKKL *NVNIW*LVLFGFSSKNHL/WSGAVAHT FNPSTLGDRGRRITQGQEFQISLTNMVK
909	14810	A	916	14	299	YQKLPQKKSPEPNAFTDKFYKIFK*LTA ILQ*LFQKI/E/KETPLPK*SNESSNAL I*KPDKDIT/SKNYKPISVSNIHAKILN KI*GYQVQQKQLYSK
910	14811	A	917	3	339	SLQPQSCRLKCSSCLSLSSCWDYKHKPP CLA/NFF/VFF*EKGICTVKN*NGDYPL GRRVTKRDHERGF*NAGKVLLVGW/CGF ETQSRFVPQAGGQGRNLGSLQALFPGLM PFSC
911	14812	A	918	2	321	GIISGIYKELSQPKMTDSSIKK\KDLNR NFTKEYVQMACKHMKRCSASLVIREIK\ IKSTMR*H*\TPTRMTKIKD\DKNTKCW *GYGAVGMLIHCQW\NTKMVQPLWKN
912	14813	A	919	51	326	FFVFCLFSLVFISLNCGLF/PTFFRIPS L/PYLQLI*IYLFFY*LKPIFLKFFRDR VSLCHPGWSTVA*S*LIEASKYW\VQ*S SHLSLLSS*DY
913	14814	A	920	239	2	DSLILSAVQ*HDLGSLQPPHPGLKQ/FL PSNWHYRCMSPCLAYFLLFLVETPFCHV TQASLELLGLSNLPASASQSAGI
914	14815	A	921	1	242	PRPRRRLLKYFILFNFLRQ/RSRSATQA EVQ*HDHSSL*PQTPRLK\HPPASET
915	14816	A	922	249	1	ALFCALKKTLCGTLMFIAALFIIAE\SR HNQTQPTCLSTDEEINKMWHRHAMGNYS AIKRNEVLIYAKI*MYLENIMLSEII
916	14817	A	923	404	1	SRPQKKLGELKCS*RPKGLNKKNQRKPG TFFFFETKFHSFCQAGVQWVYGC*SHPY LLHIIFP**VF*MFLILITV/PSRNKDL IGNSEKQIHN/WSSLYFYF*LFFLRWSL TLVPQSGVRWRNLGSLQPPLPRFK
917	14818	A	924	6	358	FFCSLLGHGGETPNNSPLPHPWL*ETKS PPKPPHPLKKKKHSLFFKIFILKKKKNG PPFFPPAGPNPRG*NPPPPQ/RPPKGPP PPKEKINPPPPPQGKNFPKGKRPPLGPF PKKGGGY
918	14819	A	925	268	2	HMYAFVKIDLTAHLRFSAGKKEIPAGKL YF/L*RKNPKNQIGNQKKKKCLPRAGRM VAHAWNPSNLGGQGAGTT*SQALETSMG NMGKP
919	14820	A	926	74	338	IAGITGVSH*ESKNSY*KQFL/WPGTVA HSCNSSNLGGQGEWIT*GQEFETSLANM VKP
920	14821	A	927	339	1	LRLFACPPLPKWWDYRGEPPRQIFFSWH

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						FFKKQGFICPIEKGRELSNCCFQKEVLI *KKVILKI*PFFFFFLMESCSVA*AGVQ WHDLQPLPP\NSWDYRCPPSRPAKFCIF
921	14822	A	928	3	416	RCWWENKIN/PFWK/S/VWPCVTKVNIH SPYDLTISLQYLPYRDEYLCSYKNLMFL IVLFIITKNYKQPKCASVG*WLRILWYL /YMENYSAIKMNK
922	14823	A	929	344	69	YKRSPLL\KSA*DGPANWKSLPRS*YKR SPLLIKAKPDQIISGWEASPLII\PRAL LQKLKPAASKF*W/NPKKKRALIS/KAI PSKKNKAEGIMFPNFKV*YRDTATKTA* WWYKNSSSL
923	14824	A	930	378	1	HGKKIDPRFIPYTKI/NLKWFIDLNVKP KTIKFLE*NIGE/TIFVIDHKK*NP*KK KLVN/WDFIKIKSFCFVH*KPAVGK*KR /QP*TRRNYVQTHTSDRGLISRICKELF *LNSKVINSIRKWAQSLN
924	14825	A	931	479	83	SRKGLGRGLKRGGFFPPPPPKGLPGGVA PPGFEGFFGSL*KG/DRG*PFLKGVKGE KGKRI*EGG/EKGGGFLPPPPPQKGFSK NFLGFYAGKKENP*GGSPPPPLFGPAQK ISLGKGENKVPPPPGNLFYLFIF
925	14826	A	932	36	440	TTYASLDEAQLPRAKFNAFLTTF*HIIK NGPILGKIGRKYMIADQ\GHRMKNHHCK LTQVLNTHYVGPKRILLTGTPLQNKLPE LWALLNFLLPTIFKSCSTFEQWFNAPFA MTGERVHLYEEETILIIRRVHKVL
926	14827	A	933	8	398	CLQGKEETLTTNWHLRYFLPFFFFFWPK KGARKNGGRPPGGSPKNQRAPCPKPFEN PGEKTPQKRGFFPPKPCPGPGPGPTGGQ GKPP/HPQRPQILPFVPQAGPQGRKGG* WNPPPPG*KGFPAPTPPRM
927	14828	A	934	1	441	TRSHPRALKEVYTEINIVFMPANATSIL QPMD*GVILTLKAYYLRSTFCKAIAAVP SDS/SSDGSGQSQLKTFLKGFLILDAI* NIGDSWEEVKISTLTEMWKKLNPIFMND FEGFKTSVEEVTADVVKITEEVQVESED GTEFLQSH
928	14829	A	935	3	383	PGFKASKDRLTFSSGNNAAGNFKLKPVL IYHSENPRVLKNYAKSILSVLYKWNNKA WMTAHLFTAWFTE\PYVETYCS\EKNIF FKILLLIDSVPSHPRALREI*KQMTIVY MP/STTTSILQPMNQG
929	14830	A	936	417	1	CFFSRDEVSPCGPGFSPSPD/HHDPPPP PSQCWDYRRDPLWVPPHICFLIHKKKRS SHMGSSMYDP*KPPHKWMKSPPPVSVLY GSIPVQVQIAPPPETNPVYFFSPPPPFW GGGRVCVCVCVSSEVCDFFGGDENVIV
930	14831	A	937	412	3	KPTRVKKINPPFFKNTKNKGGRVGGSLY SPFFGGLGQKNGFTPEAKGSINLKFPTA PKSWGTQQKSLFKKKKKKKSILKFIWNQ KINPKQIKQS*GITLPE/FKLYYKEATV TKTAWYRYKNRPIDQWNGTDRNKATH
931	14832	A	938	1	416	KNRHIDQCSGIERPEIDSHKYSQLIFDK GAKVI**RNDNLFNKWYFNNWMSTC\RK INLDTDLTYLFQNGSQT*P*NIKLLENS MGGNLGDL/GMSQ*VSSSSSSRRIHDKK LVS/WDFIKIENICSEKGIIKRMKSQTT

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						D
932	14833	A	939	4	443	DFDYNHDHDYAELGTRPGSVGQGSPDPQ FTPSRMGREGEGTHSIL*CSSLGMGVIA DLSTDPTELEKRALEVAGPDGQASAISP ASPRRKAGDGGHRRALPGCTSLTGETTG KSGEAGQDGKPPGD/GPIGPYSLPGSGP GSGESMMG
933	14834	A	940	3	404	LFMFLEFFF*KPRSC*VSQAGMQGCYLK ALQAPPPRFTP/SLLSS*DYWSLPPPLA NFLYF*ETRGFTGLTRMISIPQPTEMPG LASQTAKLIFF*K/HRVLVES/HG*SAR AVHRGDLHILEP*TPGLK*YS\CISL
934	14835	A	941	397	1	FVPNSQVANAKKKFLKEAESTTPVLSGI RKQNTFAADME*V*MVWIKDQPSYSIPL SQSVIQ/SRALTLFDCTKAERNRRGKLQ WEPAV\EGSKGWLMRFKERSHLHNIKVQ DEAVSYPEDLDKMDAVNTKHQI
935	14836	A	942	441	29	SVTLCKHTVHVPTFLRRGKRCPLFGQCQ PWPSPG/PHPLSMSPV*PRPQ\PIPLHS APPLALGPFIPMLSMAGLPFPFQGSGLR NWKPPFPQPSLLQ**HFPKPLKPIRGLR PFPPSTLSIPLPGTRPRAKLGVMRSRL
936	14837	A	943	2	397	ARDAAPEPGEHLLQGLSARHGLRPPRDS RPGPD\PP\SPPHPLPLPAVPTFVFSFG DSWLL*SPFFPAPWASEGGACAPNPHAL VPSPSGQASGLRGGAPSWKAGLDTDGQQ AGRQSPGPAPPSPPLPPSQDC
937	14838	A	944	3	449	LRQVWHEGEMPNKTTLIYHYTPI*ITNI KNTDNTKSLWGCAEARSFTHC/WMRIKM VKPLWETVQ*YLI**KLQLPFNPAVALW \SICPRKVKTY/CHRKNKTRS*MFIV/A LFVTAQTKN
938	14839	A	945	380	175	RAPAVPATQEAEVGGL/H*TWEDRLNPG GEV/CSEPKWCHCPPAWATKPNCVSKKK KKKEKRINHQHDEK
939	14840	A	946	21	331	VAPLKYGPSKETI/IQSVRQSTECKKIF AYYPSDTGLITRIYEEL*RLNRKEKLNS SVYKYAKDLI*PFSKEDTQMANRR/H*K KCSTSLIIREMRFKTTMRVDAV
940	14841	A	947	365	1	GGGPFWFFFFFFLGGFLKIGKIWAKKKT GPSFPQKKKRGPKKKKPPGFFFFFFF*K GFVAPGGGQWEGFGSLQPLPPGVKQFFC PRFLRKW/DSRFFFFFLIKSNAEQFPTL YAGVRMRYIK
941	14842	A	948	357	137	ISAHCELRLPGSHHSPALLCSPGLSRTP NLKQSSLFSLPKCWDYR\LATVPGQLLL F*ARHCISIDPSLHLNNM
942	14843	A	949	53	352	REDNHHKCIRNKMINRKWANEVNRCFSE EIQMVKKHEKLLASPPIRSMQIKRYY\L NSLA*KKEKKSD\NTKLWQGFGETKSV* RYIIN/PYDPTIPLLGIY
943	14844	A	950	937	3	KVSPYKINIHK*VAFLCTNNIQAEKK/M NMVLFTIATNKKI/SYLVIH*IKEVKYL YNKNYK\LLKKNRDNANK*KGTPCS*I* RINIIKMSVLPKATYRLSAISLKL*MQL FMELEKE\TILKVIWKNKTAHLAKATLT \QSNPGGLTLPGLYYKATVIHITW/HCY KNTHVDQ*/NRRESPEISLHFYTQLFSD

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						KVNRSKQ/WKNCLSNKWYWESWLIICRR RKLKLYLSPYKKCNSK*IKNLTVKLKAI KIVEHQKSTVLVTGLWKGFMTNTIKVNA TKIKVKN*HLIKLKNFCTPKET/T*QIC RQQRVWNKLFSNF
944	14845	A	951	246	1	AASTKTGVQTKTCT*MLIAALVITVKRE KQSKCSSVE\E*TMWYIHTMEYYSVTKR NDVLIRTTWMNLENSMLSKKDSHKG
945	14846	A	952	2	255	QGCGEKGTFLHCWWEYQPLWKTVW*FLK DPETDIPFDQAIPLLGIYPKEYQSLYYK DT\AKTWNQPKCQLMVDGIKKMWYIVDA A
946	14847	A	953	343	3	GSIYTKEMEPKVNNLQK*KASCTDGL*G EFY*TFENEIPILYNLFQKTEAKGTLTN SRDEASIILIPKPEKCTRRKENDK/P/I SLMSIDAKLLNKILAN*IQQSRIYSRHT RLIQ
947	14848	A	954	1	349	AQPPFILFILHP\IYCIFSS*S\R*QKT LKTT*FQGFIFCFFFFFK/QAKSCSRIK GRGPIIAKGTPELPGLRDPPTSPT*VAG TKGGGPHTQLKFIFIAK*FYISF*HNGK FCSRRGR
948	14849	A	955	2	351	GLKNYAKSTLPVLYKWNN\KA*MTTHLF TAMSTE*FKPTVETYCS/EKKIPFKILQ LMDNAPSHPRALMEMYKEINAVFMPVNT ISILQPMDQGVISTFKSYYL/RNTFCKA IGAIDSDS
949	14850	A	956	336	3	PTKENFEPDGF\TG*FYQTFKELIPPQT FLKTSREYFSSSSSSSSSSSSSSSSSS SSPYRPI/SLMNTD/AKILNKILTNQVR LHIKRNTHHDLVGFIPK\WFNIRKTDQS NN
950	14851	A	957	181	1	RWDLTMLPWLVSNS\GLRRSSH/LPKCW DYRFEPPCTA*GWFLIGPHWNVSTVVGS PRISRQ
951	14852	A	958	3	293	GGLTSPHVKTYYQATVIKTAWNG*RGVC MDQ/YNKTENPETDPCKYSQLMFSEVTK AIQ*RKDSLVNIENWNN*MSIHKKSSSR KHLNQYLTPYTKL
952	14853	A	959	350	3	NKKKGQSLVFRSPTLFFFFFL*IEMG\F IMLARLV*NS*RRNMTTSGSQSVGITGV SNHARPKRKLFLFSIITTIGWAGV\WWL TLVISALWDYRREPPRPAVLLPFHIQRS RMPLSN
953	14854	A	960	349	1	GGFPPPLFFFPF/PPPWGKPPPPFFYQ\ SFPPKKKGGPKPPFFFGSPWGVHKKQFL VKSPLPFFWKKKKPPPPF*KKFFPP\VF QKQPGRVKKPPYERNSWLLGPPTKKSPK KSTGS
954	14855	A	961	379	160	PGPQGEPPFFFLKNPQKLVGQGGRLF*AP LLRGVRQKNSLNPGGGGALKPGS/HLWP PSWGKKGDFLF*KKKKKKK
955	14856	A	962	184	2	TFFSPKKIFPFFFFSKKFFPKGTFFSPR ENFFFFFFFF*DGV*L\CHPGWSAVVPS RLTATS
956	14857	A	963	1	328	ARLVLKS*PQ/CDLPASASESSGITGVS HCASASQSAGITGMSHHIRPKWISLYLG FWSFNKNVLHFFCASSLEGESMNNELLS

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						KKNWEFLDKKLHGSTKLGGNHVCVNF
957	14858	A	964	1	334	HPLGGRVGGVPLGP/VVLNPPPPQ*GTP FFLKKPNNPGRGAKPVIPAPRGG*GGKF LLPPRGG/PSMNPNCPPAPPP
958	14859	A	965	206	360	QKSMSLHQQ*QDIHSSQAHKNSSW\PGA VAHTCNPSTLGGQGMQITRSGDQD
959	14860	A	966	10	332	NFFSPGAPPPPFPFGGGFFLKKGPPFF* KKKILGGPPPPKKNPPGVFPFSP/AKNL GFPPPPPPFFFF
960	14861	A	967	1	282	RKCAKDLNRHSTKEDIWISTECI*HC*S LRKSTLKPRDMPHIY*ND*LYKKNDDIK CW*GYGVTGAVFHFHWVSRMVQPLLNNW TVPRNVKFTL
961	14862	A	968	339	195	FFFCRDGVSPCCPGWSRTPRPKQSTCLS LPKCWDYR/RL*ATVPSLDYLF
962	14863	A	969	3	342	IKKGPHPQLKKPPGVFPVFQFKKSYFPP PPPLFNNPFFFR\DKASLCHPGWSAVML SYFTAAYTSW\VRSSSHLSLLSS*EWRH TQPCLFF*F*FL/CRSK
963	14864	A	970	384	6	GRKNVAGFPLSPLYTPPHGHGLGPPQTF GAGPPAHKSHQKVGRQKRGPGFVPPRPP AFLFFFFFKE*SVLEKKENNLYNSLFAY KILNKVQGETQCEGRAHIC\VCVCVCVC VSVCTCVHVCALAIC
964	14865	A	971	427	109	LNSQFELQEKRISNLEDNEKII*SEKES KNRMARN/E/QSLRETWDTFGYTNIGIM ECPEGEEK/GKRKRKTIKKKMAANFPHL MKNINLHIQKAL*TPTRITCTGPYGG
965	14866	A	972	389	145	SLQP*TPRLMLSSHLSLLSSWDYRCVPP HLANFLYF**R*GFAMLGSSNSSA/SAS QSGGITGVSHHAPVVFTFKKKLVADT
966	14867	A	973	170	419	VSFLFFFFFLERQFYFFSPGGGEGGEFG LIEPFP\PGFGNFSCLTLW/RRWD*GAP PPLPAYFGFLIK\TGFPLVGRGGLDLRP SR
967	14868	A	974	212	3	QNSMIRYSRSMSRSCLCTTILILSLNRS LKSPR*/WPGVVAHACNPSTLGGRGGRI TRSED*DHPGQHGETP
968	14869	A	975	28	356	VFETSLFRNKKEIVKGTSLPDFRTYFKP LIIESI*CLHGIGQNNAWNRVGNLQIDA /ECAENLIYEKGGISIQW/SLFNK*CWS ITIHKEEKKIRPLHCIKIKGTKDFKKLS
969	14870	A	976	350	1	LFCKEKVSLLCPGRFEPPGMKKSTLLSL PKMRGYR/RLAPPPQLEIFFHFFLTSKA TPL/CLGRSLKRLNSQMFSPFFSEGVSL CSQAGIQWRDFGSLQPAILWFK*FSCPS ILSSWN
970	14871	A	977	4	343	PLHSSLGNIVRPHLLNNSNKNDTTKCW* GCEKPGFLIHCIWEYMMV*LLWKTDWQF LIKPNIHLPYDSAVAHLGIYPR*MKTFL QKL/CP*MFIAAVFLIAKNGKQLRCPSV SK
971	14872	A	978	3	424	KRMRRQATDWEKIFAKGISDKELLSKIH KELLKLNKKKSPKQVACFKMGKQT*TAH LH*TIYR/CRRVTHRKDHSTRSWLLREL QILNT
972	14873	A	979	114	325	QQQQNN*IKKLAEDSNRDFSN/EDIQMA NK*RCSTSLVIMEMQVKVTVRYYYLTLI

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						SIAIIKQKKKQNPKK
973	14874	A	980	339	2	GPTGFKFNQGGPPPKGSFFL*KISPPS* NPPFFFGPQKGFKPFFPPPYLNPGKNFF SKKPLFFFF*KKGFFKPPPFFFFFFFF* GRVSLCCPGWSAV\A*SRLTVTSTSHVQ T
974	14875	A	981	2	377	QMANKHMKSFSTSSAFMKM*IKNKMRSH DTCIRMANINTNDT\CW*GCRSNKILMH SW/WECKMVQLL*TMV*KFLIKY/DTYH DPAISLLGSIKKKSKFCT*/T/CKILYL NVLFIMNPNWKQSNWYSMG
975	14876	A	982	1	457	INEIEARNTTEKFNKTELTSSSSSSSSS PLVGLTKRKKSQN\NEGDITTDTIEII/ TIIKDYSE*IYA/NKIEQASSSSSSSKT YNLSGPHHEGTESLNRPIMSEEIESLSQ NLPTNRSPRADSFTGKFL*TSKDELPPT LLK\FQKTEQERTLPR
976	14877	A	983	332	2	TPKAGQMQVLFPQYGSKVARAPFSVVAL PPPPPFFHFFCFPQPHCSLPPQIPPPFS RFFLQVKSSQQGPPPSLLGWGEQ/NTLP FFFFF*SHSLALLPRLECSGAISTAA
977	14878	A	984	365	2	KSSKLFNYPPLFFFLKNFGPKKK/SGPF FCPFKNFFNPRVPGPNFNFKGFFFLKKG PTVF*IKKFWWGPLPPLK*PSGVFRFFH FLIWDFRPRPPFFFFFFFLVERGFHHVG QASLELLTS
978	14879	A	985	1	153	GVQWCNYNSL*PRFPG\SGDFPTSAFQV AGITGVHHHTRLFFFFVGFFFNF
979	14880	A	986	225	1	LYIYRERERERDRDRDRDVSHTHLYIHT RTHLDNILFCHPGWNAVA*SWFTVALNS WV\KSSSRPSLPSSSDSS
980	14881	A	987	2	375	GTDEYILIALIVVMVSWVCLFFFFEKKA PFCPPAGKTGANFGLRAPPPPGIKEIFW PP*PSEEG\EPRGPNPSRGNFWFFKKRG GSPL*PRLFG/HPRP*GNRPP*/PPQRG GNNKGDPPPPPGGIFF
981	14882	A	988	55	335	HIYIDVFVSGSWLLTV/ISLLELTVFCY NVGAL*ASG\QASENRISVSDFLLPSFY LPKAGL*SFPAFMMMGHKILIPEKVIPH MLEEE\TCTERP
982	14883	A	989	295	369	ILVTRNSEL*VLPEQRTRFLEKAMALRS IPLLKR/NGRPGTVAHACNPNTLGGQGG RIKRSGV*DQP
983	14884	A	990	2	240	KKISMNLEHFMLSERSQS*KTTYYMIIF T*KLQNRQIYK\TERIYIYIYIYIYIYL FFFFFLERKFLFLFPRGEGGGPF
984	14885	A	991	463	0	GFRQLSCLS\LPSSWYYRHMSPHLANPF \TF*VERGFRHVGQAGLELLTPNDSPSS ASQSAAIH/GMSHCTQP
985	14886	A	992	82	365	EICHQLYRSFLCSLFC/DHPSNKSH*DT MNCVHFIIRLLNFSFFFFEKKFRFVPQV EGQGSNLG*LKVLPPRLKPFSCLTLRRS WGYRGPPPPPVN
986	14887	A	993	3	317	GLKQSSCLGLPKCWDYRHKPPCPTHIIF NTH*IIKVLNVSFSFCI/PLCWSIALSD HVQ/PV*LYNMLVSSFLLLLLFFEIEVV ILACLFCPVGSPILFFF*YILTF
987	14888	A	994	350	139	LFRRLRWEQHLS\QGGQCCSEP*SHHCT

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						PAWATE*DPVSKIQQNKNQDTFSHTFIL ECRTSKGVSAFLAL
988	14889	A	995	219	1	RPRRPLIQKTKAKNHHFTPTRMPVIKDN NKC*QGCGEV/WN/CRMVQPLWKT/IQF LKMLNTELP*DRAIPLTGGKE
989	14890	A	996	3	498	CLPWAAVARQPPSAHPFPQPGP*LRTLA PDTATAVNQALQRQES*TGC*SPSGWPA VPTPVAPG/PPSAG*GVVDPRAWPRHNG PPGQHPKEKTYQPVPAP*VQLSPTRQTP APMACSSLLLPALPPPAPAARPPCPAPP FLPSRTSTLPPRRLSSTIKSKTPPGP
990	14891	A	997	2	419	ADTEAAASYPDNL\ANDESSYTKQQIFN VDKTALYWKKTPSRTSIAREGKSKPGFK TSKDKLTLLLGANAADDFKLKPMLTYHS KNSRAHKNYAKSTLCFRN*NKAWTEHLF IAWF/EYFKVTVVTNCPEKK/VLLLTHN APG
991	14892	A	998	388	405	G*FFPLSASKFFFCP*ALKLWMEGCHIR PPPQVRFPLQSSQA/GFISASLKGKGFP ASMPANIGPPKGYL*PAPPFFFFSFLRQ SHSVTQAGVQWRNSSLQPQPPG/LRRSS HLSLPGSWDH/MPPCPANFCIFCTGG
992	14893	A	999	1	423	WILHD/NLRQPAQWLDQEAAPKHFPKPN SH/QKKVMVTVCWSAAGLIHYSFLNPGE TSTLEKYVQQIDEMH*KLQCLQPALINR RGPILPQDNARPRVTQPMLQRLNKLGCD VLPHPPYSPDFLPTDYHFFKHFDNFLQG KHF
993	14894	A	1000	2	406	SDLFRAI*ETTSVIVYDVSMDYLEIDSE MIRDLLNTFPV\HLELQQDSSGVIQGAG ITEASTINAKEIMHLLMKGNRQRTQEPT AANQTSSRSHAVLQVTVRQRSRVKNILQ EVRQGRLFMIDLAGSERASQTQN
994	14895	A	1001	290	3	VTQLPETVPHFLRDRVSFCCSGS/DHSS LQPQTPGLK\YPPTSAT*VGGTCHHAQL IFIFLRDGVS\SVAQAGVQWEDLSLL*P PPPGFKRLSCLRNR
995	14896	A	1002	143	408	IKKKIKREI*KYLDISKNK/DTYQNLWN ATKAVL*GKFIGINVYIFKNRKN*NK*F NSTSGKLKKLEKKEQTKLKISRKETIKI RAKINE
996	14897	A	1003	84	409	DKLAALPSSWTLHPGSPLGVTRAPPPPP PPPPPPPPPRVLEPVPRSLYPGLAVPVV PRALH*PPHPGSLPACPAPGLLGGTRQC S\QTILPKKKPPPLDADPANEPPPP
997	14898	A	1004	392	2	EKNAVHFDQKNLVSIWEPLQVPTQVCIQ NKTNSWGIAGYPFHFLKRNQRFFNALKV PGPFSK*TIHLVNLKNLFFF*DRVSFCC PSWSAVVKS*FTAASTSL\IKQSSCLNH PSS*DCRHTPLLFFVRMRS
998	14899	A	1005	2	421	FVSLLLLITSAIVAAGAPTGRTVYPPLS GNYFHPGAFVHLTIFCLHLEGVSSILRA INFIASIISIIPPAITQYQTPLFG*SGL ITAGLLLLSVPVLAAGITI\LLTEPSLF TTFFDPGGGGDPILYQHLF*FFGHPEVY
999	14900	A	1006	1	428	DIHYG*IIRYLHADGASIFCICLLLHIG RGLYYGSFLYSET*SMGIILLLATIATA IIGYVLP*GQISF*GATEITYLLSAIPY

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						IGTDLVQ*I*GGYSVDSPTLTRCFTCYF ILPVIIARLPALHL\LFLLETGSNKPIG LAS
1000	14901	A	1007	1	419	SPIVPIVMAMACLMLTERIILGYIQLRP GPNVGGPYRLLQPFADAIKFLSKEP\LK PATSTITLYISGPTLTLTIGLVL*TPLP IPNPLVNLNLGLLFILATSSLAGYSIL* SG*ASNSNYTLIGALRAVAQTISYEVTL
1001	14902	A	1008	411	27	GQPGQHRKTPSPLSIFYF/ELAGGGDAS T*FQLLRRLR*EARLSLGI*GCSEL*LP PCPPAWVTK*DPVFGGRKKKERLSQLRK LRPREVKSLVQHYVAHKGGNWDPNPGPM ATQPGRSCTTLCVPLCHR
1002	14903	A	1009	21	377	MSLGGQQDSAQTTRSPQFAGFFGQRSIP DRTGLGFHLCVCKCVCACVQVSVCKCVH MCACACMCTRTPMCECVQVCECVQVCVR VSMCVQVCACVRVCACVCSGACG/CTCV T*MSLACG
1003	14904	A	1010	1	412	HKANTSTYLLTLVNTFSG*VKACPTTHK TAEVVASTLIEQIIPRF/GPAFISKIVK QVTTTLDVNWKLHTPYHPQSSGKVERAN SLVKQHLIKLALKTRQSWVTLLPFALAW LWAAPQSPTGINPFELLY/SAPLPLSN
1004	14905	A	1011	1	410	FRAVAGASRQENGA\TVILRDIARAREN IHKSLAGSSGPGASSGTSGDHGELVVRI ASLEVENQSLRGVVQELEQAISKLEARL NELENSSPVHRSTAPHTQQVSPIAPVEP PAEKPATPT*DDVDDDIDLFGRDND
1005	14906	A	1012	269	32	NISRIYKELLQLNNKKT\SISKRAQYLN RNFTKDI*MAKKPMKRCPTLLVIREMQI KTTMRYYFTPARMATIKKTDNNEY
1006	14907	A	1013	21	443	RIRKKNSYPHYVKSIVAYTFIIRLFPTT IFMCLDQEVIISN*H*ATTETTQLSLSF KLDYLSIILIPVALVATWAIIQFSL*YM \NSDPNIKQCLKDLLMFLMTILVLSTAN NLCQLLIG*EGA*MISFLLIS**YARAD A
1007	14908	A	1014	1	309	SSRAAAIHGGACLWLQILHRLRWEG*LS VGGQGCSKP*LHH*TLAWATERDFVSQK KKKKPQKANP\HLETSCKKKKKKPMLGP PKSQRKEGPKAPQGRTLWP
1008	14909	A	1015	3	256	EKNQILKWTMDLSRHFSKK\NMQVGNRH MKKC*TSLIIREIQIKTTMKYHFTPVKM AIIWPGAGITGMSHRTQPSPTLLLTHVV A
1009	14910	A	1016	397	3	LFFSPPPKWGFFFFPPPRFFAPPPFFFF PPPPFFFFFCEKPFFFFFFPPGGGAPPL SPPFFFFFFFPPPPPPPFFFFK/SPPPP PKKK*KKK*KKKKKKTPNTPKKKPKKPK KKKKRAAARDLELVGRVGGRV
1010	14911	A	1017	2	164	EKERRE*KREE*KERK\RKEGEREGGRE RERERKKKRKRERKKDRCMFIVHFRE
1011	14912	A	1018	1	406	NSSPPKNKN*NK*KQHT**EKNFANYIS DIELVFRTYNELLQLNKTGNPIKNSF*K NQFKNKGK*PNFYITQSF*RNKPI*KF/ AKDLNKRFSKEDM*IANKRIKTCITPLA IRKRQIKTTVKSSFKA/IYMVVVKET
1012	14913	A	1019	302	2	IVEPLFLGWLCLFLQNPRVKGPGPYFSK

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						GKANPVVFPTV\SKQPFKKPAFPVYQKQ LPLF/PALVDKKKVL/RFFFFF*DRVLL \CCPGWSAMVQSWLTTTSTS
1013	14914	A	1020	47	382	AKIALLHSSLGDRVSHTHIHTHKRSNEI ELVIKSSPKKKSSGLNGFPIEFYCSFK* ELIPIFLKLFQQ\VEAVGILPNLF*EVS ITLIPK/PRQEQNSNKTIYRPISLMNIG GK
1014	14915	A	1021	273	1	QSKERRQRTQEEMGKTFHNNRENGTLFG FSQSCLKDEIIIIIFETGFRSISQAGVQ W/P/NHGSLQPRFPRLKQSSCFSLPSSW DYMC*LPH
1015	14916	A	1022	327	1	KFLKGWPIYLKKGFPFVPQGGGQWANYR SLVPQIYGVK\YPSAFASKINSTMGMCP PAWVTFGMAQLINGD*IF/IFFLRQSFA LVAQAGVQWHDLRSPQPPPPGFKRFSC
1016	14917	A	1023	3	407	THLTQR*/HNIQTPP/WV*TGTLSTVLM NFYLWM*FHFQSITLFILRLLTTKLTMY QGWLDVTQQRSYQGHHTPPVQKGLRYRI ILFITINTFFLEGLF*ALYHSSLFPTLH *RGDWT/PTGIIPLKPLEDPLLNTFE
1017	14918	A	1024	3	425	LPPQKKRGFPKIPPREF*KTPPKKKKII FPPPGKNWPPTK/RFLKGPPPSRFIPFP FFPLPSSPSPP
1018	14919	A	1025	430	1	GGFPPFPPPKNFFFPLSP*IFG/RGVCPK FPPPKKRFFSKNPQRGFNNPPQKKKKIS SPPPVNFAPPRDLLKRPPPFFFFFFFFF FFFFFLFMHPSFPTSVPQWQITSFLCLL LILQCCVCVLIGMVVGDQSESSPSHHLQ PRWL
1019	14920	A	1026	463	494	RKTGFPRLT*HLDLDFFFFFFFWKGIFV APRAGGRGRNLG*LKPPPLGWAPFSGLT PPKSWN*GAPPPPPFNF/CVF*RKTGFP RLTR
1020	14921	A	1027	606	1	AGGPGPPKVVPGAFGWG/SLNG*S*LKG KGSKGAPIPQSGPTVFPGGIPPKESPLR PPGGMQGRRGPRWPGASGC/VG*DSVLR QP/GVTGEAPCPGASSPQASQAARRGSM GKGGAFHSVWGGCVLSAAWPGWQPPGSH G*/PGRRGGQSGCSCPKG*AWWRPCLAG SHSSAKHKGMSSEGPAPRGRAISPVSAG SIGPIAARGF
1021	14922	A	1028	436	1	GGAPQGVLKRAAPFFFFWKQNFNFVARI IKGKGGVLSPRQFPPLGFKKFWGPTPL/ SRWGFKEGLKPPGSFWFFKKRWGFSMWP RWV*\IPGPKEL\PPPFSQRGGIQGGT/ HRPPIIPPSLF/CFFEMETHSVAQAGVR WRDLGSLQPL
1022	14923	A	1029	1	436	PPKKIIFSPKP*IFWGGGGPNFPPPKKS FFSQNPPGVFFSPP*KKKKIFPPPPENW GPPKIF/YKRPPPPFFF
1023	14924	A	1030	28	366	EDHLSPGGWGCNEL*LCHCTPA\WRQNK TLSPKEKDHK
1024	14925	A	1031	3	142	FDCSALQEFGTRLYCPSWSQIPELKRCT HLSLPKCWDYR/R*ATTPGLRIVLELQK KLRR*CRELLYTPRSVTPNINDI*HWGG TFVTINEIISIH*YIALAGLRFLSSSDV LTSASQNVGITGMSHHTWP

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1025	14926	A	1032	7	361	PALRPSARGQQYYDETKNKTLCRNAQND SYLPDPNPFSRFSTL/DHSWHQLEAPDA *KAPFGLYWNCGARVCR\QGISAK*TEA CGLGTIKPSFFLIPLKQGELLGYPAYNE NLKKKKKK
1026	14927	A	1033	472	3	TKQQMLNVDRTAFYKKMSSRTFIANAEK SMFGFRASKEG*LLGANTTGNF\LKAML IYHSKNPRTPKNEAKSTLLVP*K*NNKA LVAAHLFTA*FTEYFKPPIEIQIITADN APGHPR\MYKEMNVFMSAN\TSIL*PMY QGIISCRIPAARIEVKGA
1027	14928	A	1034	488	0	PLR*ILAQRSGIHSMKT*SGEAAAE*KS EARSSWFLRFKEKSHLHNIKAQDKAAST DGKAAESYLED\TD*DGNTK*ICNGDKT AFY*KEMPSRMFPAREELMPGFKASKDM LTLLLRANAVGDVNLKPMMIYYTENPRA LKNYDKTQLC/PVLYKW
1028	14929	A	1035	114	491	NYFKNFTFSNKLTL/CLL*LFLL*KLFN F*TF*LLC/I*HLA*NTNTLYSCTKIFS FFIFLFYKHFLKFIYFFYFLDFII*GAY *SLCYY*VVYFSCQFCQVLFHVFWGLCC HVLVRLLYFQTDEPFY
1029	14930	A	1036	114	496	LLRAILTYLKYKISAMNLVSA*FIYLHL TYHCVF/DHPVQGR*LLNK*INELFCYR SFGF*WVFSYSHLSED*ALEEKYLRERS RWVK/DLNVTSETVKILEEILGKTLLDI GLGKEFMMKTSQANITKP
1030	14931	A	1037	381	45	KNRGRKKNS*LGGF\SDKFYKTF*KLIQ IIYKLFQKNEKEGTL*NSRPISLINIE ANIQN/RAVLAMIIQKHIKKIIRHNQVV F/IPGR*G*SNTCKSI\NVIHHIKQRRI KSIEF
1031	14932	A	1038	134	394	SFCDKFTNCISESLCQ/SYSPTYIIKIF VLFKIRSGSITQPGVQWHDHSSPQP*TH SWAQTIFLLSSQVVGTKGMCHHTWL/IF LFLFVF
1032	14933	A	1039	483	30	YDGGSEIINYVLESRLIGTEKFHKVTND NLLSRKYTVKGLKEGDTYEYRVSAVNIV GQGKPSFCTKPITCKDEL/AYVSTTIYT SETCTFVDL**DINKNDLPL*LQILAPP

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						AHIISQEKEIKKIQI*YKEEKLPLFTSS SLFI*VKNLMEFAKKLLELINEYNKVER YKINIKNILLAKNTWTLKF
1036	14937	A	1043	50	457	TKYQLANKNMKICSTLPIIRE/MQIRPH EISLTPIMMALSEEQKNNKYWGGCREVE TLVHCWW*CKTVQSLRKTVHRFPK*LKT ELP*ELPPK/PGSQRDICTPMFIAALFT IAKRFWKHPKCPSTDE*IKEMWYIQS
1037	14938	A	1044	2	469	LKQSSCLGLPKCRDYR/R*ATVPG*FIL *NTTEDPNLTKN*ILNTNH/WCYSVQLI LGESNSTIKTSLSFSQASSHQNTTVQFL STSPSFKNCQWLAILPRK*GLTLSFCFA FERQGL/NSVAQAGAQWLHHGSLKAQPP RLKQ/FLPNCPTLMECYRLQP
1038	14939	A	1045	42	200	LICT*MLIVALLVIARNWKQIRC/SST/ DEWLNKLW*IPMEYY*AIEKEPTIGTC
1039	14940	A	1046	475	36	LNVN*LNHPIKRQKLAG/YVRKHDPTIC CLS\QQSRFIFKDTNRLNIKGWRK\TFH ANSNQKIA/GVAVYVSNKTN\FTRNKE* NYILIKGSIH**CIIIINICATNS*NLK I*NKLTEMKEEIHCSKITVED/YNTLF* TMDRQKEFHRMQ
1040	14941	A	1047	3	326	FFFFIIIIIFETERDSVSKIIIIIKNKK DLF*FLVTQVTPEITNQYISTLPLQSKT KWDRPGTVAHSCNPSTLGGRGRRI/TLR SGVRDQPDQHG
1041	14942	A	1048	403	15	EVKNSSFSYRLMTEIMPFGYVSKLYNCD SGS*LS*SFNVCKMNRY*Y/LEERGNTS FKSLLLLMWKLLHSAIFTSA*TPRGL*I YFIYMYVLETWSHSVAQAGMQWHNQGSL QPSPPGLKEFHRTDIVYAR
1042	14943	A	1049	25	457	YMWWNSHHSCMFTLLFDSSFPPPSLCFI LRSLFLLYAELPLAFLLVKDSFILFV*I MSVFHLILKLQ*NIHNIYFTILTIFKCT VQWH*VYSHFSVAKTAT\ISRTCLIPSS WDYRHMPLCLANFFL*RQGLALLPRLVL TSWLQ
1043	14944	A	1050	14	478	FEPYCRH*TTRWN\CWWGYELVQSLWKA TEQYVLKPDICVF/LEPGVSLLGMYSKE LCTLC\YQKTRMFIATLFALVKS**LPK SS*MVE*ITKL*YFHTMEYYTAM/KNE* ITI*TTIWMNI/TIILNERSQTQK
1044	14945	A	1051	2	465	GIDQPSKPIPL/TQSFTQTKA/LTFFNS VKAERGEEAAE/ER/VEASSD*FMRFKQ RSHLHNIKVEGEAATADGETAGS\SYPE DPAITDEGSHTKQQIFSVDETACCWKIS SRTFAAKEKSMSVSKASKDRLTLLLRAS AAGDLKEFPRLV
1045	14946	A	1052	392	24	DFAPRRKKRETRRSKINSLTS**KELEN QVKTNQKGSRKQEITKIKVELREIETLK TFPKKKVNKSRSWFYEK\INKLDGTLAR QINKKRKENQ/DTIRNNKGDIITDPMEI *TTIRGIPPLWR
1046	14947	A	1053	204	488	CAVCYTQISLTEWVDL*SLDPGFETVSH LFDRVNQP*DCRRVTDMLMVF*NLHFVI LFFLFWF/DFVFVLRQSFPVVTQAGVQW RDLGSLQPLPPG
1047	14948	A	1054	498	2	SVVVCLFLSPGITSHTYVPMIFKIGAKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						VHWWKSILFNKSCWRNLISTCIRMKVDP M/LTPGTKINTNWIKDLTPSAESIICLK ENIG/THFHDIRLGNAFWDMTPKA*ATK EN*IPWITSK*QT\FCAAKNTVN*VKR* PMD*E/RIFAKHISEKRLICVIYKEQLE LN
1048	14949	A	1055	28	209	IDGRSRGLWW\CVVLASQLLWEAEAGGS LEPKSLRLQ*AMIM\DCTPPW
1049	14950	A	1056	163	479	TSFLGSQSAGITSVSHCPSREVFFLKLI HWRQGGQVALLVATPHSPCCPQYRLAPI PRARHDFACASLIFVCILLVHVLLMPRS VAGRGVGSGLLG/CQAGR*L*TC
1050	14951	A	1057	2	1258	ELFPWHFQPSRAASLVVAKAIRDKVPGT RRWPVPTDGRPEGFALSEPHHSCLHGRH QGPERCRHMAASP*EAGNK*PKDKDGHP GERTETAAGVHTGCGGKGPAAAGGR*AQ GGSGEAGAAAGGAGAAVGGAGAAVGGSA GGRWPAGLLGQHGAG*GEGPCRQHGPPP GVSAGQAASPAKAAGQPGPGT*GAAGQP GRG*GPAGPRGGAAAERAGAGAMPAQGP AGAAAEPAEGEARPGAGDYGPAANHPGA RTGAGGAEGAGAAAGGLPRPAQAHR\AQ IHGPVPLGTGGRSSS/GGIPDNMSHRLW QRHRSHGEASAGQRHPHPGPTGGER\GL QSMLSKIREVAQQGGLKVGLRGRALGDQ EEAPIQQQVFRLCPGNLWR/RPPHHMRP *AVLL*NIFHISRRREDVMDPMPSSPIC PL
1051	14952	A	1058	2	437	ERSVRTACCKQSRGLSSLLCPPPAPRLS *TGSPVTGSSALEPRSPHPQP\PSLRPR SPGPQPLHPLGPRSPSPSPEQTVPSHPA RLPSLSPERTQG\PKAQ*SQLPPPSLAL AQPAPAVGGREEVASPACPSWKDKSRLR AVPGSA
1052	14953	A	1059	47	456	TRCYGTLLRLDAPGKLWTRKM*VVASTY ARTDRKSSASFRPLLPLPRGFQLSLHFS LTSPSCLAFSANTHRGLRGENYHITK/C DMAPKV/HN*TQAVVQWHDFGSPRPPPP GFGRSSCLGLPSGWDYSPLWHHEQIL
1053	14954	A	1060	484	13	FPTSASQNTGTTGVSQHAQPIIF/LFVE MGSPQV/GPASLKLPTSRDLPTPASRAA ESVSAHHH*FLNFL*RWASGFVAPSWS* TFLL\KQSSCLSLPVC*DCRCYNHWAWP HSVFSSQFLSLFPFNFSFLFFLSFSFFK DRISLCRPGWEFHQTVQWSR
1054	14955	A	1061	1	494	GSPGHPVCGRRRSALENPGQPCSLQPGV VSGATGAIVRVQRTSSAWATAAAMGAYV E/TTRFRYT*KAGVGCDRLWGAWLKADG LGETKAEHTLHDG/PPEDALYGLIEGDD TNFTIQGEVVHCWYTGTLPDGTVFDTNI QTSAQKMM/NAKPLSFKV/GIGKVSH/G WDE
1055	14956	A	1062	3	395	SDPSPCGGIRFDEMEKFLENYNLPKLKE /DKINDPTFVK*IGSVMKIFHTVEP/PS HKCFTSEFY*TFKE*IAPISHKLF*SRG IMGTATPPVMFHLQENVIPK\PTEKK*T YRPVSLMNIN\KILNKILTYK
1056	14957	A	1063	402	260	WYCPPKV/LLRFSVYSSPPEVWAVGSIK

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						AELYMLRPLFPRTREVD*IF*ICPV/LK GSPKNKDFCP*GAKTFEYFYPATLGLNL KI*IFRQRW
1057	14958	A	1064	66	379	EFGRGCGEPKLRQCTPAWVTEEDPVSGG KKRKRKEREKT*REPSVSRPESH/PPSQ EAFWVVQALSRPVLPNFISGRSASGLGK SEAIKSLFLYLAVCSTTEEQA
1058	14959	A	1065	223	437	KSCMSCDSNKIFFLRQGLSCSLTQAGVQ WHYLGSLQPLPQGPK**SHLSLLSNWDY RR\PPR
1059	14960	A	1066	414	65	NKSPDRNELAS*KCTQ*THTSIARDFFA KTIQWGKNSLFNIWC*DNWISTSKRIKL DPYIIPYTK\TNSKWIRDLHVKAKTIKL LEKNGPGAVVCPCNPSYSGGLLEARSLR PAWAT
1060	14961	A	1067	418	1	LWVFFFSRQSL/DSVAQAGVQRCDLGSL QPPPPRFKRFSCLSLLRSWDYRCRPPHV ANFVFLVET\GFTMLARMVLNS*PCDLP AAASQSAGITGVSHHARL*FCGF*YIHR VAQPSSQSI*DDHPIKKFCIL*QPTPFR S
1061	14962	A	1068	24	440	EV*NLYSENYKMLLKEMRGDLNKWKSIP *S/WI*RLNIVKMAVLPKLIYRFNLIPI RIPDEFFVKSTS*L/CKFIWNCKRLRIA KTIF*K*RTK/SGDLILTDFKTYYKTMV IRTI*Y*QKDRCID*WDRIES/PEMNPY IY
1062	14963	A	1069	442	26	LRNQVSTPSSKTPRFFFFFFLKRQTGAQ RHNHSSL*PRTPGLKQPSTSASGVSRTI GASHHTPLIFFYFFN*GKEGWGGCSCFV AQAGLQL\RLQMILPPQPPLKCWN*RHK PPSLTYPIFLKRTP*SCFSKEKATRIPP
1063	14964	A	1070	294	46	KNKLKRKERKENNKKKAKINDIKNKSML EKIHKDKN*FFERNNKIDKLLATN/RIT KKTQIVIFMNKIRDITTYPTDIKNVKR
1064	14965	A	1071	141	469	PKKQGVQLTQNAPLPFRVGGKRGLCPKK KKERERDREIISIIIIIIKLPTKKTPGP DGFTDELYQTYK*LTSILLKVFLKKRRE CFL/PYSMDPAVPAIALNPPP
1065	14966	A	1072	49	472	EFQIIKK*NSFFADTEKALVWIENQNSH NMPLSQSLIQSKALTLFNSMNAERVGKD AEEKLEASRGFWFMRFKKPSP*HKVQGE AANLDVEATASYPEDLPEIIDEGGHGKQ /QIFNMDEIVFYWKMPSRTFPAREERSM PG
1066	14967	A	1073	82	419	LTVGFRETRSSSWVCSSSPKRALHALRF TPALKF*FFFWSFSRLFFFFLRDRVLLC CPGWSPTLGLK*SSCLGLPKCWN\YRYE PP
1067	14968	A	1074	1	407	LEDGFFKITQSDKKEKKRI\KKCK*NLQ EVW\DYVKHSNLQVIEIPE*EVKCLENL FEEVIEANI/PHLASYLDIQIQAVQRTQ RGYIARQTSPKHIVVRLSKVNMQEKILN LPKEKHLITYKGNSIRLTAKPSPKPT
1068	14969	A	1075	3	396	LHAYHIVKLSP*PLTGALSE\LLMTSGL TM*FHFHSITLLILSLLTNTLTIYQ*WR DVTRESTYQGHHTPPVQKGLRYGIILFI TSEVFLFAGFF*AFYHSSLAPTPKLGGH

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						WPPTGITPLNPLEVPLLNTS
1069	14970	A	1076	250	47	VAACQNAFCTFSCYWL*NLLCRK\MDLD ISLLP*TKVNSRWIAGFNVRALTIKILE ENIGSAFGNRHSQ
1070	14971	A	1077	2	393	PLTGALSNLLLNSGLAMRDDLHSITLLI LGLLTSTLTIYQG\WREVTQESTYQGHH TPPGQEGLRYGTMLFITSEGFLYTGFF* AFYHSSLAPTTQLGGHWPPSGITPLYPV ESPLLNTSALLA*GVSIT
1071	14972	A	1078	2	500	LHVIGVSEGEEN\GMKQNKIFEEIMGPN F/PNLVKYINA*/IQEMQ*TPNGIHLKK TVHRYIIFQLVRTNNKERILIVAREKWH GIFGGTML*MNDDFSSEFIKARKIEMMF LKYKRGISSSAKHC*SRILCVAQISFVS KG/EITTFSDKRKLRAFIISRPAHRNAK GK
1072	14973	A	1079	419	1	LRWSFALAAQAIVRWRNLGSLQPLPPSS SNSPGSWRLQ*ANTAPLRSSLGNKNETL SQKKRK*KDNSEWEKIFANHASDKGLVS K*IKNSYNSITKN\DI*KWTKYLNRHFS KKDIKMANKHMKRCSTS
1073	14974	A	1080	468	2	KLPPPRGAGSSAP/PLFFPPTKKGFFSP PPP*KFFFSPNPLIFLGGFFPIFPPPKK NFFLKNPKGFFFSPP*KKKKIFFFPP*I FAPPKFFFKSPPPLFFFFFFFFFFFFFF FFFFFFFLRTRGRTRGRTRGRTRG
1074	14975	A	1081	467	1	PTYKFNAIPIKIQ**FFKKIENCILKFL /WNLKEPQIAKTVLK*NKVEGFTLPDFK \LTVTKTVWS*HKDRHRDE/WK*TESLK IKPYKYDQFFFFFF*FSFL/HFF*YLTY SQHHKLIFNRMPKPFNKERLFNK*CWEN WISICKIIKLDHYLTPYTK
1075	14976	A	1082	387	3	LKQPPPHKSFVKNKNGVSLCCPG*F*TP GLKRSS\HFDLPKCWDFRCEAPVLSLLN NIKL*L/CGRGLIKPQFP/SVK*K**AP SWSAHLAETFFFFRQGLTLLPMPGVQWH DPGTVQPQTPGHK*SSHFSL
1076	14977	A	1083	2	435	FHPPTNWGGFSPPPP*KFFFSPKALNFG GGVGPNFPPPKKRFFPKNPRGGFIYPPL KKKNFSFPPPLKLAPPRV/SFKRPPPFF FF
1077	14978	A	1084	447	47	PSRKFFFLAPPKRGFFPPFPLKNFFFPL GGLFFG/RGVFQFFPPPKKGFFFKKPRG VF*PPPKKKKNFFFPPRENLGPPGVFLK RPPPFFFFFFFFFFFFFFGRRFVK
1078	14979	A	1085	438	2	AKNHPKGFSPFKKFSPPFGGGGIFIRGQ L*KSFFFFFKKPKFLV*KPPFKIFFF/I FFFKQRVLAL/CPPGGNKGVPQGPFPIF FSRVGKPLFFNPPKNWGKKNPPPTPGKI FFFFCSFFL*RQGLTTSHRLVLNSWA*A ILPLQPPK
1079	14980	A	1086	43	265	IKHKLEYIKIKNFCASNSNR/TERQPME WEK\MFANLISDKGLIPRIHKQLL*LN/ TKQQNSPI*KWVKDQLQWPYL
1080	14981	A	1087	11	412	IASGLHDFFNKKKKKKKKKGGGPLKKTP GGPKFNRGGKKKIFSFKGGEKKTPGGFL EKNPFLGGGKMGQNPPKKKKPFGEKKNF *GERGEKKPKFPGGKKMSPSPQE/NKAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						RDDPRPPE
1081	14982	A	1088	2	292	RSLPASADSSSLVAASLAGVRDRVSTCW PGWS/AV/VQTL*SARLGLPKCWDYRCE PPCLAEAPSFMRSGKASCTLETVWEDKH KYEEAERRFYEHEAT
1082	14983	A	1089	376	3	HIGLYIASCKTLLKEIKGS*IDILCSWI ERLNTVKKAILLKLIYGFNTIAI/KILS GLFIETERMILKITGKCNRSQTANTILK PNKVGRLALPNFKTYYKATVIQTVWSWH KDRWYGFFCVPTQI
1083	14984	A	1090	277	407	QIKAERSHHKQITSMRNVKHCSSENYDS *RKPAPGYIIIK\F*K*LIKRKILNSGR LKNRPIKEE*RYAYQDISETIKVRR*EN DIFKVL\KEKKSCQPRLLYPLKIS*IEV KYFFDKSKLKEVITNRSPV*EMLNIVLQ /INYDSPYEP
1084	14985	A	1091	421	2	GHPGVLFKG**A*NEKSL*NCSFFNY*S SFSNMQTRIKNV/WPSTVAHACKPSTLG GRGGQIT*GQEFETSLANTVKP
1085	14986	A	1092	369	3	FLKEIRSVTPVNT*ENLIAD/IGEKVLV VWIENQTSHNIPLGQSLIQSKVL/TFNS MKTER*/EKLQKFEASRGWFMRFKERSH LH/NIKVQGEAESADVEAAGVYPDPAKT IVKGGYTQ*QIFNVDV
1086	14987	A	1093	71	506	FAEDNGL*LHPCSCKRHDLAVFYGCTSF VLTFGL*PWFLTQS/FLNPLEFS
1087	14988	A	1094	118	385	SDLGKDFMAKTSKAQAAKTK\IYTWDYI KLRSFFSAQ*TKQSTE*RRQSTE/WKEK IFADYSSNRGLISSRQETQTTQWLKKIN KNALCTL
1088	14989	A	1095	419	1	DAKIPGQMVAR/RIPRPIKKIFCPDQVW FIPGMQGGFHIGKSINVAPHIQMG*KSF NNIQHPFMI*KKKNLSTGTTHEGDITQH /R*MLHEHTTNAILNREKLKAFPLRTGI RQGCLL*PLLFSIAVKT*P*AMRQEKEI N
1089	14990	A	1096	34	464	NSSKKEKRKIPHDLGLRFLDMTPKT*ST NGMMD/KDFIKIK/FCASKDTINKVKRE *EKLQIIYL/DKRLVPRIYKDSYYPIRQ LKKWVNNLNKHCFKEDTQIANKHKKECS T\SIRE*QTKTR*RSHFISTRVTKIKMS G/N/NKYWQGC
1090	14991	A	1097	458	28	RIIKVDLKMCTHNFDSLEEMNQFFKKSR WPR*NR*FE*SYNH*RN*IHNLKVSKSS GPDAFTGEFYQTCEEELAPILQNLFQKM ESIRSNSFYKVRITLIP*GDNGS/TKKE NYSVVSFMNLDAKVLIKILAN*I*VFIK REFH
1091	14992	A	1098	41	500	FWIRHFLSRHKQRKNR*MDFIKIKNLYA SKDTVKEVKR*ST*WENYFQI/RMFDTG LVPRVYKEFI*LSNK\DNHI*QWGKKAV SRGFSKGNTQMAKKHMQRCSMFFVIRKM *I\KPKMRYHFTPSSMT*EKNKDNTCFK SDGEYGILIYYYWGI
1092	14993	A	1099	1	484	RRAPFFFFFFKRSFPFWARAP/LQWAFF GLVQNPPPRQIPPPGLHPF/SCPNPPKK WGYKGPPPTPGKILGF**KGGGPRLNKK IFISRPCDPPAPTP\QKVGIQGGTPPPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						PFFFFEMVSCSVAQAGVQSCDLRSLQAL PPGFEQFSCRGMPLKWIGSHPSPHP
1093	14994	A	1100	144	260	ILILDSALGHPEPHEFNTKGIEVVYLPL NTMYIIQPLDQ
1094	14995	A	1101	265	457	DPAAPLLVTYTREI*MYITKRYTAALF IKTKNWK\RPKCPSKGE*INKLWYICTM EYCSAIKNE
1095	14996	A	1102	387	40	RLRADILRILVYNNFLQRLKKQRYLFTG PQYRFLFLELWLCVCVCVCVCVCVRANF *IISRDKVLLCCPV\CFCFLNPPCVCVC VCVCVCVRACAIINKLLVETRSCSVAQS GLR
1096	14997	A	1103	465	208	QNMTKTFQDYRPISLMKIYARKQQYRYR Y*RMLHNYQMGFTLGLRGWFNI*K/SII IHIN**EKKIMIILIESEEAFDKC*QSL II
1097	14998	A	1104	57	250	MTCSRMQ/RNIKLLRYKSEKL*EENSTS RNEITILSEEDSFTNVKLEN*MKTVKQK KKTSKKTGVYKMAIKKQISEFKGKTSNF Y*EQINT*EKKNFKENWSL
1098	14999	A	1105	2	378	YVDPRQCGGILKGVLKGEFTISNEKANP GRGSPSSVSKD/L*CQNIKTIESKKTCL IQKLIKVKAEIYERESRKTMEEINETK/ SQFFEKI/NKID*/PLARLTKKKKKTQV LKSEK\GNITTNHTEIKRV
1099	15000	A	1106	291	1	VSIYVSYNLDSCKGQIRIKSCDDQYIFK RLYFFEITFLKFLN*K*VLKKIRDNVLL C/YPGWPQTPGLKQSSCLSLPSSWDYRH VPLHLAPINYFLW
1100	15001	A	1107	24	397	DIDHVWEFETVFYHVGQAGLKLLTSDDP TALASQSAGITGVSHRTRPSSGHFNNTP EPPEASSLSSHPKLHKSPVT*NGAGL/Y GSSKLLSCVLNGPISLVHSTLRLRKGGP QGNISQISLMAPP
1101	15002	A	1108	64	414	AQLTPTQPQGRAALHKGHV*RKTAPTCL FMAEKNQAASFFLFPFPSICINKE/HFK KKKKKKKKKKKKKKTRQKKKKGPEKPR KQPGGGLLISKILVVAPPPGFFLTREGP PPIFF
1102	15003	A	1109	62	475	FEPLFYLMCLLNLFPLQLPRHPFLFLTV DLVNTWGCPLPSSPQ*EWLLAAPHRSTP PPLSSGFPARRQLEPGAGARGP/HHTQA LHLSFFFVFLRRSL/DSVAQAGVQWRGL GSLQPLPPGFV\ILSSPLSLPSLTY
1103	15004	A	1110	76	477	EEWKKLYRWRENISNLISDKELIC*IN/ NQTFNIQPLKTKNPTKDVNDLKTFTNED TQKYTYIHQ*R\SHMKR*SP*LFI\KMQ MSTALRFLYPPITMDRIQIPENIKFWRG CGILIHSW*TRKMFHSL*KAFWPF
1104	15005	A	1111	1105	3	KEERSETLAKGKLIAAGA/YN*KEERSQ INNLTLHLKGGKKTNDKPSKR/QE/I*Q IRAEISRIRPRKKKEKNNEFVFLKINKN FKTHSYIKKKREISNTKIINKRGDSTTD ATEMKKITRD*CEQPSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSS SSSSPPKKKIPGPDNFTGEFYQTFQEEL MPALCKIFQ\NVQKPEGDI/PNPFYQVN IYLVPEPDE/QPFVIKTLKELVIYGN/Y

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						L/K*IKIIHEKLTANIILNGEKLKSFPL GSGIR*QHLFLPLLFITVLEFLLRIISQ EKVIKRMQIGKEKV\KILFTDNRM*WV/ ENP/VNSQNIGKIMKFNKVSGYSNTHKS VAFP*TNNEQSANKILK
1105	15006	A	1112	37	466	DRAAEFPTENPLELISKASKVEEFNVSI QRPIVFLCISNKQLENEILKIQFH*/PI SVASKNSKYGGINLRKYL*DMHIDNK/P LNKNRGGLCSWSATSVLPKLIDNFSAIS GNYSRFFFFGEIEKLNLKPIWKYK*VRV AKTVSY
1106	15007	A	1113	33	436	PGLN**CWKNRISTCKRMKLDPNLAPYT KITSKWIQDINIRPVTIKILKENRGKGL QH*MWQ*FF*I*PQKQE*TNRTKSDFIK TAQQRKQQNERQSVEWEKI/FANQISNK ELLSKIKFRLLPLDNNKQLT*KWA
1107	15008	A	1114	2	391	PLTHSRMAIKKETK\NYKCWQ*SGGIGN LGNCW*ECKMF*PLWKIVLQFLEKKKRN TELP*NPLIPILGIH/YKRNVCIQMFTE ALFIITK/SWKQPR
1108	15009	A	1115	3	458	IRDPLEEAVCPFADLKLHAGRTTTLFRA VRQGPLSL*KLLLPFVQLSHVPRGGVYR GSQASLSCGGLHPVQAS*LLCLPTQASA MADAP\PPASLPPCSSISDCCASSERGS VGMGPSEPGMGYNLLVCRLLRPLEKPSI RVGVSLFSRYHM
1109	15010	A	1116	204	13	PKMKTDSRWILGLFF*FLRQSL/SSVIQ AGVEWRNPGSLQPPPPRFKQFSLENQGI PPHGLVVS
1110	15011	A	1117	34	454	IHISVVEFLTSKLYGTLTSQYNKKTNIL IK*MGKRFNAHFT*EGI*IVNKHMKRLP TSSVIREMQTKTTVGFRSVLTREAGIKQ TDS/NQAWVRKWSNSTLLCCWWKHRVLQ PTWN\TAWQLLIYKMIWQLHFYAQKDIY VN
1111	15012	A	1118	83	451	CFLKFFLYRELISPFLL*Q\FVRPSPAF RRKPPPWVAFFFSDPS/FSFLVFFPKGI VFFLGDALKKVLT*KKNFFFFGRD*VLL CCPGWSRTPALKHSSCLGLSKCWNSTTR P
1112	15013	A	1119	316	441	FIFFFFLKTNFNFFAQVGGHNRNLG*LK LPLPGLKQFSCLTL
1113	15014	A	1120	67	312	RQIDQWTRIES*ETDPREYSQLIFDKGA NPIQWRK\LFNKWFWHNWTSTCKQIKKN LDIVLASFTKTSTSHRLRENLYRIHI
1114	15015	A	1121	27	490	GTQLHSREKKNSPFNK*YWEN*ILTCKR MKLDSYFIAYTKINSKWIKDLNVSLLGL LAKIK*SPKCKIQNY*TSRRK*KGKDLG Q*FLGYDTKCKATE*KNK/LNKWDYIKL KNFCIA\NKTINRMKRQPTVWEEIIANI ISDKVLISRICKKTNR
1115	15016	A	1122	490	48	EHTNNKRDTLTVDIGKVLVI*TEDQTSC N/IPSNQSLIQSKALTLFNSI*AERGEE ATE/EKLEASKGWFMR*KERSHLYNIKV QGEAASADEEATASYQEDLAEIIDENG\ KQQIFNSDKIALHQKKM/PREKSMPHFK VSKDRLTLLREF
1116	15017	A	1123	2	259	IYGQLIFNKGVKTIQ*RKNSVFNRCYWD

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						N*ISIWKRM\GLDPYLTPHTKINSKWIK DLNIRTKTLICSSWRKKKRENFLKKKRK KL
1117	15018	A	1124	206	24	CSIFFCIYLFIYLFIYLFIYLRQSL/DS VTQAGVQWHYFSSLQPLPPGT\GLF*RT SYSWDF
1118	15019	A	1125	3	351	RRGRGFTILVWAQTPDLM/HPPALASQS AGITGVSHCARPICLFFKRQGF/NSVAQ ARVQWWDHGSLQLQPLTLR*YYHLS\SW DYRRM/PAMLGFFVFYAYPGITLLPRWP WISGLNELP
1119	15020	A	1126	2	349	STNHKDIGTLYLLFGA*AGVLGTDLSLL IRAELGQPGNLLGNDHTYNVIVTAHAFV IIFFIVIPIIIGGL\GIWILP
1120	15021	A	1127	362	2	RVSLHCPGWSQTPELKLSSCLSLPKC*D YRCEPPHPAYLTSFITEDSKNFEYVTTL F*NNIY*TMFIEIPP*VHYIGAHLF*DQ LSTFF*SF*N*FFVCLFFRQSHSVAQAG \VQ*CDLGS
1121	15022	A	1128	1	349	IYFLTRSHSVSRAGVQWHSSGSLQP*PP RFKRSSPPLSLLSSWDHRTWG/HMPP/H SSSFSSSLFLRSGWGGKGVLWS
1122	15023	A	1129	367	24	INCVFYPCKGVTKKPWYT/HF*RKGFII INIFHGPFKLTFVCPEGGKNSETLYPFC FLPLSLAIKKSRPLGVFLV*KGPLSPPL QGNYGVGWVGFFFFSAFVIFIKKLVLSP YYKN
1123	15024	A	1130	61	299	IPRVDNYCGYVREHLFSFLFFFKRSLV/ SVTQAGA*WRDLSLLQPLPPGFKQF\SC FNLLKNHCYRDVPLLLNTLCIIFKT
1124	15025	A	1131	2	261	FFFFLVFSFFLLRLFLLPSPSSPPPSVF FFLPSSFSL/CLVSRDLLTLSQTKVQWR DLGSLQPLPSRFKRFSCLSLPSS*DYGR TPLW
1125	15026	A	1132	2	381	EFYFFF*SSQMESPSIAQAGVHWRDLG/ SIAPYASWVQVIILPQPPPPGFESFSCL RFPSTWDNRHAPPRLAKKRNKI
1126	15027	A	1133	2	221	PSLLKKLARHSGRCL*SQLLRNLRNENR /CVPAWVTK/GETPPSKKKKKNPPPKGP GAQTFETPGFGKPKGKIKV
1127	15028	A	1134	331	2	RGPPPPLKEPSGVFRIFQFKNLESRGGG ERGKQSPPLGPPIRRGLSPKPPPPEKGL TVFFFFFFRCKDGVSFCCPG/WISRTPG LK*SSCLGLPKCWDYRHEPPHPAPAL
1128	15029	A	1135	3	391	AVNTQMMRK*KSLIADVEEV*VVWIEDQ TSHNIPLRQSLVQSKAL/T*RAKPSMKA ERGKEAAKGKLEASRG*FMRFKENN\RL HNIKVQGDTASADVEAAASYS*DQAKIT GGCGYTKQQIFNTDETAFY
1129	15030	A	1136	107	350	TYSIVAIVMRFYFFIIFYFLRWSLAVVI QACCCHPGNWHDGSLQPLPPGFHKFSCL SLLSS*GYRCPPPCQA\IFIFLVEMG
1130	15031	A	1137	35	297	TLMHYTNRVKEKNIIISIEAEKAFDRIQ HPHM/IKYLNTIKAVYNRPTASIILSG* NLKAFPLKSVTQQGCPLSPLLFNIILEV LSTRP
1131	15032	A	1138	378	1	PFTKINLKWIIDLNIKHKTIKLLEDIIG ENLDNLGHDYDILDPTPKA*AMKKILIN

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						VALC*NHESFCSENDTVIRMRK*ATDRK KIFAGDMIKDCYSKC/NEKAEVNNMKKN NPIYKWAKDLNMLL
1132	15033	A	1139	271	361	KW/YWNPIHIISQVCL*GPEIYQHVYGQ MTKQRCQGNSM/WAKDSLFNKWC*NKWI FF/C/RI*NLNSYLTPYRKIK*KWIRDQ NITVTTKLLEENMRFSFAFGIGKD
1133	15034	A	1140	28	340	LLYF*YKRGFTMLSRLVSNSRPQ/CDPP TSASHTAGIADGSHHARLLFFLEK\EPA FGPPAGRKGANFG*REPSPPGFRGIPP/ LPPPGNWD\YGGPPPPKPNFGFF
1134	15035	A	1141	94	128	GSQMPRHLVD*MTRHLATLRES\CYSR\ VYPRFIEFLHFDIQSTGQKSHR
1135	15036	A	1142	85	492	VWVGLLSLEGSPSKFGNFIEFGVLLSSG GFSAWRLFFFVYFLRQSL/NSVAQAGVQ QWRDLSSLQPLPPGFK*VLKQRGVCLFV CFETESHSIAQAGTQWCDLGSLQPLSPE FKRFSCLRNSRSLRRDIEPSEGNQC
1136	15037	A	1143	372	3	KMNR*PISIKEIDFIVKNLPK\KFGPDG FTGILY\RHFKKEIIQTVCNLFQKTEKE GMLS\IYKASIAQIPKPEKDKQTKATD/ YKPSGIEAKIINRILANGIQQYI\HDQV RFTPGMQGWSNIQI
1137	15038	A	1144	56	482	TMKTLLYWQKNG*VDQWNGIESPEIDPY K\YIQLVFDRKAKTCNV/RKDSLVNKWC TYAKKKKTLNLFFTPFTKITSKTYLKNW N/SVNFLNTPLGKTLGDLGFPRDFKFLN TPKAKSLEKH/MDTLNFFKGKICS*KNM VKKNKKT
1138	15039	A	1145	190	482	RQGLALSPRLECSGVIIAYRSLKLVGSS DPPTLASQIAGITGIRHCPWPKTLFLAS VIMPAHNS*PSLSPVPSP\SLPSPPLLA SQSRRSQ
1139	15040	A	1146	138	485	IFFPSV*TIFLLLALFFS**MYLIFVKS SLSIYSVYQF/SFLCFWSPISDPKSQRF SLLSFIVCFFVFPRNRVLLCHPGWSAVV *S*LTAVSNS\LLKQSS
1140	15041	A	1147	101	426	GDWKKFYIYKHSESKSPLILFEKKKGVL EEYSSFDI**AIKVIYHISRKRK\KNQL ANLTDAEKALNKI*HPFMRKTTQQFSNR SFLHLRKGIYKKPTANMIIKEQIIF
1141	15042	A	1148	458	15	VFVCLKICKHRKGTAKKWYYNFMGLPLY MRSVVDQNGTM*KMTIYAPNIGAPKYIE QILMGANREVNSNTILLGDFSIPLSTL/ DKELPELNFT*NKTDLTDIYRTFHPMAA KYTYFAGTHGTFSKMCPVGFDIRVILVE FRRSTYGLDW
1142	15043	A	1149	1	507	KGPPAPPPYYKKKFQGGPKKFPP*SHPF KRPRGEDP/YKPRNLKPPWAKKKNPPFP KKKQRGKGPKNPPPWKVKPEKSF*PSPK KTKIWPPPPPGGQKKKKKPPPPKKKKKK KSVSSSPKNI/YRSLFCTNLKKSFPT*F *NLMP/TKLPV*EFPPPPYNSF*SAP
1143	15044	A	1150	436	32	NLCMYVYMYLIYVRTYVCIYSIYVSIYL IDLSLYHHHYLSICMCVSIYPIYLSLIY LCISLIYHLFNLCIYISIYLIYLS/YVC M/SSI*SMYVCIYLIYVCIFSISLYYLY IYLSIITIIYLYLCMYCLFYLSSIEF

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1144	15045	A	1151	3	657	QDCKIQNEHKIQNTLFLYTRNAHIKIKF HLHSKKILAVNLTKHV*NFYAENYTTLM KEKI*IERNKDLHRKQ\NLNPCIWIVKL NIVKIPVI\PHR*RSLTIPIIIPAK\FF GDKEKIILKFIWKGKGIR*LRF*KIRIK GGLNLPN\LRLTVVTVIKIV*YWWKERD RYLNQ\WNKIENS/EKLKPRKYVQLISF VFDTSG
1145	15046	A	1152	430	438	TFWVKKFFLLNLPK*INPGFKKKKNKRG G*KRP/SGSQVLKKLRGKIALTPEGKGK IRDCFCPPPPPLRKKKKPPIRP*KKKKK KRKRDPPFGNHYSNSYRHTSCYFTLLHL TLQIFFTSRSPVAMSCRINL
1146	15047	A	1153	104	478	ELLLEGSPCLRAESKAGPAGRLVPTLLS WRVQSPGVLCAWEEECEEPPSTGEDAPS LAIRETQIKFITRNHLSPLSMAIFQTNN DN\RTKRK*CWHGCGEIG/T/LLHCWWE /CKLTFP
1147	15048	A	1154	171	476	NSSDYYYYFLRQSFTLVPQAGVQWHDLG SLQVTSDDPDLR*FARLSLPKCWDYRRE P/RMSDSNYFLK*VPVN*KARA*LLFIP SSCQAG/ASAGQTLSVS
1148	15049	A	1155	3	562	PDYQTARRRQAPADRCQPGPAATICPR* PKARSSSMNRSNPTVTRTAGP*PSWKTG AASKSQTGDGDRKELIPPNRTPNN*VST AAIK*QVRPYLTQKVPAG*TFCPHQKLQ GVRPLCRGPP\RPFGSPAVTDNRQAKLK TPTQ/HPADPPEQKRPPARPPVGRHAEV KQPGPPFPAGPRPAPSTDGL
1149	15050	A	1156	67	417	TLSCETQPGQHGEAPS/PTKNA*IALPL SWARPLYFPAPARFTARGGPVFTSKRVP SPPNRRGWRPPP\QFCHAWNPSPKFLAP KIPPT/GPLPPNKEPSKENVNPG/PLCP L
1150	15051	A	1157	446	87	PDCINVISCFLTKIYHVFFFL*RQGLTK LPRLVSNS*AQAILPP/SASQSAGITGV SLHTRPIMYFSSYYIIFGDTVLF\ETQS HPAAQAGVQ*CNLGSLQPPPPGFKRFSC LGLPSRRMA
1151	15052	A	1158	1	938	FFFFIFATYLFNKGK\LTGKRQSD*SIC KHLKGYYIKKDILTASKH/V/KKCPTSL AIREMQILTGIIKCC*RCEGNGIFTHYW *ARALAQLLWKNV*QHILKLSMCITYNP TILFLGISNRKVYM/CCPK/DPCSRMSR AAQFVI
1152	15053	A	1159	370	3	AFKAAAEGAAMSVTGGQPVLNSWVVLGG VTTTT/CPTTFIMPDNTV\RGDILELTR \PLGAQVAMAVHQWLDIPEK*NKHK/LV VTEEDVELMYQKALMNMVQNNKKAAGIM YTFNAHAAIDEFHR
1153	15054	A	1160	55	471	SPPPGLPKKIFFWPLSFYVWP*PQRFCP LFAPFKQESNPLKVWPPFGALQNKRSKG CSPSM/SARQES*PLFPKNLETPPFGGK FLKFFFFFF*DGVSLGHPGWSAI/IDSL QPLPPGFKQ/SLCLSLPAS
1154	15055	A	1161	3	467	GYTNQQIFPVDKTAFY*KMPSRTFMARE KSMSGFKPSK/DRAGDFKLRSMLIYHSE NPRALKNYPKSTLPVL\KNKAWMKHFCL

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						QPPVETYCSGKKIPFKILLVIDNVPCHP GALMEMYEEINVVNTATNTTSIL*P/VT SGVIS
1155	15056	A	1162	216	464	SSEGPGSPGELPYGAQEFVMKAPQGILV IR*T*FFETESHSVAEAGVQWCDLSLLQ LPPLRFNQFCLSLP\SWDYRRPERHPAN
1156	15057	A	1163	29	433	AVEFGGDSCSPQHPLNPPLGSPQHSPPP LIGICT/REE*GWGGGLPVPCPPALPYP STPSWGGICVCYGRGGVAPPP*HPPLT* LGGGSTPTSALPAPGAPRHPGHPLMVLQ TLPWGPHTPARKPYINKVLSCVDF
1157	15058	A	1164	486	11	STCLGLPKCWDYRREPPRPALRCPFFLN ILLFLKFTLSEINIPTPAFF*LVFAWYI FFSLFSF*P/DLEHYI*SGICVDTM*VG SSCFFNPT/WSISSF*LVCLDHLYFFLF FFFLRQSL/DSVAQAGVQGQDLGSLQPP PPWFKRFSCLSRIPAHFEWSRA
1158	15059	A	1165	467	131	NRSLEWAKMYKTYDEIKLVTNLPT/RKS PGLCKITAKFYHIYKDGLVLLLNILQEI QVGFHPNS*YQ\IILIPKYSEGTTKKGN CRPIFLVNIETKILHEIRAI*VHKQIRT LE
1159	15060	A	1166	455	32	EEGVLKAKRGCKSGLLHQTVNQVVN/AN LEKFLKEIKSDTPVNI*MIRK*NNLTAD KEKVA*IQDQTSNNIPLTQSLIQSRALT LFNSMKTERGEEAGEEKFEASRG*FMGF KEKSHPHKHKSASKAASADVEAVASYLN S
1160	15061	A	1167	26	418	KIWDYVKQTNL*ITGIPERGGEKVNNLE NIFEAIVQ/ESVPSIFKEVDTQEQEIQR ASSSSSS
1161	15062	A	1168	64	313	KWCKGNSYISKDLKELKYLGV/QLK*VQ /DL*SENYQILLKEIKEDLNKWKDIPCS *IRRLNIKMVIFSKLIYRFNAIPIKILA A
1162	15063	A	1169	464	36	QQAEAAESL\DPGGRGCSELRSCHCTPA WATEQSINK*SINQSIK*KSKLC/CWEN TLVKHIFHKRLTSRIYKEL\QQLNKKTN NSL*K*EKDVNRYFIKKIYEDI*MANEN IL\IKLVIREIQINLKEWLSWFCCCCCC FVLFVF
1163	15064	A	1170	290	487	GSLPHHTPKR*PFLF/CVFETGSRSVT* AGVQWHNHGSLQP*PPGLKRSSHLSLPV LIFLFSVEMGV
1164	15065	A	1171	2	413	GKVFI*FSTLH/GCNMK*SRS\LL*ALR FIFLFTARGLTGIVLANSSLHITLHDTY YMGTHFHYVLYIGAEFAIIGGFIH*LPL FSGYTLDQTYSKIHYTIILIDINLTFFP HHSLGLSGRPRRY*DYPDAYTTRYILS
1165	15066	A	1172	381	2	PPKLQKNFFFSSTGKFFLGGGRAFSPPP KKGFFSQIPRRFFFPLPKKKKIYFCPPP CFGPPPTFFLRAPPFFFFFFLLLFCSFL VGVKFILFL/FYLFIFRDTV*LCYPGWS AVVQSWLTAALTPRP
1166	15067	A	1173	9	405	NLDKKGRNRTPQSWFQANPMASMTFSKK KKKKKKKKGGGALKKKPWGAQKKPGKK KKNFFLKGG\EKKTPRGILEKKPFFGGG KKGPNPPKKKKPLREKKKF*GEKGEKKP

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						*KFFFKKKFPPPSKKTP
1167	15068	A	1174	410	0	FSYYPPPTRGGCPSSPPQIFLPPPLLGV FFPFSPLKIFFFPRGFKFFGGVVPFFSP PKKKVFFKNPRSVYKNPPKKEKK*SLQP PG*VWAPPGIFKR/PPPPFFFYIFS
1168	15069	A	1176	319	3	KEARSVFRVEGRG*KNFSASGPPGGGNP GGGRPGRGNFVFLIKKGGPPPGPKG/SP FFDF/GGPPPPPPPPSGGGSGVNPPPPPF FFFFEMESRSVSQSGVPDAWADAW
1169	15070	A	1177	385	1	SASFGLPKCWDYRHEPTRPASVSVTVTS SRLSGA*ARSGKGTLVFWAQMVFK\RIP LTKYSDHSREPSSLQLCMQSTPSKAEFT VAKADKRLCCTAKSSTAKSIAQIKCQND AGRSPQESLHVSGRV
1170	15071	A	1178	147	808	KLKEIKKLLEENAGINLYDLRLGSGFLD MTPKAKQQKKENLKWDVIRMKNSCASKD TITFYN\YRSDKGLV/SKKYKELNSITE RQPNF*KDLNKDFSK/EQMAKST*KTTE RLFIREMKTKTT/ME/YHFLSTRMAKI* KDSNR/RLCRKTGTLIHCW*GTAPANLL KNCQPLFPF*GTVWQFLKRLNLELPDDP AIPPLVICPKEMKT/C/CYTEICTQMFT AA*III
1171	15072	A	1179	1	398	SRSRHCTPAWVRVTLVLKKKEKEKEKEE KKRCPCYIVSHQSL*KPAWQFL/RNVK/ LELPYDPAI/PLLGKCLKEI*KYAYTKT CM*MFIALFIIAKKYKQLKRLSTDEWIN KMWYIHAI
1172	15073	A	1180	3	389	GYDRVIPNP*PLTGA\LRALLLTCGLAM *FYLQSMWVLILGLLTDTLTIYHRWSDV ARKSTYQGHHSPPAQKGLRYGIMLYMTS EVLLLGGLF*AFYHS\SLCPTPQLGGHW APTGMTPLDPVEVPLLNT
1173	15074	A	1181	354	2	ANSSDACILDGHRALPLQLPPCGYSISP AAQSSTVPMPLLLIPPPHCNRTPSLWHY SPASNPTNPSPY*TAPSPPPPIPRNNP FS*KFPYYVWVYTSLTTCSQPPVSSPNF TQPSVL
1174	15075	A	1182	3	384	GANVSG/DL/KLKPVLIYYSSNPR/ALK NYARSILPMLCKQEKKEKKKK\AWMTAH LFTAWFT*YFKSTGET/CAKEKIPFKIL VLIDSACSHPRALMEMCKEINVVFMPVN *HSI/LFCMQPMDQGALSTYKS
1175	15076	A	1183	1	410	PPLP*KFFSPGGVQS*KGGRFWPPP*VG VLPSSSP/IIFFTPGNWGCFSPFSP*KF FFSPKGFIFCGGVGPFFPPPKKRFFSKI PPLVFFSPPFKKKIFFFPPPVNFGPPRV FFKRPPSIFFF
1176	15077	A	1184	406	62	PPIINMLCSLAPPFFSPPPLRGVLPPFP LKNFFFP*GVYFWWGGGPHF/SPPPKKG FFPKFPPWVFNPPPLRKK/YHNFPPPGK FGPPRVFFKAPP
1177	15078	A	1185	337	383	RSYISFQK*VKDLNKHFSKDDTQMAN/K HIKRYSTLVIREMKIKPMTRYHFTPTRM AVPF
1178	15079	A	1186	3	471	LAPSDK*ENRLPGNRPL*EVRSPSARQP PHLRSEEPLRPAATPSGK*GASPPSSHA VREGGGGQPPPGQPPRPGGEGRLCPAAP

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						TGK*GAPLP/EPPPGLGG
1179	15080	A	1187	2	406	FLVETEFCYVGQAGLELLTSRDPPASAS KGAGMTGVSHQVQPQ**S*LWT*/PSSV EAGTSFGLSFLSSSWALSAQEGCLAVPS /SGSRGLLVGALLLWTKPSPQLSPVPAS QRLSSLSLMPPLPQPQHLTHTSIET
1180	15081	A	1188	160	459	NFMTIDMLCSAVVIHFCSSGLDFQL*KL FKSQ*ENNLINKWAKDLNSFTIFSYG*K LAHEKMLNIIREIYFTAIMS*YTLTRTV KVKKTDTKCW*GCTATGNLIHCCKNV*P LRNTAWQ\FHKILNIYLPYHPAIPLSDM NSRE*KNI/CHAKMCAWIFI
1181	15082	A	1189	232	2	KAPPPFFFFFFFFFFFFC*SGSHSVSWA GI*W/PGV*WHHHGSLQPQSPRLK*SSC LSLSSSWDYRYVPPHLANLKK
1182	15083	A	1190	2	402	PRVRHASGSPSPPPPPPGL\SHTSPSQ* VFSWPSY*TPCLSALTLASVLSLL*QRS PRTLFITNKC/DF/PASHSSCRIPAGL* ALGRQGLFSCFFCFFETESHSFAQAEVQ WYNLSSAQPSSPEFK*FS/CLSLPSS
1183	15084	A	1191	19	390	WCVPAVPATWEAEPRRSR\RSKPLTGRQ SKSLSY/NKKKKKKKKKKKKKKTGGGP *KKLLGGPKYKGGKKKKFFFFKGEKKKS LGGILKKKTFFWGGKKWPTPPKKNKALK GKKKFLGGRGGNPP
1184	15085	A	1192	485	112	QRPDPR\SAEAAIKYFLTQATASIILLI AILFNNILSGQ*TITNTTNQYSSLIIIM AIAIKLGIAPFHF*VPEVTQGTPLTSGL LLLT*QKLAPISIIYQISPSLNV
1185	15086	A	1193	55	385	THAFADAWADAWGLFKGILTENFPNLQK YINIQVQGG*RTSSRFNTKKTNSRDLII ILPKVKDKLSKKKKKN\AENKKILKYRG GPF**KPGGAQFYGGGRKSFFFFFGG
1186	15087	A	1194	408	3	CQSA\LLGGASQLG\SRGSGVRDPLEEA VCPFSDLQLHAERTTALLKAVRQGHLSL PRLLLSF\VCLCPAPRGGACRGRQASLS CGGLHPVRASRLLCLRKRAWAMASVPPP ASLPPCSLISDCCVSNQ*DSTGRV
1187	15088	A	1195	5	371	LFSTNHGDFGPLYLFP\A*AGVLGTDLS LLIRAELGQPGNLLGNDHMYNGIVTAHA FVIIFFIVIPIIIGGFGN*LVPLIIGAP DVAIPRISNISF*LLPPSLLLLLACAIT EAGAGTG*TVY
1188	15089	A	1196	76	404	PTPLRTHDQSSKVSRYKVNIQKVGAFLY MLSTRTTGI*\IKSTSFPFASPKVKYLT INLTKCVQ/DLWKEKKL/NEIKEDQNK* /NVPFSWIKGPNIVN
1189	15090	A	1197	50	334	ILHMVSIPSISIY*HLLPAG*AGTHIG* LPPA*FFWVMG/RDRVLLCHPGWNAVVQ S*LVVASNSW\VK*SSHLGLSKY*D*RH EPSYPASGTKLN
1190	15091	A	1198	250	1	QYYLVSSNT*SIIDFLQLPQKCIFTVGF SK**CICGFIFKNI*LFF\FCLFESESC SVAQAGVQWQDLSS*QPLPPVFKQFS
1191	15092	A	1199	2	402	TDARHHTWLIFVFLLEMGFHHVGRAGLG LLTSSDPPRPAKLNFL*R*GHAVM\CPG WPHE\TCLGLPKCWDYRCE/HTAPKPHH FLFFFFFSEKNFIPVPRRGGG/WKNLN*

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						MEPPPPG*KGFFCPGPPKYWN*KAP
1192	15093	A	1200	50	437	STLYLEREKEQISLSVIVSSPLPSTSTG PTAAAQSSISGPSLPLPPHNGAGDAPAG LG/YGQGPSGPPWGPS/SGPSPR*ALVC PTDPSGAARGGRGG\SRGSCCAPAGPAG LGDHRPGGMGEGPAAPPKSS
1193	15094	A	1201	86	313	PPPPGGYPHFSFXXXXXXXXXXXXKSLL PPGKGPNPPKVGLPPFXXXXVSPKXXXX XXXXX*NPPHSPPRAPGGPP
1194	15095	A	1202	105	485	VQQTTMARIYVCNKPARSTPRFTKQILL DVLK/YIDTQTIILRDFNTP/LNSVMSW RQKTNKDNLDLNLMLGQLDLIDISRILH VSTR/YIFFSSLHEIYSKSGHMLSHKAC HNNF*KIEIILIILLYHC
1195	15096	A	1203	1	476	PHFGPPPPPQDPRF*G\GPSTRKGFFPQ PPGFFPQAWPRAGQPPPGGT/EPVFPPP KHP*RRNPYPKFGSPPLPGKIHQGSPGP SGQFR\PPRWGKKRAQPTFWAHPPPIFF FF*GVLLCHPDWGTVARSR\PPQPPPPG
1196	15097	A	1204	1	269	VVEFETYNLGIK/WSKDMKRNFTKEDLM MADEHPRRC*HHLTPPRTAQVKLELEP NE/WQGCGEAGPATPCWGDAAPVQPLLQ IGRRFLKK
1197	15098	A	1205	459	42	KLKPMLIYHSENPRAFQDYAKSMLSVLY K*KNEAGLRAHLFTAGFTENFKPAVETY CSE*EISLQI*LLI/GHPR/SLMEMYKE MNVVFMPANTTSILQSMDQGVALTYEYH YISNILYEAIDNTENPLIDLGKANAWVG PG
1198	15099	A	1206	408	1	EMKTLTEMSSPGMPTEKVSELED/DIN/ EMHRKLQCREKR/IKRN/EINVQEL*YH YKRCNHHVMRMPEKEQRKEEIFKVIMAE NFPNLATNNKSKVKEAQRTPERIKTIYI YIYIS*LQKAKEKESILKETCQKTSKPK
1199	15100	A	1207	7	383	LDIGCFWWEDKYSSCYFSLATSGKLKYF SFSCLIHCFLVCVCVRAHK\CI*SRAS* CVCVHK\CI*SSAS*CVCVCARTNGI*/ CQCFLVCVCAQV/CI*SSAS*CVCVCTS GI*/CQCFLVCVCVCVC
1200	15101	A	1208	405	214	AEAGRSLCPGGGGCNEL*SPPCPSAWVT \SETLSQKQNPHHHKKKTGQVRGQSSYL PLWEVNR
1201	15102	A	1209	384	2	GVTHH/ARARFFC/LLDTGFHSVFQAAV Q*A\NHGSLQPQPPGLKPSSCLSLPSSR DNK
1202	15103	A	1210	403	2	VPSIQTNGKSLTYFDFFFKQLFKTKLKL DASFVNVCVNVEPFRTFALSKTQSLLCL SLFLLIF*TINCNFCFLRQN/LRSVAQA GVQWRDVGLLQPLPPEFKQFC
1203	15104	A	1211	156	405	ESKQMLIQCKSQMLYC*RI*TV/CLCVC VCVCVCVCVCLTCGTKRVCIVFLFIVVL NCK/PLCEPCC*CNRQGWAPWLLPVIST RW
1204	15105	A	1212	70	408	KAFSLLPPGVSPGPLCNPRRPNFIGGGP KKKPPPPPQRVVTQGFFNPPPFFFFLWG G*GQD/PPPVAQG*MDPPPRPPK\GRGP RHEPPPPAF
1205	15106	A	1213	410	3	KKSMPGFKASKDRMTLLLEAQAAGDF\N

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						LKPVFI\YHSENPRILKNYAKYT/PVLY KWSNKAWMIANLFIA*FIKYFKPTVETC YSDKKIPFKILLLIENAPDHLRALMEMY KEIHAVFMPANTTSILQPMDQGVILT
1206	15107	A	1214	3	340	KIRVEVNKMYNRKLLEEIKKIKSLFFEN INKIDQFLPRLRKTRQKMQINKIRNEQG GISINIMEIKYSYKEML*AIICKKLNNL HEMNKFL/EHRVPKLTQVEIENLNYIYK K
1207	15108	A	1215	1	57	RGLKIQNVNEIKS*CFEKIKIDKFLARQ NFKRKRFKFRD*KGDIMADITEI*GII RAYY*QL*GNYLENLEEMGKFLVTYNLP KLNH/DIENLKKPVTT/REFKSVIKSLP LKKSPLHDSFTAQFYQTFEEE*VSVLKR
1208	15109	A	1216	350	1	QSSFFSIYPNFHLLSFLFCFKDFLFFYA SVLATNSLPLFFPQISRYFP\PFERERE RERENVVL\CCLGWSAVMQS*LTPALNY W\VRQSSLLSLQAS*SYRCGPPHPANIF HFIFCR
1209	15110	A	1217	139	358	KNTFFVVVEAKRLFVPQAGGQGGNLSFK FPAPP/NLRG*SASSPSSGDYRPTPPCP ANFFFFKKNRISPWGSGW
1210	15111	A	1218	361	50	WGDHGSLKPQPPLRSKNPPPLASLVTGT Q*LG/HPVAPFPIQLIFFFFFLRRSL/D SIAQAGAQWCDLSSLQAPPPRFTPLSCL SLKKKGNPVFVITWMNLEDIMLS
1211	15112	A	1219	1	361	LKQHVSNVEKTAFYWKTQSKTFVARE*K GEILSSNRGECLLQSFKGQPLLLGANAA GDFKVK\PMLLDHSEN/PKALKNYTTS
1212	15113	A	1220	292	362	HIPVVPAIQQAEVGGSLEPRRSRP*PPR LK*SSHLSLLNSWDYRNVLP/RLANFCI FLCPVR\FKLLGSNHQNASVSQSARITG VSHHAWPILKLKKLFVCLFEMGSHYVAR AGLK/PPGLK*SSRLSLQNCWESRREPP HPDTIH
1213	15114	A	1221	372	3	RLFFLLPPRPKGDFFPTLLIW*RHGFSP PHVFKPPPLNLILGALKKKFFLPS/LPY VKFYFFKRAPLFFF/IFFFRDRVSLCWS *PPGLKQYTHLGLPKHWDYRHESACLAN NHNNNNTNFFFETE
1214	15115	A	1222	3	291	RSGDQDCPGQHGETLSLLSLTFVNLSLI CNL*TLSLIFVKIQKLAWHGGVRL*SQL /LRRLRQENHLNQEG\DCIPAWATEKDS VSKKKKKKKGGPF
1215	15116	A	1223	379	19	HMQILTIMRYYTPIRMAKMKKIGYTK/C W*GCAATGYI\WECKMVQSL/WQNTWAD S*KLNTHLSYDIAIQFL/GFYSKEIKAY IHTKPCT*MFTATLIIKSQI/MKQYKCL STDKWIKQNRGIYI
1216	15117	A	1224	387	40	KKTLSTP\PEKHPTPPLFHPPPQKGGKA PPSFKPPPPKHPPPPKGISPPPP*IPPP PIYPPPPPAKPPPDFFL*SPPPPPPFSP PPPP*TPPPFFSPPLFFFFFFFFLLIR LLV
1217	15118	A	1225	21	477	IVSRLITVRLQKPRLDPRVRPRVRRKEN YSSV/SFINIDRNVLNKIL/SSQIQQYI KKLIRHE*FWF/IPGIQGWFNILKSVIV TYVNK\QKWKKHTIISVDTEKAFDKIHY

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						LALILIKKKKKKRALPQSFIPGDLFKK PNGGFPGLKMMGRAPGE
1218	15119	A	1226	1	398	ERINHTLFFLAEAQKRLPTGISGRGRPA IPHNTPQRAPDHAYLPAALAAQHRAGGQ QAPPPG\SSPSSPYDEVKDREGDVTASH GLRGNGWGSP*ATSLVLNNLMYMTAKYG DEVPGPEMENAWNALANNEKW
1219	15120	A	1227	3	238	DAWVAGHDG/RTP*SQLLRKLRWEHRFS SGDRVSDP*SCLCTLAWVAE*DSSSKKK KGGPFKGTKFNSRGGGRNYFFYGA
1220	15121	A	1228	207	2	NRVSPCCPVQWHDHSSLQ/PRTPGLKGP \SASAF*VAGTTGVHHHAQLIFHFFFFY *DRVIQAGVQWRNL
1221	15122	A	1229	15	413	RKSVNVIIHHSEILKKKNYMIISIDTEK SFDKI*YPFMTKLSEN*DSLNLINNIY/ AKP/VANTILHSKRLNAFPIKQGCLQGC \PPFLFNIILEVLASTKGRKEIKSLQIR VEEI/KPLSLFADNM/IVYIENPKES
1222	15123	A	1230	363	1	AADPFACRPVSPHPPLYLVTSSQSLLTS VSPKKQPPSAGMQLGVGDSLSGWGWGRT KKTRLFFFKTRSLSAAQTRRQWCEHRSQ P*PPGLIKRSSHLSLPSS*NHRHMPPHL AN\LCLFV
1223	15124	A	1231	3	402	QANSCIFSRDFGSVGQAGLEPLTPGDPP ASASPRCRDYRC\GPHAQLLLTFC*ISI LILV/CIS*MKDYFITCIYFFNYS*QII FYRRASDFFPFLRQGLALSPMHDHGSLQ PHPPRLN\HPPTSAKGVTGT
1224	15125	A	1232	3	396	FLSQHGFLFLFFAGIDKLILKFIWKDN* NNYEKED*RGVITLP/QYKAYSVATVIK MVWHWQSDKHVDQWNREPRNRPNYYMSQ *FPL*YVSQRNENLPLHKNPYMNVHNGF ICNSRKQSRYPSTGEWVNKL
1225	15126	A	1233	3	395	LPKCWDYRR*PPHPALF/LFF*KHPKFP KMQVK/WRKH*TENRLVMYFSEKFGD*L KDQHKLYYLDMAFQFIFTFTYVMRYSIL FKFNIR*LTLSSVKMAVFLVETGF\TML ARMVLIS*LRDLPTSASQNAGI
1226	15127	A	1234	416	2	KIDKLILTFIWKCKRPLLAKIVLKKKNK I*RLPLPSFKTYGKGMV/TK/TKWGWPK NRPIKGTGF*VQKKKTPHIYGQLVFDSG ARTITN/WY*DN*IST*KRMKLDLYLTI YKINSKWIKDLNVRAKTMTFLEENIWVI LD
1227	15128	A	1235	384	22	FFQEI*NAIPVNTQMVRKQNSHPANIEK VL/VVWIEGQTSNNIPLSQSLTQSKALT LFNSMKA/E/RGDKAAEEKMETCRGWFM RFRERRHVHNIKV*GEAARSCGSLAAGS PLKHLLLHNTLIC
1228	15129	A	1236	379	2	SPYTKIHSKCLKGLNVRPLTFKPLEENP G/VMVPDLGPGKKFIS*APKAWATKTKI IQWGYIGLK/AFCPAKEAIPRVKTWPSE SEGIPAGHAFYEGFIFQIFKGLQPFHSK KKKDLILKLDLLSADIS
1229	15130	A	1237	1	407	YRVGQAGLKLLTL*SAHLGLPKCWDCGR EPPCLTIIAL*SVFSLVLPAVLIKLINF F\CRDGGQTMLPRLVSNSWPQMIC/LPW PPKVLGLQ

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1230	15131	A	1238	3	380	ELSQRTCCMDIMSYYKAIVITMAWY*FK DKQRVQQNEVESPKTLLYIYRLWIYYEG DTTDKG*TF\NKWYWDSWI/ST/CKNM* FDYHFTQCIKIN/SQWM
1231	15132	A	1239	1	396	FADDMIVYLENLKDSSKKLLELVNQFSK VSGYKSKV/NVHKSVALLYANSNQAE/Q IKNPTPFTIAAKKQK/YKQKNNLGIY*T KEVKDLYKENYKTSLKEIIDDANKWKYI PCSWMGRIDIVKMTILPKAI*RFS
1232	15133	A	1240	392	58	SFSMLARLVSNSR/PSRVLPASASQSAE IIGVSHYAWPSKLSF*LTIDQTHLSCNL FIYVFFERRSCSVTQAGGQWYGHSSLQP *TPGLKQSSCFGLPKCWDYRLEALPRLM
1233	15134	A	1241	500	204	SLSLSFS*DGVLLCLGWSSTPGLKRFSC LSLRSSWDYRCVPSSQTNF\VFLVEMGF HHVGQAGLELLTSSDNARLGLPKCWDYR RVPPRPAAFFLFFKG
1234	15135	A	1242	2	397	NFMINNLPKKKALCPVVFTGEFYLPFKE ETIP*VIRISLSL/IFSIIFQKIETEGI LPNSFYEGCIILISKPYKDI*\ENYRLT SVMHIDARFLDSILANPIQQCIKVIHCS HVAFV/SGTQDWFNIQKSM
1235	15136	A	1243	12	362	AGFYHVGQDGLKLLTSSDPPASASQSAG IKA*ATVPGLSPLNFCEVRFMESWSWKR P*RTS\VCSALAKCWDRNASQVVDKLPS FPT/RM*SPCLHPAVSAFCGSASVLPGI IVTTSV
1236	15137	A	1244	183	383	KQAGRGGSCL*/LPRCWDYRRELLHLAF MPG*LKK/FFCKDGGLTMWPRLVLNFWP PVILLPRPPKVLG
1237	15138	A	1245	410	2	FSRDRVSSCWPGWS/PNS*PQSDQLALK CWDYRCEPLHPAFC*MNFLKVSC*HGTS /DSKY/CQHVSPKNKDISLCNYNIIIIP KKFNIL*YIWFLDFFFFETEFCSCCW*D LGSLQPPPPGFK*FSCPSLPSSWVHRHV
1238	15139	A	1246	440	46	KTEGANINKNTTYQ/NLWDADKAVFRRK FRALNAYTRK*ERAQLNLSSTLKTRKKE QNKLKADRR/QIMQI**KLGKVENKQTK TIQQIH*TKSWFFEKISKIYEL*QA**R KKGEKTTITNVRNKRYSGRVG
1239	15140	A	1247	266	340	RKCWPGAVAHTCNLXTLGGQGGRIT
1240	15141	A	1248	3	391	DAWADAWGSRSRAVALFFFFWGFLGGGG LKTGFYFIPQVERRGLNFD*WNPPPPGL RGSSPPT/LPKQWEPGGGPPAPSNFWFF FEKRGFPQVTQAGFKLWN*GDPPAGPSK GVGITGGTPSPHPLFLKKR
1241	15142	A	1249	3	323	MHHHA*LVLVFFCGDKVSLCCPG*S*TP DLKRLSHHGLPKHWDYRC/RATTPGFFS LFFFFFFNPPEFLLPWAPPSYSLKQNKI FLKRFLEPLAPPKGLPLKRAKGRI
1242	15143	A	1250	3	405	QPDSYSPQPGRLSAPPEQEGGPWLILPH ACAPSQICVGPHGASILSYQERKGTKVL SCEGHCKLSSPVGLVGQSFCWQQPDAVQ WVPFRRRTQTPGTVAHACNPSTLGG*GR RITS/RPGVRDQPEQH
1243	15144	A	1251	407	2	PFLKKTKKELP*GPAIPALGVPSFFPFF FLPYKRKEIKGIRTPPMRIAALFTIAKI LNQPKYPSVDI*LHKRHTSNTTLLSRMK

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						H*WIKKT*/HTDMMEYYSAIEKNGILSF AATGMSPKDIMLSEICQAQKNRY
1244	15145	A	1252	1	253	VADVRESLDPGD*GCSELRLCHCTPAWA T\SRTTSQQQLKKQNENTT*KTYGIQLM NCQIANYCSKLLYFRKMSNLQSNLKKKK K
1245	15146	A	1253	3	372	KKKAQKSGTIVLPCNPSYSGG*VGENA\ WARSQPGLIS*KQQ*QQQNQQQTTSKTD PYIYG/YLIHDRGGK\NTQGWDRLLNRW GWGIWLMTQRKIKLELYLTPYTRTNSTW IKDLNVAGCGGSCL
1246	15147	A	1254	2	410	KNLTPIVGLKAATN*ESIPPQT/SRKKK KKKKKKKKRGGALKKKKFKGGGGGKKNF FKGGKKKKLGGGVKKRGEGKKPGGKKKK RFGKKSFFSRGGKKKKNRSSSSSSSSSS SSSS
1247	15148	A	1255	61	487	GRPGPTHAFVVIDSFFMGNEARFINHSC DPNCEMQKWSVNGVYRIGLYALKDMPAG TELTYDYNFHSFNVEKQQLCKCGFEKCR GIIGGKSQRVNGLTSSKNSQPMATHKKS GRSY/RE*KKNKKKRGGRFKGSQFSSPG MQG
1248	15149	A	1256	118	5	MFIAELFIIA/RRWK*PKCPLTDEWINK M*YSHTM*HY
1249	15150	A	1257	390	1	TQKNTPTPKPKPTSQQHHQKNKPTPPGF FFFSPPGK\GGFFPSPLFWVPPGFFPPP VFKTRPPEFIFGAP*KKFFFSPPRSLNF FFLRGPPSFFFFFFFFS*VGKEGSSPSH ENPLFVPTEGW
1250	15151	A	1258	378	3	GAFFFFFPPPKKGFFFTPFFFFGPGFFF SPPFFIPPPQIFFFGPKKKKKFLPPPPQ KIFFFLRPPPLFFFFFFFFFFFFFFFF FFFL\DLD*NVLSGTSAPEKNQELLGMV AYACNPSTLGGRGG
1251	15152	A	1259	462	287	RDG\FHHVGQDGLHLLTS*STRLSLPEC WDYRCDLPCPAIPAVTLYQIQYRPLGLE SKA
1252	15153	A	1260	446	34	NVRAET/IKTLEVNTGVNLHDLS*/GKA FLDARPKAQVAKEKSRQPSLHRRLR/FC ASKDPIKEVKRQPTE/WEKINHVSDKGL EFKIHKELLEKLSNNPI*KWDKDLNGHF SK/ELQIASKHMRRCSASLVIRKCNEIV DPD
1253	15154	A	1261	2	383	GSQRKWFLEMESTPGDNAIDIVEVTTKG FNYYMNLVDKAVAGFERIDSNFERSSSV SKILSNSIACYR*IFCKKKSQLMQ/QTS LWFYFKKLPQPPQPSAATTLISQQLYTL RQDSPPAKRL*FTDGL
1254	15155	A	1262	476	50	FFFFFSDTGSHSVV*AAVQWHDHDSLQP *PPGP\SDPPTKSSTREF
1255	15156	A	1263	143	472	TGAVPIRPSWN/RPPAMIFF*NAQGILF AEFLASQRAILWEFFEKAYHESVLRKSA KGLAEKCPGKLHQRVLVQYDNALAHFSH QTRTTKSSTRQFR
1256	15157	A	1264	179	489	YIFFFLSLFFFLWPRPEYRGAITVHCSL NLPGSSDPTASASSVAGTKPH*YIFFFL SLF/CFSVAQA*VQGGNHSSLQPQPPGL K\YPTASASSVAGTKPHPLIFFFF*KKK

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						FL\CFVPQAGGQGHDFG*L*PPPPSLKQ GGGLTLSRIGDYRGPP
1257	15158	A	1265	1	536	FRGGWGSVRRAPGTASCYLALAGGPPGQ CPPAAISCPSPLPWGS*TE/PYVPRRPG DPSAAP/PSW*VPRPGVPRNVPGRGRVG QDGCGQAQDIQAAASLMADTAPDSPGSA GSVRALPACVPEISGS/SGLPPGAALP* VAA/RPTPGRHVDTHPRQHSFCGGQEGD IRAFPTLYLEVYPGPP
1258	15159	A	1266	403	2	TSLHPRGYMRLLRQGFISAPCGYMRLPR GSSLHPRGYMRLLKTGVHRCTPWVHAPS QTGVHLCTPWEHTPS*RFISAPLGAASH VT/GSLSIQHIYIFVFCLLRQGL/NSVT QAGVQWCNLGSLQPKLPQAQVILTK
1259	15160	A	1267	2	401	FVLNPGGRSCSEPRSLHCTPAWATRAYL QLGKKKKEKKKERGEENKNQGPPRPLKR EVGTPGQKKPL/WGGSNGAGQKQPA/QK KGGKKKADHKGQRGKN*KRKREGGGSTS KNNSRGTGAKA*NPTIWGGGGKKI
1260	15161	A	1268	49	416	LRGRALDPRLLRECGDLGAPPAPEVALR AGTCWTR/CTL*APPRGA/DRSPWPPRS PMCKAG/DECQDGIPG\MKAWSCGLRTR QCPWP*PKLPCGPGHPAWRT*PLPQTA/ CGPGPAAPCAG
1261	15162	A	1269	420	47	GPPGWASFRLNFPKARR*GEWKTPGESG GAFFSPPGKNF\AGQN*GRPPNPPPPGP GKGGIQTRGGAGLGKNPFRFWGGFPNPG NK*GGGTKKKEGPPPPLFFFFLNTDFCN LIKRDRLGVGAHL
1262	15163	A	1270	404	1	AEILELKNVIDILKNVSESLNSRIDQAE ERISELEDRLFENTQSEESK*KRI*KNE ARQQDLENSFKKANLRVIGLKEEVEREM GVESLFKWIIIENSPNLEKHIHIVQEGY RAP\FNSNKKTSRHSIINSHTK
1263	15164	A	1271	387	2	KKEKKKEVIIIFVLLLPLK*FQNIQVWL VRELEKKFTGKYVV\FA*RKILPKPTQK RCTKNKQKRPRIHAPTAAHVAILEDSVF PGEIVGRRIRVKWTQQLTRVHSDKAQQN NVERKVQTFSGIDKKLR
1264	15165	A	1272	1	393	FRMGRLPGGGAPHFSDGVAGQRRSSPHR RSRGRAEALLTSQTGRLGRGAPHISDDG RPGRDAP\PS*TGWQPGRGAPHFPD\GQ PGRGAPHIPDDGRPGRDAPHFPYGVAAG QRLQSRHFGRPRQAAGRWRL
1265	15166	A	1273	3	317	SSYETKGVMIASFSSREADNHTAFIRIK TNASDSTEFIILPVEVEVTTG*WKTDEI ESCFVFSIAYSGKVKNNC*LFFFP\APG IYSSTEMLDFGTLRTQGKKIF
1266	15167	A	1274	92	368	LCPPGGRAGQGQNLN*GVPSPPGPKGFW GPTYGGGGGKRTTRPGGGKPEKSFD/GP PGPPPGGTKGNPAPKNFFAQKERGPFFQ NGGPGNKLF
1267	15168	A	1275	401	3	DMCDWFKKEFSDTTPKA*SIKEKQLTSF IKIKSSCSPS\KNTIKGLTRQEKLWGKI FANHMSDKGLVSRIYEELSKLN\K*KLN F*KWAKQ*DHLLKKTH**QICKERYSLG KGKITMRYHSTSIIMCIIKTIHS
1268	15169	A	1276	298	426	GATMLVLLF*LAFDLRQSL/NCFPQAGV

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						QWRDLGSLQPSPPWFK
1269	15170	A	1277	421	1	VSFKDQKL*INKENHPIKKWKKICNQPL PQIRYMDANKHIKIFSTSLAARETNMKI TT/RILWKTVWQFFKKVSIYLPLEPAIS SYLFTQEK*KHIDGSCSPSRVATAKLLA LQWRRPSWNCMHQRAGSWKQIGAPPFSK L
1270	15171	A	1278	1	218	TRSGVQDQPNQHGETLSLLKIQKLASYG GVCV*SQLLRELRQKNCL\NGPRSHHCT PAWAT\EQNSI*KKKKG
1271	15172	A	1279	88	396	TFLFSSSFFFFGGGVPPCPPGLRPG\PN FASLHPPPPGFGGFPSLTSPRA*NWGPR PPPQATLGAFGLEGE*IFPPGRPPEP*L WGPPPPPPQRGGMAWPTPL
1272	15173	A	1280	94	399	TDFLFL*TDFLFLCLCSLKNKIWVNEFR YGGFSLGVSNTQALPPSQEVNDAIKQMK KHLKLAK/DKISIVRCITKMGM*LLGYR SSWQVKRITWQLIVLNMLAYRAVFGI
1273	15174	A	1281	236	2	TQSRLVFFYMTGPAVYLNHHALRTHQGS HLCFFFCFEMESHSVTQAGW\VWWRDLS SSQPPPPRLKRFSCLSFPSS*DY
1274	15175	A	1282	37	410	KKKTLKKIKKLCPPGVKGEFNPPFYVLS KVFPKKERGLFFKVTFVSLTPFFKKKNF KIGGGSGFPPPLWFFFFFY/RDRVLLCH PGWNAVTRS*LTTSVDSSDPS/CLRLPS SLDY
1275	15176	A	1283	404	232	LSSWDYRCLPPHPANPLYF**RRGFTVL ARMV/GPRDSPASSSQSAGITGMSHCAQ PG
1276	15177	A	1284	3	402	MQIKITMRNYCTPVRMP*KKK\SRTKPR C*GGGGTTKILIPCWGDYKIGE/PLW/K SVWQFLIK*NNHLLYDPAILPLIFYTRE MKTYVHTITKYCNHNEK/CMQGFTEALF /TLPKTE/SQPKHSST
1277	15178	A	1285	1	253	LRGKFMTLHS/SILKRG*SQINN*TATL IK*KKKGKIKPK/RSRRKVIIMNRNK*D *KQNNNKFNETRSWFFKNMKKIYKSLVR VT
1278	15179	A	1286	400	105	FNFKKKKKKKNREVSE*QY*QAKYLKRN FTKNI*VAEKHMKNAQYVIKEMLI*LTM RYYYTPIK\MAKIKLTDNHKCQQLKPSY MVGKEFGKFLIKLNM
1279	15180	A	1287	400	119	TVFHHIGQAGLELLTSSDPPVSASQSAG ITGLSHW\PASSSFHSNHSCPVPLEPHQ VAQLDSFGYEKVCSFSN*VPGAQDKNDL SEN
1280	15181	A	1288	157	386	NDLQFHPFYCLF/DLFCQSLKKAGMQWH DLGSLQPLLPRFRRLLCLSLPSSWDCGH VS/PMPG*FCIYTHIYFLVEMGF
1281	15182	A	1289	400	124	FDAPAKGQGGDFGSPPPPPPG/AQKIFP PHFSQ*IG*KEGAPMGQPIFVSFSKTGA PPPGQGGFQIPTPCGGPPQNFGIQGGAP APGPGGGFF
1282	15183	A	1290	419	3	KNFFFLERGFFFFPPGGRAGGGF*FPPP FFFQGKKISGPPPPKKRGPPGAPQKL/R EIFLVLKKKGGPPLWPGGFLNPAPKNFA RANFPKRGGSRVGPPSGGPNLFNLGGGW FFRFFFFFFFFFLVFETEFRFCCPGWSA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						M
1283	15184	A	1291	397	39	WGQVWAKDWIHGLGPKTQGCPPPLGVFG CP/SLIPPNLFFYGIPGGLKIFVHKNPP FPIKKEPANWIATFFPPGVFLFFL/CFF ETRSHSVTQAGVQ*RDLVSL*PTSGFKR FSCLSLPSSR
1284	15185	A	1292	399	1	LNFFFLHRQKLCNILGSDDKVPAFSIYP EPRICYVFSLLFEIIFSFDFNKKIRIYK KHVSRIYKDLLKFNNKDNPVKKWAKDLN RHFSKDGIQKVKWHIRNC*TLAIK/EMQ NTTTMR*HLMPNRMAKIRKTI
1285	15186	A	1293	412	1	ARMVSISRPLGTPIWRSQKGGNKRVSPP TRPNPLFLKNPKKCPKSRD*NKPPLLKK KKKWSGPCPAQ/SCPGQNPHP/SPPKQL PPSPSTPPSRPSPTLAFPMAS*LAISPA HTHCCWRELSGTHTLSIPCLKPLRGP
1286	15187	A	1294	229	1	FFFETESHSVTQAGVQWCNPGFKRFSCF GLSSSWDYRYAPPRP\ANF*FLVETGF YYVAQAGLKLLSPGDLPALAS
1287	15188	A	1295	401	2	STLPVH*KWTTKAWMTAHL/FTAWFTEY FKPTVQNYCSEEKIPFKILVLIDNAPGH PQALMGMNKEMSVVFIPV/NTTSILQP\ ADQGVIFTLKSYCIRNLFQHQCTPAWVT QLDSVSKK*INIFQPGMVAHACN
1288	15189	A	1296	1	336	KKTPRRKTHKEHHNGEK\LRAFPLRSGI KQ/GCAF*P/YILNIVVA/VLAKEYGKE IKASFRKEELKLCLFIDMIIFVEIPENS PQKL\IN*FSKVAG**VSTQNSVAFLFF FFFF
1289	15190	A	1297	3	384	HTNMQKVLV/VKTEDQPSHNIPLNQILI QNKSLTLFNSIKAERSEEAA*EKCEDSR GWFMRFKKKK/RISITKMQGEAASAVVQ AGTSYPKDLAK/DEGSYTKQQILNVNET VLY*KMI/PTEDFVVRKDKSM
1290	15191	A	1298	3	395	SRSVTRAGVQWHDLGSLQSPPPGFKQFC LSLLRSWDYRLSPPHQQMGGIFL/VFLF FFFPGKGVFLGGPQAGGKGPNLG*WNPP PRGLGEFFGLNPPRGWGFQ/HPPPHPQL F/CCFFRGKGGSPRRAGRAPNP
1291	15192	A	1299	260	4	GFIVSSAVFPLLKCLLDILVSSSVLLYC LWNFKIQKSFRFYNLSPLVSSFKNSH*N SNI/WPGAVAHACNPSTLGGRGGRITRS GD
1292	15193	A	1300	91	219	LSRLSAWDY*HVPTHVFFVEMGFHRVVQ ASLELLS*GDPPALA
1293	15194	A	1301	277	441	TVEF*GVQSMKEEI\ELCLFEDDMSVYE ENLKELTKN\LLK*ISNYSKVAGYKVNI *KAIAVLHTSNEQ*NFEIGNTILF/TIS TPKYLGINLTKYAQGLYEENYSNLMNEI KELNTW/RDILCS
1294	15195	A	1302	256	482	YNVYFKICIGPGTVAHACNPSTLG\G*G GRI/TLRSGVRDQQVQHG
1295	15196	A	1303	182	460	VGREFLDMTGKEFIYKFLYIRKIN*SSS KLKTFVLPKTLLRD*KAKLQTGRKYL*I TYPVKGLVSRLCKKLSKLNSKKTTQLKK WAKDMNRHF
1296	15197	A	1304	1	468	FKQFSSLSLLSSWDYRHPTGNFCELAPY KQNAPSCSNVFTDNVPVIST*QGLQALS

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						PNVNEQSPWRETKKTAVDLCGVIWKPCQ VFLRKKPKTKTGQ/HEQQIFGF/CFFSE TESHSVTQAGVQ*HHLGSL*PLPPPFKR NSTTRTSDYDGP/HVPP/HPA
1297	15198	A	1305	880	1026	EEHGAGLSGSQDAAGGVPAG*GGWAQLW VTRRASLFLDKTHWPVDEQNLGSLYTIE ATAYGLMQKLELGRYNETHAIAKWLLEK QELGGGFRSTQ/SDGDPRETTVVALEAL TRFREAVPFKGIQDLHVQIRAPKTALNV NWYIDHSNAYQQRSAKFLAQDDLEIKAS GNGRGTISILTMYHKSPESREDNCNLYH LNATLHSALEENKKGGETFRLRMETRFQ NN*EATMTIMEVSLLTGFYPNQDDLKQL TSDVERYAFQYKTKTSTSDSTVVLYLEK LSHEKNTELGFRVHRMLQAEFLQAALVT IYDYYEPSRRCSTFYNLPTEQSSL
1298	15199	A	1306	3	726	RTDHYQFQSLKHCLTGGEALNPDVREKW KRQTGVELYEGYGQSETVVTYKWELSYE DANTYIVK*KTL*TQKEEG\IICANPKG MKIKSVSMVKESLPYYVHIVDDEGNVLP PVEERNVTVRIKPTQLLCILNCYLDKCE KTAVS*QGDFYITGDRARMDKDGYFWFM GRNDDVINSSSYRIGPVEEESALVEHTA VLESTVVSSPYPIMGEVGKAYIVLTRAY SSHDT*ALTRVLQEHVIK
1299	15200	A	1307	230	486	NAICPNGSKGSLGLGSCSVTQTGVRW*D HSSLQPRPPGLK\YPPTSAS*VA\GPQA GVQWHGLDSLQTPPPG/FKRFSCLSLPS SWDY
1300	15201	A	1308	463	440	SAIPVHT*RRRKQTSLNADMEKV*VVWI EDQISHNIPLNKSLIQGKALTLFNGMKA KRSEEAGEGKFEASRGQVMKFKERSHLY NVKVQGEAAGADGEAAASYPEDLAQSTD EGGYTKQQNFSIDV/TTFYWKKMSSRIF IAEFHHTD*GDNGSVP
1301	15202	A	1309	463	59	EVISTLTKMGKILKTKNAK/CWQDCGTK RTFIHCWWGYKLVQPLWKRV\YTFPYNL AIPLIGIYP*/NMKIYSHKRTCTKMF/I NSLFIISKNWKHLRYTFTREWIK/M*YS HTKDYYSAIKRNKLDMFSNMHESQKHYG
1302	15203	A	1310	438	29	PGGKGGGGPTPAPFPFPPPPPKVGVFW* GFPRPFLFKPPPPNKAPFPGAPHFF/SL PPFPRVFKKTFPTKKKFFPPGGGGKKKP PPPLQGGKKMGSALKFPSGGKKPWGISP QI
1303	15204	A	1311	2	310	HNQKNEFGPYVTSYVKVKEAK*IAKTRK LLEENIGVNIHDIELGSGFLAMMP\EA* AIRLKIEKLDFIKIKNSCASKDTINKVK KTGRPGMVAHAYNPSTLGG
1304	15205	A	1312	19	348	RGQQDVLPG*RGQQDVLPGRGTYSEYGL IFSARNPSMEV*SVNHRPFHHHGVP/HQ NCSDSGSYFISKECGN/WVSACGIH*CC LVPCLPKAADLGE*WNGDFSLSGKEKKK EFYLIMTFSQ
1305	15206	A	1313	2	424	ENKLTNHGKTGNGGAQSQ/PPECEPRTH LQRGLEGRGGGEPWGQGQPD\PPSNSSL KNPQAGVPPFSSLKGKVKRDRSVSVDSG EQREAGTQ*TFVNGKKKKKKKKKKAKKA

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						AYSPDSKA/PSSKSSPKSS
1306	15207	A	1314	375	3	KKRTLLIPLMNMDAI/MNKILAN*IQQH IKRIIHNDQVQFVPGMQGWFNIQKNINV IPYY*LFY*CYINRIKDQTLIIISIDTE KNDKIQNSFIVKTLRK\IKENFLTLIKR IY*KSSNNKKNID
1307	15208	A	1315	403	3	LEGVSFFFPRVASQGSILGSCNPPLPRF HHFS/CPHLLSKWGYRFPPSPPA\FFFF FLKTGFFFFCKNFALCSFP*KQASPPPP LTVFFFS/HHPFFFFFFPLFFFLRWSFA LVAQAGVQWHDLGSLQPPSLGFKRF
1308	15209	A	1316	38	427	PEXPARPTRPRPSAWQPPRLRSEEPLRP AAAPSEK*GASPPGSHPIWEVRSVSARQ PPRPGGRWWGVNPPPGQPPRPGGEGRLC PAAPTGK*GAPLPGQPPRPGGRWGGYPP ARSAASYGR*GAPLSSRP
1309	15210	A	1317	43	399	LTFFFFLGEGARPPPPGWGPGAHQGITA PLFWGGQCNPPP*PPGEGEPS/QGPPPP GGNVFFWKKKGSPRAPGGPWTGGPKGLP RPPPPKGCE*RGNPPPPTPKFLGFTTFQ KKGKNSGP
1310	15211	A	1318	437	54	MNEQKGERGLSSLGLPAR*D*GKGNVKE GR/EGVTFSPREPKEESLRWSTPQKEIV GVINHPRGQRVDRQGAGSGCEGFALRAQ TGGPPA*EITRAGEQKAGGGSKGAQTLQ RETRPPRGQRGGGRSASL
1311	15212	A	1319	351	133	GGGWAEVPLTSQVGRSGRGTPQLPDGAA RQRRPPPPRRGSWAEAPTSQTGRPGRGA PHLPDDGRPGRDAPHLP
1312	15213	A	1320	474	11	KINSPSQKKKKKKQCSSIRKLA*/DQNR HFIEEETQIPNKHMKRSSIS/LAIKEMQ IQITKSYCIIIRLCK*LIKNSDSIKCWQ GCREI/GSLIHCWRKLKMNSTALQMVYK
1313	15214	A	1321	485	33	CPASRVAGITGAHHHAWLIFVFLVEMGF HHVGQAGLE/LPVSWGNGGHL/RLCLLF GYCGQCCYKPS*RRFFCVSFYIRA*K*G FVCLFV*MVSCCVTRLEFVVTHRCNHSK LQP*IPGLKCS\PASGF*VARTTGLYHG VWHVSNSTALTSGLQ
1314	15215	A	1322	451	145	THPFGRPRGGVFKVRKLNPPWLKKENPL FIKKKKKKPGPGGGPFIPTPSEG*/GKK KGFNPEKEASNKPKFAPSNPQTGLGKKK KPPSLKKKKKKKKVYSLIF
1315	15216	A	1323	470	151	GKAEERHDPGSRACSEPRSCHWTPAWAT \SETPFKKKKKKLCISWPGTVESCFSVR T**I*LRQYVLYLFLFQPKNVIYLFICL HDKANMVMFLDFKYYFCFLFLD
1316	15217	A	1324	64	367	TWEGEGSWLTSQDRTTAPLHPSLDNRVK LRLKKKKSVGFLSPSILLAKNQIKKPAP FTMA/SK/RIKYLGINLTKDVKDLYNEN Y*TLMKNLKGGAMCSFTSL
1317	15218	A	1325	193	381	AQLFKTSMGNSETLSLQKKKKEKS*LTL PSSWDYRHPPPRPVNF*FLGEMGFRRV AQAGLEL
1318	15219	A	1326	410	7	GFFPYP*LPK/SLRC*GKDFYNQGSGQA RWLPPVIPPPLEAQAGGSP*GRSLRPTW PAWSNPSFLKKPTPLFLKFS*GRRIALT PKAKVSVNWDSPPALQPGGPSKTFFPKK

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						KKKLRIIGPGVVAHACNPNTLGD
1319	15220	A	1327	295	3	VCHFGIYFCVCSLYFTCLYFPFLIFL*V TLTFLVFYFDFTVLFIISL*YFNDCSRD CNIHM*LLSLPVLIFHCCC\FVFRDRVS LCHPGWSALASSLL
1320	15221	A	1328	2	392	RQASRPP*SAPPAPAGKEGSGE*PPSPK /PPPPPPKVVPPRGFPFPPAGPPPPPPP KKSPPPKTNPPPPPP/IKPPPPPPPPPP PPFFFSPPFP
1321	15222	A	1329	378	7	TDDLILKFI*ERYKPNQF*KRTKLKDSL PDFENYYKAKVVKTRW**YKE\KHIDQW NRIESR*QIFNIASII/HIEKEYLCNKW CYRTTKMEEKNMNLKPLP*TIKFNSK*I TDLNIKTITIWLKL
1322	15223	A	1330	403	2	VETGFRHVGQAGLELLTSGDLPTLASQC WDYKHEPLRLGELRSLTAAWAMQQDPVS PNK*IKIK*I/P*SEQFSGI*SIHNVVQ NRHFYPDPTHFHHSKVKPLTHYVVSPHS FLSPTPGNHQCLLSVSMDFSIL
1323	15224	A	1331	1	389	KMKSQAIDLEKIFTKHISDKGLGYGLYK ELL*FN/R/RCQTTQLKMGER*TNSSTM GMSFEWMVSKHMKRCSCAFPSLVTREMQ VH/TTSLFVERYHYTPTRVAVIKQSDQV \W*ECGIRTLIHC*WECKMIAT
1324	15225	A	1332	392	3	NNFMPSSA/PPPPPPFFFGGPRVFSPPP FFKPPPPFFFFGPQKKKIFSPPPPLKFF FFLRPPPPFFFFFFFFFFFQKNLGKGFF F*PRPEKKKKPPPGGVFFFSLFFLRCSV ALSPRLECSGAISAHCNLCI
1325	15226	A	1333	394	1	SQVVGPTAIHYCAWLVFKFLGHFSKTTI SAPLLK*TSTRAETSKSFS\CPRKMERA EGRRMFLGKSLLKQIVLLF/LISGSCVT AS*FL/CFFQTESHSVAQARVQ*HDLGS LQPLSSRLKRFSCFSLPSRTRG
1326	15227	A	1334	416	1	LTLLPKPTPYNTRKENYRPISLINIDAK IL/NILAGKIPQYIKVHN\NMGLTPEMQ GLFNI*K/RKSVNVICHINRKEEKKILL INA*IVFDKNPTMI*KNSWQ\GEYKEIY SNILLNGKMLKACHL\KTRIN*GCQLSP DAW
1327	15228	A	1335	391	57	WQRVCNWDKNLYQKEKRQDNVREK/WAT DLIINFTHEEMQSVNNLQKDTHPHSLVI REMQIKTTSY/HLLAKILNSDNSSYW*G CGGMGTL*CCWWVSKEIHALWEIVWFIY SK
1328	15229	A	1336	285	2	IFFFPWRGEII*HLSLINKGSRQNERAH \KDNGDFSQIISKLKLMYKYKILNQTTI KYMFFPKKHRTSIKIEHILGSKGSLNNC QRISVLQTGRV
1329	15230	A	1337	34	391	AKIASLYSSLGNRANSVSKQNKKTKNQN LKN/IKTAGGLGVVAHSCSPSTLGGLH\ DPGV*GCREL*WCRCTPAWASG\ETLSQ K*INKGKERKKKMKNCWWMNNSLIQLTS FSFTKTDWSS
1330	15231	A	1338	292	1	GGGISKTPGGEGAINPKKPPALPPGGKK EAFSPPQKKKKGERA*RDISSEDI*MAN KHMKSCPPLLMIREMQIKSTMRYRFIPI RME\ILKKQKNS

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1331	15232	A	1339	369	16	DPWQNEQLSRVTCPGPRRASMFRIT*YK VIIAALMAYSVGPRAVSCIRALWTTYG\ IMDNYKRHERRFLKPL*WPGMVAHACNP STLGGHGRHERVGRVRSIPDCVVRVAAG VKASI
1332	15233	A	1340	394	1	TQSGVQRHDAGSLQPQPPRLKQSPHPSL PSSQDHRRVPPCPARPCSSHDSYVLREG PCGRW/HESRGRVFLVLFS***LSLMRS GGFKKGEFPCTSSL/SCLPPST*DVTCS SLPSAMNVGPLQPHIFMHGF
1333	15234	A	1341	400	161	KIGPNLPCFSTKRPWKIDKIQFWPPGKV F*/SPPPPKKILFFPPPPSGPFF\PPLP PLPKSFFPPKNPNLPPSFGFDIPPP
1334	15235	A	1342	377	3	NRHFPKAETLKASKHLKRHLPLLVIREV QIKTTNICHNIATRLAKM*KADNTKCWE SCEPVLTFY\C*WEYKLVQPL*KMVWQK PKVCVPYYLAILLLQHIPEGTCAS/CY* DIHKRLLTAMLFAM
1335	15236	A	1343	170	369	RCNENKITKEVYFGEIFVRLDNKEKNTS FFYFYFLFY/CWR*GLALLPRLVLNS*A QVVLLPWPPKML
1336	15237	A	1344	385	2	SDLRRSTHLGLPKCWDYRC/RATVPGRL FIFLMVSLKHKSFKF**RPIYLFFLSSL MLLVSYLRNH*LIQGHKDLLPMFSSKSF MILVLTSRSILSLLFCFLFFVLRQGL/N SVTQAGVQRHNHGSLQPQP
1337	15238	A	1345	1	281	HMATKHMKRC*/SEMCTLKPQLNTTTPD HQNG*N*K*LVNFKGWQ*FGAVWNLIHC W*DCKLAQPFWKIDLSIKAKISMSYSHV VRKIFKLKNK
1338	15239	A	1346	176	1	SVIWNIKEP*IAKIILKKKTIVGGLTVP DFKTYYKAMVI/KTV*SWLKDRQRNQWY RED
1339	15240	A	1347	398	2	PRPPGPVRRRCPS/LTATSGSSSPPSSP FYLGYPQGFPLPAVLNRGPGILFWGPHK KNITLPARGR*IGSS*TAPPFFF/SLFS FLLFSFLLFDTGSYSVPQAAVQWFNHGS LKPQPPGLKLSSQLLRRLGW
1340	15241	A	1348	9	395	GLQNPCVGFLVSGFFFFFFFPPKKGLGV PPKKK/RGPNPNGPVGEFLATGPFFWTG PLKKNPAPPRALFWGPPPPPPWGG*NPP PFLARGSPFFKKFFGGPDPFFYRTNPRG PNKRGPPWPLKWGNPPPK
1341	15242	A	1349	119	1	ENVFRNM/WPGMMAHTCNTSTLGGQGEW ITRSGV*DQPGQ
1342	15243	A	1350	58	396	GIRVGKVCFIIFFFGFFFFFGKGVSLPP GRETGGPPL\LIKPPPFGVKGIFLPPPP GGGG\CGPPPPPRVIFVF*GKGFPP*GP GGF*PPAPKGSAPPPPPLWKNWGNRIFG GR
1343	15244	A	1351	396	1	GPTKGPGPFLDGQGFPPPTLKQNFFFPA LFFPPLGKRLILGGF\PKPGGLLQPPT* KPLRFKPGGESDCFPKFF*GRIVCFQQS LCFFPPPKKKKTAFGKRFKKKTLLFFFF SDGVSLCHPGWSTVAQCRL
1344	15245	A	1352	1	250	RRL*SQLLGRLRRQNGVNLGSGACSERS \CSERRSRHCTPAWATKRDSVSKKTKCR RHQHVGSLTVRLRPGYWIRHCGCHWWP

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1345	15246	A	1353	249	3	CGATLCPKKYMKITPSFFVEIDN/AILK FIWKFKGPRIAKTTLK*KQG*RTHTFHF HNILQKAIIVKTMWY*YKHRQSPGRVAH
1346	15247	A	1354	15	416	LLTLSSSLKITIHTNKGRT*SFIRENII IFIATTNLLGLLPH*FTPTTQLFINLAM AIPL*AGAVIIGFRSKIKNALAHSLPQG TPTPLIPILVIIETISLLIQPIALA\AR LTANITAGHLLMPLIGSATLTI
1347	15248	A	1355	2	416	IKYLNVRPETLKLL*/ENIE*NPHNIGL GSDFFNLTSNSQGIKEKIDESDYFKLKS CCTESDTTNRIRQLKNERKCLQITCDKG LIF*KKLK*LY/KQKTNNH*K/WSKRLK YFSRKDIHMAKRY/MKKCSTSIIRENKP K
1348	15249	A	1356	426	85	HARLVL*FVF/LFETAYLSVAQA/GGAM AQSAHFSLELPGSSDTATSTSQVCYHRN T/RLLF*IFCGYG/RLCCLGWSRTPRLK QSSHLSLPKCWDYRWEPLYARPYLSCFP ENARLG
1349	15250	A	1357	2	301	GGLLEVKVQDQLGQHNKTPSL/IKIYIL PIYTQKN*KNLTRHGGMCL*SQLLARLR *ED*SSPGI*GCREP*WRHWTPVWTIQQ DSKSRGEKKQVIFTHYT
1350	15251	A	1358	2	389	FLHVGQSGCELPTSVDLPASASQNAGIT GVSHRSWLKFSLLDVPSPLTP/VSSAVP LISYLATGWRQAAIAASPIFLHQLARPA QPAREAAADS*LPADSAFPPKQWTC**M FTGALFKKKKKPCFVAKK
1351	15252	A	1359	309	3	KWDHIKLKNFCTAK*TINKVQRQPMEW* K/IFVNYPVDKGLITRIYKELKQLYRKK KSNNLIFKMSKS\SSLAIREMQIKTTMR YHLTPVRILVYVLPKRARS
1352	15253	A	1360	300	2	KRAFH*KKMPSRTFTAREGKSMPCFK/A SGWATPVIPAL*EAKVGESLEPRSSRPA WATRRDSCLF*K**INK*KLTLLLGANA AGNLTLKLMLICHSKS
1353	15254	A	1361	396	60	HKVTRKSDGMLCHSGFCSINQLAFCCLF FQPGGPRGTPLP/PYKPPPQKTPKKTGP GGGGLYSPPFGGGGRGNPFFPGAQGFF* PPSPPPPPPPGGRKKIFLPKKKKKSLLF FF
1354	15255	A	1362	37	385	ALFSFSFFFGFFWGKKIFFFGQGGRAGG HSNLPEPPPPGGGAFPRPNLSGGGE*RG PPIS\GEIFGFLKKTGVPPGGRGWFKPP APKEPPPPAPPRGGISGQDPLPPPVLPG WGKKN
1355	15256	A	1363	12	421	EPWEPQTLGICTHLQTLFHDYQVLMKML VVTVRYHLTPVKMPFIRKTFDTAGM*KK KKGCYQGSKKGGMLI/HPPWGAL*MSIV KKKTWGTFFKKIQKELPWDPAIPWLGMY PKEGNSVFQRGMGLPSVIGTLFPIAG
1356	15257	A	1364	278	3	CCTGEKLETFLLR*ATRQGCPHLFDNVM EVLANAVRYEKEIKGIQNGKKKVKT\SL FPGDEIV/YAENPHKS*PKNSL/KLKSD CSKVNIQKPIAF
1357	15258	A	1365	265	330	WPGAXAHACNPSTLGGRGERIT
1358	15259	A	1366	379	1	KRKLMYCWWECK*IQPGWKTVWHFLKKL KLELPYDSVILLLYTFLKES/PVYARDI

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						CTPKFIATLFIIA\RCSLTHD*TKKMWY LSIMEYYSAIKNE/YLPFATTQMNLEDN IFSEESQA*KHGVFIFP
1359	15260	A	1367	1	376	HLPGAESQPPPV/DNSWDRPAGRTQLLW TPA/DPHSYG*GGAGPHPCPSQPGCCAP VQSCS*APSEAQSLGAADS\GPAATLPA RQLITKKKKKKKKKKKKKKKKKKKKKK KKKKKKKDDSGKG
1360	15261	A	1368	2	409	EEAMPKAKMG*RPFAPNSQILNAKKKLL KEIKSVTPVNI*MIRK*NSLIADMKEV* VIWIEDQTSHNIPLSQSQIQSKVRMLFS SMKAERREEASEEKLEVSR/GWKSAGFM RFKERSNLHNIKVQGEATSTDGEGA
1361	15262	A	1369	220	416	PQPLFDWQMYTYTLHNDILVNDGRLSPG GQGCSELSLCHCTPI*MT\SETLSQKKK KKMGQARGLS
1362	15263	A	1370	310	289	AFR*AFHSKGSK**H*EKKVN/WNFTKT *NFCTAKDIIKRMKRQPTKWEVIFANHI YLTGILIS\KIYKELRTTQ*PETQSLK
1363	15264	A	1371	3	322	HASERTHRRGKSTETTTPAWATERGSVS KQKTNKKTNK/RNTGSSIHNMVSDFEKQ VTQTF*SSMQMSNKPLKRYLTSVIIEMN IKPEYHFTPIRMAIIKKTDNTKC
1364	15265	A	1372	3	332	GKEVS*EDIMMLHVYAPNNRASKHMKQN LIEMQGEI/DE/HPVIIGDFS/TPLSII DRSGQKIIKDIV/ELE/STVKQLDLI/D IYRTLYLKRVEYVF\FTSLSKTFATINC ILGHKV
1365	15266	A	1373	381	2	CSVAQAGVKWCNHSSLQP*TPGVK*SSC FSLPSHSDYRHE\PALFFKFFVQMGS\T ML*FS*ESCIKGSRQPCSYTYLHSPPIF SSLFPSLAPESIKRQEPSFFFEMESCSV TQAGVQWRHLSSLQA
1366	15267	A	1374	1	385	YKKGINAKIFNKI**V\ESAISHDQVGI VLVLQGFLSI/RNKSISVTHHVNRLKN/ HMLI*IDAEKAFDKIQQSSHGKIGIKGN FFDLLKSIYRKPMANVILNSEKMKCLPC KC\KTSQGCQLSPLFFLFFF
1367	15268	A	1375	1	357	CSGVISPHCGLKFLGSNDLPALASRVAG IIGMTP\HAQLIKNFCCCWWR*CLAFGG *RFKTMCRPIVK*NKSINK*NRTVCMSG CGDS/RQLLGRLRWSPGLRNVQGCSEP* WHHCTSACL
1368	15269	A	1376	1	375	HRPKFKSISLLEENMGESFHDLGL/GSD LLDMAPIVQSIRDKTSDFLEIKKSCSSK GTV*IMKKQATDWE/RTFVKHTSNKGSI MYEEL*NL*KL*NNPI*KWAREFSRHL/ EDTQMATKHMK/KCSTAL
1369	15270	A	1377	260	400	KRGLGKTVFPWPKKKNGPFFFFPKTTSK GRKTLMVNPE*PKYYSVKKKKKKKGGGL PFPCKIFFPNLTIQTTFFWPKTNPLTLK KRKKPPKKTPTFWGHFFFERGTKKTQGG KKNPFKKGGWEKLFFLGQKKKMAPFFFF QKPPQR/WRKTLMVNPEP*NLLKKNM
1370	15271	A	1378	403	1	TGVSQALSLFFFKYFKPRMVEFLVEPSR *KGPSVYGLQIFFSIPKVPFPCPFWAF/ SLV*SSPPCLSLHLLPAFGVLPKRSLPR PMLQSFSPMFFARIG*FQILLLNFQSLL

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						S*FFFFFGDRVSLCRPGWSAVAP
1371	15272	A	1379	195	381	AERYQTSRSTADRISCLFI*SAEI/VFP DSGKKTGGNNNNNNNNNNTNNKDNNNNK ISLSLKP
1372	15273	A	1380	361	39	PPVKETAKDVNRRFPKQPMTNST*SDA* VDEVVCL*FQLIGRLK*SRRIA*AQEFK AS/HGQHSETLSLKNYLKKKRFSTLLFL REMQIKTTTRYHFTPIRMAKK/SHHTKC *QGLAMLPRLALNSWAQAILLLHFSLPI SWNYRHTTSSTQASLHVLFVIGCLGNRL LTSFAVSFTGG
1373	15274	A	1381	400	90	LPSSWDYRCAPPLLANFCVF/M*SQGFT RLVSNS*PQDPPTSASQSAGITGVSHHA WPAFFIMWFSSSYSR/TMH**QHPHV*K LHICPN**KS\LSCPQVPTIIVV
1374	15275	A	1382	1	431	DNIPKKSAVYYWITLFKKG*DNVEDEAY SGTLAISIC/EENIHLVCSLSDEEQHST AQTIANTIDITVGLAYTILTAKSKLNKL CT**MPKLSYPLF*KIL*KNKTKNIV\P NQLQIKAELPVEILHNCDQDPETWLGGV AHTYN
1375	15276	A	1383	2	432	ELSADVSFFFITTPLSGVL*QNWGIAAF IPIELRSPTEVTFSFDVGNGPFEISLQS PTHFSDHQWHHVRVERNMKEASL/QVDQ LTPNTQPAPADGHVLLQLNSHLFVGGTA TTQRGFLGCIRAL/RMNGMTLDLEERAQ VTPEVQ
1376	15277	A	1384	1	421	NPPALASQRAGIADICHCAWPLLRLSKP QFSNL*SKKFALGDV*SSNIL*YIYIFF EMESRSVTQAGVQRHDLGSLQP\LPPKL SLLPPKLSLLPPK\SASCLRLAGSWNYM HVPPRPANFCIFSGDGVSPCWPGRTRTP G
1377	15278	A	1385	2	416	IFSVDETALYWKMMPSRTWYL/RKEKSM SGFRDSEERLTLFL\GLNAPGELELEIL LI*HPEILGPLNYVKFTLSVFY*WINEA LITAHMFTAWLTECFKPSVETYCLGEEM PFNILLLIGNAPGYPRAPMEIQEINIIV
1378	15279	A	1386	170	1	DGVFLIFGGQNEKLNKNKDG/DLTKLPR LA*NSWARQSSCLAFSKCWDYQREPPCL A
1379	15280	A	1387	47	418	FWGFFFFFLKKKKAALGPWTPPPPGQGG PPPPPPRGPGKGGPNPPRQTIYGFWGQR GPPPGGGGEPGPPPPGEP\PAGPPQTGG PQNWPPAPGP*KGF*GASKGAP*KGVDP GGERSQVPNRGA
1380	15281	A	1388	58	503	RPTRPGNYIMIKEFIFQKDRTI*NVYAP KNIALKYIKQKLINLKGKRDKLTLTVAN ISTCP*VTDITSR*KICKGTEELF*QPA \DLIDIYRTLYPTAA*YTFFSSAYNYSK IGNSIGHKTFSN/CKRNDNIQWLFSDHN GIK*EINIII
1381	15282	A	1389	2	401	LVSQVVNSKNRILKKIKNSTPVHT/RQM IRKQNNLIADMETVLVVWIEDQTSHNI\ SQSMTQSKALTLFNSVKAERGEEAA\EA GRGWFTRFKERRQL*NLQVESEPPS\AD VEAVASYPEDVAKIIDKDGYTKQR
1382	15283	A	1390	294	3	KIVIFDFNDVKNCSS*KIVIFDFNDVKN

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						CSSKTVIEGKVSDCKKIFSKHISDKYLI SIIYKELSNLNNNQQPN*KWAKDL/NNM SSKHRKICSISFGKMQIKTQIRNHYIPT DAW
1383	15284	A	1391	3	422	PLFKKEEGTNFPFPPPFWGRFFPGGKSFS PFFFPPPPFIKGGPKVSQKGPRFFFFFF F*DGVSLCRPGWILFPPQVTEALLRGFL ALSSLCFRLDKFFFFF*R*GHLLSRWDY RHEPPHLRIS*RKTKE\KGLIMLTRLVL
1384	15285	A	1392	3	400	FLYIYKDIYR*YKTFQINNKLKIIYFK* EKDLSKLFTKDVQMTNMHI*MGSTSLII KQMQIKTTMKHHSSLPECLHFNAANITC WKRLGPAGTLILRW*ECKSVKPL/WETF *QCLIQLSMQENYH/DPATPLIG
1385	15286	A	1393	409	2	IVRHFSKEDIHSTNEHMKKGFLSLVKEV QIETTMGHHHITVRRVKIKTDIFASA\N TKC**GYGKTRTLINS/YWECKIVQPL/ WKNILAVAYKIKHTFFPPRIHLSGSQKS HFSIYSKEMKTLRQHKDIFMATLSQN
1386	15287	A	1394	409	24	KSPFFFFEKGFPSPPPGGAQWGGFPPPE PPPPVVK*FSPPTPPNKWGNRPPPSW/P G*LFFFCSPGGFPPLPNWFLTPPLR*SY PPGLPKRWGFKQKPMGRG*RAFFCPPKI SKKLWSGKKKKKGRPLAI
1387	15288	A	1395	83	411	QRDSVSKTKQKKINNKSRTDLNRHFTKE DRWM/ANKHLKRYST*LVIREVQIKTTM RYYYISIKKSKINKPDHTNCWQGCGRPG TLIYC*WE/CKMVPSLK*TFW*FLKRLN
1388	15289	A	1396	308	14	NFFFFYSWSNIIYCQKGTAFTPISDKID FN*KIISRQK*QYMLIKGSIKN/DITII NTYTSNNSSPKYIKQTLTGLKGEIAPST IVVGVFNTTLSIIK
1389	15290	A	1397	321	1	KQ*CSIEYS/FKYTR***SKL/WPGAVA HAYSPSTLGGRGGRIT*GQEFKTSLA
1390	15291	A	1398	183	48	KWPGAVNHACNPSTLGGQGGRI/TLRSG V*DQHGQHGESPSLVGRVR
1391	15292	A	1399	18	422	KAGMAILIDKVDFRTKNIITE*/EKHFI ITKGSVREENISVLNV/WPHYRASKHMK Q/ILIELHVELGEHTIIVG/DFNISFSV LNRIDKESARRR*NI*NNTNHQLNLVDI Y*KTKNTTNGRTTFFPSAHKLFTIIIHI
1392	15293	A	1400	28	339	YSCDHNSVQPQTPGLKQSLCQPPE*IAG ITDARHHIWPIFF\LKRSFVFIAQAGTQ WRGLL*KKKKVGGFKKGSCLTLPGRGDY RRFREEKILIPGRGFCNELI
1393	15294	A	1401	390	1	FGLGKHVLHMTSKAQSIKEKTD*LDFLK IKNFNFSKDTIKGMKRQARNGEKIFPRH QS/DDFF*WAIDLTFPKEDKVMANKHIK RCLRLLLL\SMRYHYH*NKKTDHTKC*R ERG\ELELLCCW*EYKMVQ
1394	15295	A	1402	149	402	RFWIHLYRKRVFPPLLNPVITWKEKRGF VFVFVF*DRVLLCHPGWSAVPWS*LTAA STSWA\K*SSHLSLPSY*DHQHASPCLC N
1395	15296	A	1403	1	403	KRKSVPELIC/APRC*APCSYRPNLPSS PGPHLDPVGPTPTPSPPRPGPARGPPAA RPKEPAEPGKEERRGL\PAPGG
1396	15297	A	1404	342	3	KEDNLIDKGGSPKQQIFKVN*TALY/YT

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						ALYSKKIPPRTLIAGKEKLMPGFKASKN R/TLLLGANAAG\DFKLRPMLIDHSEL* /RPKSTLPVL*KKA*LRAHLFIALFTKH FKPTVE
1397	15298	A	1405	498	66	KNYAKSTLPML*KWNSKALMTAHLFTAW FTK\FFMPTVETYCSEKKRF/SFKMLLL IDNAHSHPRALMEIYKEINIAFMSAKTA STLKPMDQ\KVILAYKSSYLRNI\FHKT TAALSSDSSDASGQSKFK*IWKGFTRTR GRTRGSAR
1398	15299	A	1406	3	411	VSPLCLGRSQTPEIK*SSPLGLPKCVDY RHEPLYLASMGVLNCPISNLGQCIPP*A AWWSLLLGC\PILMLNLVQTPDLPSVLQ PRAPGPR\HPPVSAS*VAGTLGTHHYAW LSMLLGSTL*DVFPFLSPSLIPSEE
1399	15300	A	1407	361	2	IRVPQKKKIKSPGRGHKIFSF*RAGPPF FFSFFFLRQKESHSVTQAREQWHDHGSL QSRLPGPK*FSH\PPPPHPPVTGTTPLF IYYYYYFLRQSL/DSVALAGVQWHDLGS LHPRVRPRV
1400	15301	A	1408	393	2	PGFNISVLKKASGGLFFFSPLGKKGFFS QPFFFGSPRVFPPPPFFNPPPFFFFCCP L*KIFFSPPPGLKFFFFKRAPPFFFFFF FFFPDRVSL\CCPGWSAMVQSRFSATST LRAQAIL
1401	15302	A	1409	393	60	LNVNPNL*SYLDKHRGMLYHILQSKEFL SKTSKAQAKEVTLCKWDYNKLKMFCTAK KTL/IKVKR*STE*KKIFVKY/STTK/G *TYRIFNKLNNKNNTQFKNRAETSRSKM AE
1402	15303	A	1410	422	2	VNDRKMDGWMNGWKEGR*TQKKKGGRRK REKERSMFLEGRKEGREKEREEREKESQ KERQKRGKARKEQRQEARKQGGR/EREK ERERERGREREGERGRKSSS*TGSKVVK IILLAVKMLVHLKSLHLQKVCVFSFSRS
1403	15304	A	1411	398	64	PGFFFKKIFVENFFGPHFQFFFPPPPKG KNPL*PPQRGPG*\RFPGVFPPLKKGSK KKFPPPPRGTQPRWGKKPLLPKRPGFPF GPRVSFFCLIEIGWFFWAQVPKKKKKK
1404	15305	A	1412	391	125	EPAPFFFFPPPGKRGFFP\PP*FGYPPG FSPPPFLKTPPGNFFLGPKKKKFFPPPP GEKICFL*RAPPHFFFFFFFFFWPPRQA ICFIIE
1405	15306	A	1413	3	387	TPDLK*LTRLSLPK*WDYRRATTPG\LF FFKPFASLGSISM*YHSPVCLASKLRIL FDSSFSPSATAKHPLTSAFAAAWLSPFA LIQPHSSESSLYSSYCPVPILLF/IYLF IFLRQSL/DSVAQAEVQWRD
1406	15307	A	1414	409	1	KRSGPFFYF/SPPFKKGSFAKPFFLGSP VFFPPPSSPP\GFFFFSPPPKRGFFPNP FFWGAPGFFPPPLF*NPPPDFFFWGPKK KKNFPPPRGKKFFFFKGPPPLFFFFFFF FFFFFFFFFYKIISIKGEIGRSSVVR
1407	15308	A	1415	3	385	HRPPPVMGLSPRPAAAEGVPGPPAVLAH QHHAQFLARP*LPPHGAGLRTCSPPCLS LPNPPPWAPVWPEPP**ALPPAP/AVPG PIN
1408	15309	A	1416	2	238	PGGRGCSELLPRHCTPAWVT\SKTPSQK

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						RKKREKPGSL*EKTLFFCQTLVFGPKKK NGPPLLGRVWAKRKGGFHPPLKN
1409	15310	A	1417	3	394	NKHLKRCSTSSVIREMQIKTTNRCHFSE *KHW/IINMCW*ECGQTELSALLIRC*\ WDSEMVQPLWERKEYLKEITAESSWDPA IPLLDI\YPKRNEASC
1410	15311	A	1418	307	357	LETRKTAEKIKRRAGFEK*NLETNKNGN TISQNLRDVAKEVRREKFIAMNA*SKK KEKP*INNLMLSLKELEKDEQTKPKVRR KKKILNIRAEIIRD*KNSGKD*KKSWF
1411	15312	A	1419	341	3	IFVFLVGRGFPPLTRMVLIFWPHDPPPL PP*VIEGLFH/LPAFRPGAFLRKMVPPY *KNKIPPPRKNTFFFLKPPPFFFFF*DR VLLCHPGWRAVAQSWLATASTSQAPAIL PPR
1412	15313	A	1420	405	1	WGEELVPSGRVHELFSSALRSERDTDSV CSCGGQCHCPGAIPGAALKAACRGDPAS RVGVETGSTMGNNGFFSFFIFKPYFFRD RVLPCHA\AMAQS*LTAASTS*\VKSSF CLSLRSSWDYRCVSPHLANFKTF
1413	15314	A	1421	1	399	QPTLLTELGLRPVPPHPATMNILY**IN TILHYSYKNYFLFLFLRQGLQPLQAGVQ WQNHGSLQL*TPGVSFLSSWDHPNPANF FIIFFLERQGLTLLPRQVLNS*AQ/CNT PASAFQSAGIIGMSHCSWPYKN
1414	15315	A	1422	168	414	EWREKAGESLEPG\GGGCSELRLCHCTP AWVTEQDSSYKKKKKTPGGGKGVF/C*K LGGGINF*KRVFCFGKGPTKKKTGGEA
1415	15316	A	1423	369	1	EHFCKSQDRDSVPKKKYIYIYPMSVFMP INLTNWIKFLERQKLS*QIEEAIENLNS IY*/PNESEFII*SLPITKAPGPYGFTE FYYSFKGEAMQILHKLFQKRG*RHSFSN VIKTLKSKPEK
1416	15317	A	1424	403	1	KNTEHSKRYSIPQRYCGFSSREFFHFLV HMKVMFPLFKCAIALCLKQVYTVFFETE SCSVTR*/EVQQQDHGSQQPQPPRFQ\H PPTSASQIAETTAILENFRKICIYFLRQ SL/HSATQA*VQWRNHGSPQAPPPG
1417	15318	A	1425	401	3	FFFFFKKNFPFFFQVEGKGRKLG*QPFP PG\LKNFSAPPLPGGGN*R\RPPFARLF FFFL*KRGFSPLNQGGLGSPPFFSPP\R APKNVGFQGITPPPGNFFFFFFFSEAES RSVTQAGVQWREPGS\QPLPPGF
1418	15319	A	1426	386	27	CRINGVLILC*CECKMAQTL*I*FGNFL QKKLDLTCDSTIPLLGIYPRDMKTYVH\ KKTCT*MFTAALLIITKSWEKLLRPSEG EWINSRHPYDRIVLSNYETHNVNKIQRH YAEAKKTV
1419	15320	A	1427	398	2	GLQVHATTKFFKFFVETGSCYIAQAGLE LLVSSNPPG/SSFPKCWDYRCETRRWPF LFKFSLPIFVF*LNHLFCLHLLPLFILK LNLPCFMYYLFIPPALYSLSLLALFRND CDLSPIHLEVKKYFSKKDRL
1420	15321	A	1428	401	70	HHAQLRCFFNSFVEVGVSLCCPGWSQTP GLKRSSHLNFSKCWDYKR/AAITLPSFF *IALF*ENPPNCHSLPTPLSPPKLAALG NSCLHPWLPQPPVKGLSDSFVCMHPGS
1421	15322	A	1429	388	131	RGGGCLQRH\RGFKQENWFNPGGRGSS*

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						PRSMYCPPAWGAQGGSLSQKKKKKKKKS KNYQKILSTQKTQKSRVFIVWSKHCTRH CEK
1422	15323	A	1430	184	413	VSFLFDFYFLFF*RW/RSHSVTQAAVQ* CDCGSLQPFILFYFLRQSL/NSVAQAG/ VGSLQPLPPGFKQFSCLSLLSIWD
1423	15324	A	1431	76	533	SCKRTTGRQFPDLPTRPPTRPQGFALVA HAGG*WRDLRSLQPPPPGFKRFSCISSV LWCTKAFNFDFQEIYSFSS*I*GFDSFE VNFFFLEMGVSL\FARAGLKLLGSGKLP ASASE/SGGIIGVCHWAQLL
1424	15325	A	1432	373	29	RQGFPPMGRVVLDSLKKKKFQIPNSKIF PGGGAPLVIPPSREGEAGKFF*P\GGKG AIKQNYC/HCPPTWGKEGNFVSKKKKKK EKKMHQK*RCVKDQQ*T*MLLFPSLKSI YYFK
1425	15326	A	1433	389	73	TDCPAIGRNHRDPVRPLLSSPHRKI/YA NLYYYIIVRILTLIQSTDLM*ISPVVLV LTRVCVCVCVCVCVCIILPS/CYPVCRF MYPTTTVKVQNISIGQEKQKTKT
1426	15327	A	1434	402	39	QAGLQLLASSDLPALASQSAGITGVSHC ASPSISL*APLGLDTFSDFPCFNDLDSF EEHWSGML/SECP*TGI*DLSFFS*VYW GYGFLEDHRGKVPFFITSYQSYTPPTQL IIADVKFEQLV
1427	15328	A	1435	105	387	EFSKVAGYKINTYKSIVILYNSNE*FEN \KKIIPFIIASKRIKYLKI/QFAKAVQD FYAENYKTW*RIIKEDLNK*KNVLC*WI GRL/NI/LKMVLLP
1428	15329	A	1436	242	2	FGGGFFWVGTPNKMGPFPQIIKNLF/TR PPENF*KPP/LPFIAFFSLGFLGVFFFF *DIVSLCCPGWSA*AQSLLAAALTSPG
1429	15330	A	1437	411	0	LLFVAQECLKWFSALGGPGVPCS\LPAN QQPSVWVP*QS\EHVTVLQRFCLWPVLG PAYGQIWEPVPSTLK/PPPPGFK*FS*V SLLSAWDCRCTP/PTDPANFCIFSRDAV
1430	15331	A	1438	41	412	FFCTD*GSLCCSSWTQTSGLKRSFHLSF PNCWNYGH/RASVLGLIFFFFLRKKT/C P*KKFL*NEDLLCCQLGLELLAPRDSPA LGPQSVGTANVTPRPW/LLFL*TQNYLN SSRVRFSPAPLKYKEV
1431	15332	A	1439	1	406	HAYNIV\NPSPVSLTGALSSLLMTYGLT MGCHFLSITLLILGLLTNTLTIYH*WRD VTRESTYQGHHTPPGQ*GPRYGIILFIT SQVIFFTRFF*AFYHSSLSPTPQLRRHW PPTGITPLNPLEVPLLNTCVLLR
1432	15333	A	1440	3	422	MEKVSVVWIDQTSHNIPLSQSLIQNSAL SLFSSMKTE*GEEAAEEKFEASRAWLMR /FEERCHHNVKVQG\EAASGDREATGSY PDDLAKIIDDSGYPKLHIFNIC*KPTDT DIVDETALC*KKPSTYFLFFFLKQSLAL PP
1433	15334	A	1441	375	2	KVSSPRAENVILYNCPPLFFFLCQD/CH SVTQAARQWRHHSSLQP*TGL\ASQVAG TAGAHLYPSQNLIGRGIRSLA/SVAQTG VQWRNIGSWQPLPVRIKGFSSLSLKSSW EYRCPPPCPD\LFIFL
1434	15335	A	1442	397	122	GQASLELPTSGDPPASASQSVRITGMSH

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						CARPILGSCISLPAYPFCFLKCFLF/CC REVILL*CSGWS*TPGLKQSSGLSLPKC WDYRCEPP
1435	15336	A	1443	3	299	WEKMFAMYLSD*ATVSRPYR*LLQLNKT KYKLKLSQS/MNRHFTRGDVAMANKHTK RKSTSLVIREIKTMRYHYLLKRMAEVQK /SVKCWQECG*GGGKCG
1436	15337	A	1444	10	410	CTLFLSISPDSAGGICTMLLFQNTLNFK ISLALGVSDKCFSNFLIMTIVRNVFYIH GKKCILYCSPGCAHTHMHTLMHTHIHLK QFFLRRGLTLLPRLECSGAITAHCSLDL LGSDSPP**EMYFIYMV\EMYFILFPRV CTHTYAHTDAHTHTPETIFFETGSHSVA QAGVQWRNYCSLQPRPPGLRFSSYLSLP GS*NHRHVPP
1437	15338	A	1445	431	9	GPAQSLDSSVSPLGTISSTVKWRHNAYL AGLSGGI/PCDCFLGPRVPWGSGICQWH WAVSPTLS\PTVRPPLFRETLYFT*V*V PPLETCPQ*HISHCRCVINWCEDTHTPK KHLVCVHACVCVCVCVCVCVCLGRSRQS EH
1438	15339	A	1446	85	416	PGCLSLPKIWDYRCEPPRPPHFFIFSSI QGPLTDFFLTPLEQVQISPTAKGFLKKI PFFFF**RRGVPILARVVFKS*PHDLAA SASQKFGITGVSPHVHPIFLY/CSSIQG PLTDFFLTPLEQVQISPTAKGFLKKIPF FFFLRQGLT\RQWSTHLGLPKCWD*GCE P/PMPGLHCEFFKG
1439	15340	A	1447	376	3	IKSEIIETESRKPIEKIS/RAQSCFCGM VYEIDKLLARLDRKKMKTQLNNIRN*RD EINTDFTDIKRIIRENYKQDYGTKFNNL DETDIFLERHQLPKLTQEEKDNLNSPIT IKDIEIIV*NLSTG
1440	15341	A	1448	2	192	SKWIKNLNKELKP*DS*KKPEGNLHDIR FGNDFLDVTPKN/MATKGKIDN*TLPKF KMLMRIWRN
1441	15342	A	1449	411	3	VFLPPLPPFCFLNFF*GKGGFFFKIFF* KKKGVEGPQLGPPPPFGPFKKFFFF*IF LKAPLFVPPTLKPLF/CPPKKKNWENNP PPFFFCFFVKKTQFYFFFFFFLRNRVLL CHPRWSVMV*SCLAVASTSWAQAICP
1442	15343	A	1450	413	1	EA*TGEWCNPGGGACHEPR*PPCPPPWA TERGFVSKKKRKQEK/SRIMECFQDNLP GFFQIFSVMKNKQEGR*FWTK/VKMTKY NA*NVNGS*YWKKRENEEECYDVVKKLF QSILS*YVKKAR*KPGCWLMAAIPALW
1443	15344	A	1451	4	384	DPAIPLLGTYPREMKTYVHIKTCTQMFA AVLFTVAETSKRPKCPTDE/VNKI*CTY I/MTYYSAMKRDE
1444	15345	A	1452	3	390	LPDHPGSSVSTPRGVIITGRGFWLLFPW VSFFFFFFFLKRISLLPPNWRGGGQNLL NKSPPPRGF*NFLA*PPQGGRKKGPPHP PGAPGDKNP/QPFFFFGEKKKIFNPPTG GEKKKPPSPFKWGGGGPN
1445	15346	A	1453	37	381	LILYINVCVCVCVYIYTHTQMGSHIVAE AGVQWCNLGMW*P*TPGLK*/FLLSSGD YRLTLPHLANLYIFFFFFEQRG\FFFLL KLV*NSGPKATLPRVGITGLTHTPRPYR

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						GDLFF
1446	15347	A	1454	3	400	TEMVLHTEMVLHISVWDPLLDRPGRGVT WLMLTAELFLYGGTEAFSSSFDV*GPCS ETVECFSD/L*A*GPP*NT*SPIYRFAS FLLAFCIYLLETRSP\SVTQSGGK/WQD LTSLQPLPPRLK*SSCLSLPSSWE
1447	15348	A	1455	77	398	RAEIVPLYSSLGNRVRPPSQKMYIYYEQ LHAHTFGNLAEMDKLVERYKVLSKFT*E EI\LNSPVSIKEREF\AVISLPQKETLG PDSFTGGFYIFKEELMPILQRLFW
1448	15349	A	1456	397	69	CPPGLSGLPWVA*AVPP/RRPAPPPPPP AGIDAGLGDDPLQQTHHA/PPAAAGSAP AGCAAGPARGAPRGRSPPRRGSAGAAPP PWPPAAAAASSAGGSSAPCASSPAAPPT
1449	15350	A	1457	400	2	ALFFWAPKKKKNFSPPPGKKFFFFKGPP PLFFFFFFFFFFFFFFFFFFFFFFFF FF*RRPIFILFYFLNQKNIPRDFFFFF FLRDRVSFCQPGWTAMV*SQLTAA*TP GLKQSSHLSLPSS*DYRWVPPC
1450	15351	A	1458	343	11	QGVHSRKYKEISKLNS*KKNPTRKWAKD TNRHFTKDNIQMENKNMKDVQARCSGS* F*KN*NFKSYAL*PKCSEI/KKSVTGTN WRNSQIYDKLSTLQNN*WIFSRSLYNFE
1451	15352	A	1459	109	401	QNYRQLGQWDRIESTVIDPCKYGKLIFD QSAKATEWRKDS*NHQTS/WWKESFTRV KALEEITKRKVNSLASISVKTDVHVIKV *LKKKKKKRGGRFKE
1452	15353	A	1460	42	424	CPAN*NSFSRDR/SLPMLPRLILNSWPQ VVLL/PWPPKVMGLQ
1453	15354	A	1461	419	69	IFPLKKKKRGGGVGPPLYPPPLGAKRGG SP*KQNLKPPRPHKENSPFFYKKKKKGG RGGAPFFPPPLGGKTKKFFLPPK/IKVS FNPNLFPPPPPPGGKKKFFFPKKKKKKK SRNTVWF
1454	15355	A	1462	1	277	CHTNFLCMSFPPAISHHPLMPPHPVSRS VAQAGV*WCDLGRG/CSELRSCHCTPAW MTERDSISQLIRKKKKLIKIKKKKNKNK SVIFLGGGS
1455	15356	A	1463	382	3	KAGGSINQNSPPPPPPGEKKKKPPPKKK KKKKNPFWGGPRILPHNPPPFER*R*KI FLGPKFLTPLGPKIKPLFFFFLKKKKKK RMTY/HSVAQGPLLNKDTLQAG\LSKA* RSPPKSKSMGQSFHRN
1456	15357	A	1464	561	86	NDPILSLKAEKTFGKIQDSFLIVSSSL\ NKPGIEGNLLS**KASTKQNPIMNLRV\ LNVFPLRS*TRQVCLLSPLLFNIVLEIL AHIISQEKEIKKIQI*YKEEKLPLFTSS SLFI*VKNLMEFAKKLLELINEYNKVER YKINIKNILLAKNTWTLKF
1457	15358	A	1465	3	221	RFHRVSQDGLDLLTS*STRLGLPKC/WD YRLEPPCPAKTCLILNGSC*VFLCYLSC FKAQERPSQNSWGAFVTL
1458	15359	A	1466	2	396	WWPAWTHTPGLKQTSRFSLPECWDYRRE PP\PGLVKFLL/IQYRVVTQHVGLGDWV QDHHPHIEICLHKSVI*NGIVFAYNLRT SSLTLFYLRRGLF/SAPQAGVQRHKLSL LEPLPPSFKRSS\CSSLLSSWDYR
1459	15360	A	1467	349	413	RLGL*PRKDITD/HVSLRKDTG/WPGAV

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						AHACNHSTMAGHRRQIPRSGV*GQPGQ
1460	15361	A	1468	403	2	LPVEWKGGIFGSFHPPPLRLKKFFSPTP PKS*D/YRGGPPPPGYFFFFFLKRGFSP FGRVIFKFPPPGVPPPPPPQNFGFKGRS /HPSRALFFFFKRVFF*IYPFFFFFEME PRSVPQAGVQWHDLGSLQALPPRFM
1461	15362	A	1469	423	3	IEFSFFAPSKDKGAILGPSTLPLPRFNN FFCPPFPINKDIRRGPPPRPNFFFFRKR GGFPHWAGMFLSFNLQEGPPPSPPQ/SV GF*GRN/HPPRAQFFFFKKFFF*CYPFF FFFEMEPRSVPQAGVQWHDLGSLQALPP RFM
1462	15363	A	1470	13	427	RTRGLVFDKTEFKPPKIKKKKKA\GPFL RGNRSILKKKATFPKNLFAPNPGPPKFI KKVLSDLQKNLNPPPRMGGNFTPSLLK* NKSSKQQITRDFRDLTSPLDQGDL*KIY KTFYPKTTEYTFSSAPHGFY/S*FDHKI
1463	15364	A	1471	378	1	FVRPPFFFFSSSRPFFKVVGGPLPPAPQ FFFKTPRGNPLLRG*KPPPQTPVGGAKG SPPW/VPPGFPKKGGGVFFFQQGL*KIS PPGPAPP*LVWGGESPPFKKKKSRPGVV AHACNLALWEAKAG
1464	15365	A	1472	412	53	SRLSFFLSSEPHGPPSPLGPFATNKVAF C*/PPPPF*PSPPPKFFFF*GPKSVIYF YQR*PPTSRIFPPKGGAGPP/PPFWGFV NPKKK\LKPFSKPSPPAAKFKNPEGTKL GFFKKKKKKL
1465	15366	A	1473	116	34	DWNIKPVLISNVMTGLMSMIITLLLQLF LL*LFFFK/WELTFFGGKFHQRVDPSFQ GSLGRGRQFFLLTKTEYHIFFLIKVFNS KTEGAGLAT*IK
1466	15367	A	1474	42	428	EIIMESINRFDVITF*NFCL*CYLMSKI NRQASSW/ENV*NQYVGEKILIFLIYKE CIQINKK\KLRPKIDTQVKDKQISEEGM QMANQHMIQC\QPSLVLNKMQIEIAEGH HLPYQINKDSKMMVEERRQ
1467	15368	A	1475	87	433	PQSSPFSDHCSYQRLFLHLVKVSTYRLQ KIRKIHKSPGNNEYFGGFFLFFSFLFFF ETGFNFVPQAGVQGQDLG*LQPLPLGFK GFS/CPQPPRTFFFFFFLRVWGGFIQKK KFLFV
1468	15369	A	1476	212	430	SLILMTSNGIHFIYFLFLLLLFFFF*DR VSACHPGWRAMS*SYFT*ALTSQVK\QS YLSLSSS*NYRHTAIMP
1469	15370	A	1477	493	2	PGAAAHACNPSTLGSQGGWITRSKIPEH PG\TLWNPRSY*KTKMCGLEAP
1470	15371	A	1478	454	492	HRVGEERF/CLFETESHSLTQDRVQWHD LGSLQPPPPRFKQFSWYHI*PHAW
1471	15372	A	1479	2	213	IDQERERLMEGDRERDTETDAEKDMGRE /RNRYRERERLRG\RRERRKRRDRMT*M PRERERENLNSLYRETYRDFETEWVMDR ERQRLKRRLL*AVIVPSHSSLGSRRKTP FQKKR*REGERKSEFLIQRDI
1472	15373	A	1480	77	453	SFGDSLTLSPRLAVQWVYLGSL*PPPPE LK\YSPTSASQVIHYLLFFFFFFGKKVS FCPQGGGEGPPFGLLEIFAPGLMPFFCL NPPKGWVWR/RPPTMPKLFFVFFIKRGF SPGEPRGVSFPEPGT

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1473	15374	A	1481	398	96	KRPVVCFFSPPPKKGFFPPLIFVGPRFF SPPPVFK/SPPPFLFFFPP*KKKLFSPP PRKIIFF*KPPPPFFFFFFFFFFFFFFF FFFFFFFFFFFFVFILLLS
1474	15375	A	1482	484	64	QKRQMANKYMKICSPLFVIREMQTNTTI RYDDIPTRVAKNKTNK*KSNSTKYCQEC ESARP*IYCWWKYKMVQPLWK/S/VWQY LLKLNI*LPYDPVIPLLSMYPSQIKTCI PTKTCAQMYLVTLFIITKNQKLAHSARV G
1475	15376	A	1483	2	400	YNKKGQGVAPRYDVDTAANFPKELAKII DEGGYTKQQSFNIDYTALYWKKTPCKSY SWR*IH/SLASKDRLT\LLVGNVVGDFK LKPVLIHCSKNPRVFENYTKSTLPVLCK WNSKAWITAHLFTAWVAEYFEPT
1476	15377	A	1484	459	65	GGPPPPHKTIDFFFFFFRGESPPPPKK KKKKKKG*DNAEDEAQS*RPPPSI*EKI MHLICALTEEY**LTAEIIASNIHISTG SAYIILTEMLELSKLST*WVPKLFYPNQ LRT/RAEL*MVILNK*DQQF
1477	15378	A	1485	2	518	PPPPPQRFGLRGGAPPPPKKKG*DNAED EAQS*RPHPSI*EKIMHLICALTEEY** LTAEIIANNIHISTGSAYIILTEMLELS KLST*WVPKLFYPNQLRT/RAELSMVIL NK*TSDP
1478	15379	A	1486	122	501	PRDPPALALQNAGITGLKQSYFLSLLSS WDYKHKPPCAPGYLK\VFFLEN*YLALY VF**SYQGTSVLTQPPSLIPRHSSPGVS VQLFQKK/DLQHGCLLTPSISGYSVTWD GVQWRDHGSL*P*PPRF
1479	15380	A	1487	491	425	IPKNDI*AEP*RINKR/CAKRKMVRKGF EAESTICKALRYEEIVCSRNTEFVHGWL *ENRGQIMKGFGNSVEKLEHN*KFYEG* LLYRFE*LAAGFIVFQQ*VSKEIVKAWP GTVAHACNPSTLGGRGGWITRSGDRDHP G*HA
1480	15381	A	1488	441	17	KKTNIYDQLIFNKGAKSTKLRKNSLFNK WCQDKIS/IIQKMKVDPYLISNI\NLKW LKDLNVTAKTIKLLKENTGAILHDLGFC NAFLDGKPKAQTTKKKQVK*TSSKFKSR CQWLIPIISTLWETEAGGSPELRSSKPA WPT
1481	15382	A	1489	413	1	LFWKEMVFLFWPGRVGNPGPK\GWLRLR PPPF*FSFQPFWGPPVGLLFPKNFYY*P PGGAHGPNPPPPGGKG*GPPRVGGGKFN *PKFGPCPPGWATKQKPVFQKKKKPNKI KNRTVKVPKVTKFIYYVPYLNGVSN
1482	15383	A	1490	359	407	RHRMITFFT*IVTQNFPYL*KKMDIQIQ ED*RTPN/RDQHKHTPRHIIIKLSNSQ\ NSKRILKTRKK*LVVY*GTHIRLSTYFW PKS
1483	15384	A	1491	397	39	RKFRGRSFAKTLFSGPGQG/PKGNPGLI PEGPPPFFFWPAEDGGFFFPPGQLPPQG PIRGPGPFLGFPVPPPEGEGPPPTGP*K PGQKRPKKRGWSPQKKGPKKKTLFFFFF CQMESRSVT
1484	15385	A	1492	378	1	FGVFWFLAPRRKGGFFPSHLIWVPPGFS PPPGV/SNPGPGIKFGGPIKKIFPCPPR

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						GGKFGPFKGAPPFFFFFFPQDGVCSVAQ AGVLQ*AEIVP\FPPT*ATEQDPVSKKK PTRPPTRPPTRPPTRP
1485	15386	A	1493	3	428	IKSP*PDRFIAEFYQTFKELVPILLKRF HKI/EEGTLPS*FYE/ACVTLIPKPGKD TTK
1486	15387	A	1494	3	417	ILNNARLKPFLLR*TTRQGILLLSLLFN KI*VLEFLAGAISQEKEIKVIQVRNEEM SKTLFSQTT*S*GRNPFIKIPLPKMSVV N/NFIKVTEYKVSIH
1487	15388	A	1495	429	4	PFCLGSKRFPPFFNPPRGGKF*KKKKIF GPPRGGPPLFPPLWAPKGGGPPRAGGSG PPPPKGGNPLFINPKKN/PPPPGGAIFQ SRFLGGVNPKIFLFPGGKFLTDPGFPPS LPPGGKKKKPRFQKKKKRKKRKVKEKKY FL
1488	15389	A	1496	3	433	FSKEDTPMVNKHMKD/CCTSLVIREVQI KTTTRYHLMPTRMAMCIYIFNYILFLK/ SKNNKC**RYREIGTLIH/AQWKYKMLQ LLW/KTIWQLLRMLNTKLSKDQE\IPLL GI*KKKKKKKKKRGGRFKGINFTDPGVE RINFYNSAPK
1489	15390	A	1497	3	326	WPACL*AVAAVALLVPEATRLTMGNNLT VCTPHSIAELLSSKG/DLWLTDNR/LLK YQALLLE\DLQLRTFTCLNPATF/VPEE TGEPEHDCEWVVVQTGKRNNKDHCLYSL
1490	15391	A	1498	345	22	KSKWLIDLHGKCKTLKR*YRKPTK*\LG HGNDFLDTTSNAWFI/RKIDKLDFIINK NVCSGKVTVKRMKR*TTDRDKISSKGIS DKRLLCKIYIKILTTQQ
1491	15392	A	1499	194	432	PVVCVCVCVYVCMCVFETQS/HVARAGM Q*HNHSSLQL*TPGLKQVSCLNLSSSWD YRHTPN*FFFF/CNFYLERGGVS
1492	15393	A	1500	2	417	RD*FMRFK\EKSYSCNIKIQREAASANV ETMASY*EDLAKIINEGSYTK\SQIFNV DEVAL\KKMPTRTFIVRERKSIPGFKAS KDRLILFLG/ANAPGNIKWKPVLIYHST NPRAFKNDAKSILLVLYKLNSKAWRIAH LF
1493	15394	A	1501	414	0	SSSSSSSSSSSPKWTTGALQP/LLSRTP LKDSSEEESSQ*AEL*AVHLVVHFAWKE KWPDM*LYTDSLAVASGLAGWSGT\WKK HDWKICDK/DWGRGMWMNLS
1494	15395	A	1502	3	125	RLGLPKC*DYR/RAATTPGLH*F*SWKE QRPQ*LALGRKPVNRNKNTQKYIHIYTY TH/PIPTNVYICIYTHIHTPV*YTHIIY IIYLFKVLVFGFLRRSLT/SVAQAGVPW RDHSSMQPRPPYKQLTCH**LASQSARI TGGSHHTWPALILKLERTEAPVISFRTE TSK
1495	15396	A	1503	406	172	DIILDR*RQKQRLRLRQKQRETETE/RR DRGRERQRYRQRQVQRQGRRQRQRLRHR Q*QRQIDRLRQRQ/RAERDRGRGRDRDR GRDRGRDRERQRLRQRQR*RERQRHRQR /RERDRQRQRQRDRGRRRDRETDRGLDR G*DRGIDRGRCSDRGGDRDRGLDIGSDR DR
1496	15397	A	1504	3	420	ITGVSHRAWLPS*FLKFFVVVEMESHSV

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						AQAGLK/PSGLKRSSHLDLPKCWDYRHE P\PHLAFFQFF
1497	15398	A	1505	407	1	PISIYHSKDPGSLKSYTKSTLPVF*KCN NKTWLTAYLFTAWFPKFFKPTVETYC/S RKKSPFKMLLLIANAPSHPRALMEMHKE IPVVFMSAVTSILQPMDQGVVLTFKSYY LRNTFCKAIAAIDNDSSGGSGQIQ
1498	15399	A	1506	1	408	PPGFKPFCLSLPSSWNYRHPPP/RPG*F FVFLGGTRFHHVGYTASQHLTSRETHAY ALQ
1499	15400	A	1507	2	416	EPRSHHCTPAWQLSKTLSQKKKKKRKR MVFTGRKKGLFFGN/LKNLGTLSREYPL GPGIKNRLAQKRKPLFYKKRF*NINPGG GAHPGGPKSWERGGGRKI*TPVGKYASN PEYHICIPPGKRNQNPFLQKKKKRRAD
1500	15401	A	1508	276	14	SPPPYFLLIR*GRKGRGQF**LRLFFII NLRQCL/DSVSQAGFQWHNHSSLQPRTP GPK*PSFLSLPSSWDYSHAPQLLAFYGA NCFN
1501	15402	A	1509	1	391	NIFKEIMSENFPSLMSENFPSLGKEIES QIQEAQRTPNKMNPKRSTPKQVIIKF*V RE/MLKTAREK*IVICKGTTLRPAVDFT AETLQIRRE*DDTFKTLKGKKKKKKTLP AKLTFPSILVFKKTRGGSR
1502	15403	A	1510	2	419	PRVRSRATNVISKYKQHKKKNTSK*IKD LNVKPEPIKLL\EKTTGEKLLDIELGND FLDS/TPKTRAPKANLTP*NYFKLKSFL TAKETFN\KTPTKRGANHISDRGLISKI YKELTIQ*QKNNLISK*AKDLKRHFSKE DV
1503	15404	A	1511	392	122	SVSLCVSLQSSGMFRC/LPTMPLRR*RQ ENPLTSAGGGCSEMRSHPCTPAWVTQQD SVSKK*INK*IK*/Q*LRQNVKIKPSPI FCEQGKRRK
1504	15405	A	1512	2	281	GGCSELRSCHCTPAWTT\SETLSQKKKK RKKICIECNTLKSH/ILSFVCGGKYHSP VSCTCL*WSLGRSLKRSLERHQKNLNDP YPIFQNETNIH
1505	15406	A	1513	242	382	QGPNLG*LHPPPGGLKGFSPLTLLRSWK NRLPPQHPFYFCFFRKNKV
1506	15407	A	1514	1	388	RTRGTERDT/RFRERRRERDRGREGYRW RYRERERHRERES*V*RDRVRDGDRVID RERERQSERERLR/RERDWERDTYIVRE TETERETEGERDIERERDIVRDRYM/RD RDRDILRE*ERDRETALDSEK
1507	15408	A	1515	4	285	TRXQICNGDKTALY*KEMPSRMFPARVE LMPGFKASKDTLTLLLRPNAVGDVNLKP MMIYYSENPRALKNYDKTQLCLYSTNGN KAWMTDYRFT
1508	15409	A	1516	415	2	MGDRESLPPSRVFLFFLAPCPKGILFHP V*FGSVRSFSIERCYR*GQRNEFWGPVI RVKASSSRAG*VVFSSTAPPLFF/CFFE TESCSVAQAGGQ*CDFSSLRPLPPKFKG FLCPSLPDAW
1509	15410	A	1517	1	324	PTRPEMGFRHAAPAGLELLSSSDLPTSA SQSGGITGVSHRTWPILASNNY/SMDKL CAI/CERFILPFLKNILLWILILFIFIY FCLIK*CITINFSQNSLLPHSIHLYI

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1510	15411	A	1518	2	163	ACRYPWLNFVLLVEMGL\TMLASDLERS G*PQ/CDLPASASQSAGITAESHHGWP
1511	15412	A	1519	425	52	VLRGAQFLFQEARLKWDFGPGGMAPPCN PPPLGV*KGPLPKG\GGPNPPGPPRGNP VFSKKPKITPPGGGAPEVPPPWGGGAEK FFYPGGPRVQGTE/RKTPPPPPGRQKGT PLPQKQKKKKPWSL
1512	15413	A	1520	3	404	THASGKSNIRGLTLPVFKTYYKAAVIR/ TVWP/WLRANTNRQNRL/DGPEVDPYKC SQMIFDKGAKAIQ*RTDNNLLNKW*/ES *TSTCQKKKKKNQFR/DPAFLIYTKFNS NGRKNLRVIGKT*KVLKKNIKQNWGDLG
1513	15414	A	1521	332	39	TSRETGNFQLDLTAFLNEVGVLFLWRKG KGKIDIGIGTKEMP*FPI*LLMFSYIVI ERERKPE/LSLSPSLECSGMILAHKKNS LPGSSDSHDPASRVAG
1514	15415	A	1522	482	0	RARTSGVLLCSPGWS*TPDLR*SLCLSF PKRWDYRT*ATVPGLLYSLYSRFSP/DE LKGCEKSRTSPA
1515	15416	A	1523	1	417	NKC**RCEEKGMPVYYWYECK*GQPFWK TKERFFKKNL/NIELPYNTAIALLNMRP Q*I*SQ*RKVCSCMLCAT\PTPNK*IKT MW*VCLVEYSSPLKKN\LLFSTTWINLE DISSNK/LRHRKSSISRFHLLL
1516	15417	A	1524	1	397	RDSTYQGHHTPPVQ*GLRYGVILFITSE VFFFAGFL/WSAFTRSSLAPTPQLGGHW PRTGITRLNRLEVPLLNTFVLLASGVSI T*AHHSLIESNRNRIIQALLITILLGLY FTLLQASEYFESPCTISDGIY
1517	15418	A	1525	2	376	LKAKTGQKLGLLHQTVSKFVNAKEKFWK ELL\KSATPVDI*MIRKRTSLITDMETV *VV*KEDQTSHPIPLS*SLTQSKALNLF KAMKTDRGKGAVE*KSEANRGWFMQFKE RSC/RFCNIKVQG
1518	15419	A	1526	3	386	ESMLKAKTGQKLGLLHQPVSKFVNAKEK FWKELL\KSATPVDI*MIRKRTSLITDM ETV*VV*KEDQTSHHIPLS*SLTQSKAL NLFKAMKTDRGKGAVE*KSEANRGWFMQ FKERSC/RFCNIKVQG
1519	15420	A	1527	127	388	KRKSQINNLLLQFKELEK/QEETKPKAS RRNKKKKIRVDLLKIKKGKPLEGVKKKG GFF*RTNKRDKPLLKLPKKKGGGRIKTF HKTS
1520	15421	A	1528	3	402	HENHMKICSTSYVIRELQIKTTMK*YYT PVRTTAIQNTDHTKCWQG*REQ/GSLIY CW*QCKMVQ/PLWKRVWQFPTKLKHSLN I*SAVVLLGIYP\KSGKFNVHTKTCT*M FLAK*PQCSSVDEERKKM/WYMYGFE
1521	15422	A	1529	2	365	IEKLYRSGAKFFCRDRVSLCCPGWSRTI GLKQSSCFGFPKCWDYR/R*AALSGRLL LTISSH/REQIEQEFTHYPEKSAKLFMQ DGPPRRK/HPPTRPQASNIQNKFSFFLR QSL/NSLAQAG
1522	15423	A	1530	1	418	GTDTE*ACDKIQKPFPDKRLNKLG/IRK KHLQLDKYL/WKNPIASIILKSRRLKSV RLRPGDGRQGCSFPAWLFNIILEGLARA IR*EKQKQKQGQ\QIGKKEVNLSLFIED IMLYIENLKESTKKPIIIINEFSRKEDF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						RP
1523	15424	A	1531	381	3	ILQGFVIRKKSKIFQKACHTSDLWTLTN LSCLHMKGLPPHRLYSSCTVLLFLRKPV MRKTTLSCCFLT*DFFLPLLPPCFFR*F ILLIF*LYFCKDKVSLCCPSWSKLLP\Q QSSCLSLPKYQDYKA
1524	15425	A	1532	38	479	DEACGPQDPYLTPYVKTQWIKD*TRNKG IQFLEENGKN\FDIGFSSDLLDMTPKTR ATKVKL\NDIRLRNFCASKDTINLSLLC R\KR*PVEWEKISANHISDKGLISGIYR QPPLNSKTSHLI*K*ARDFNRHFSEEDI QSALYRWVL
1525	15426	A	1533	105	447	LIFCRVFEYLHSLHLPQEICLSLALFSR FTFCVIICEVDVWSVIFKVPFCSKRNKV AVHTMLYIQIFVSLFI*PQNWKQPKCPA TVERINKMWYIHIV/EYYSANKR
1526	15427	A	1534	76	471	VWVCLLSLEGSQSKFGNSIEFGVLLSSG GFSAWRLFFFVYFLRQSL/NSVAQAGVQ QWRDLSSLQPLPPGFK*VLKQRGVCLFV CFETESHSIAQAGTQWCDLGSLQPLSPE FKRFSCL\SLSPPWPSG
1527	15428	A	1535	45	338	SNNEPFLDWIVM*RKVDFIRQPAMTSSV VGPRRRSKALPKAKLAPKKVMVTIWWSS ARLIHCSFLNASETIASEECTQQIDDMH *KLQRLQAALINRK
1528	15429	A	1536	425	1	FFNITFHSVSFSPLSQKCILTL*ILLKS IVKNNMRNFQRSLVRK*AKDMNRHFTDD HVQMAS/KHMKRCSLVIGEMQIKN\TVS YHYPPIRMIKVRNSSNTKCW*GCGQTGS LMRCWW/NK*NQLLWKTGIPPHGLVSTR SRVF
1529	15430	A	1537	4	443	ETFVDHYQCGGIRPFSDLQLHAGRTTAL FKAVRQGHLSLQRLLLSF\VCLCPAPRG GAYRGRQVSLSCGGLHPVRASWLLCLPK *AWTMEGTSTPASLPPCSLISDCCASNQ RDSVGIGPSEPGAEYNLLVPRFLSPSEK RSIWVGV
1530	15431	A	1538	487	3	TQNGGVLLSAPRSVFSPTTLR/CTLQAQ C*AFWWGGTQQAASSTAAMAAMKPLGIW AGGAAGILPKLGFQD/LPLSAEADPAGK ELSIGRQRAWREQPDQSAEPPFSQAPRP GYPPSPQPLSMRRGPGANPRLARPLRGP VRVRLRRASSERQKRSRGGSGPLG
1531	15432	A	1539	394	489	IYLFIFETESRSVAHAGMQWRDLDSLQP SPTG
1532	15433	A	1540	475	202	PGGGWFSPPDNFSLKENSQGGPPVSHPP PPPGNGEGGKTPGAGHSGI*NPPPPLKI N/LEKGGRGGPPGPLLNPPFPKEKPRGG KKKKKKKR
1533	15434	A	1541	14	468	LSMWWNSRLKARRLVLVSQVVNA\KERF LKEIKSVIPMNTLMVRERNSLIVAVEKV LVA*VKEQTSHNIPLCQSLVQSKALTLL HSVKAKRG*EAAEEKLEAGKHWFLRFKG KSRLHNIKVQGEATSTDGELQQVTYPDL VKIVGEGDYPKQ
1534	15435	A	1542	479	141	RKTDSWDLIK\SFSTAK*AINEADGQTT EWEKTFANYASDKGLISRKELKQINKKK ANSPIKK*AKDTKKQPTNMKKCRTSLII

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						REMQIKTTMRYHLTTESE*LLIKSQGRA L
1535	15436	A	1543	17	474	NPKKKKKKKIDLLDTYYTLYPK/AEYTF SSEIHKNWLYIN*LRANLNKFIN*KIKT ILSDHNRRQPEINKCNKTKR/RVT/TQK FKNLILSNYWVKGELQTQIAEFLKRNVN KNTIYLNT*NTIKVLNSGGST/ALNTYI DKNFKKRVPS
1536	15437	A	1544	89	481	ICLKVISLRQENATSVACIVSCLSEGSR ASENLVLHNASPNSCGLGIAFTCLCNVV SSGNKITDCYD*LSSS/WLGFFFFFFLK KSFLFVAQAGGQGGNLG*PKPLPPGLKQ FLPPPRANFCFLEKTGFFLF
1537	15438	A	1545	1	300	PPPPAPXXCRPY*XPWXXPVYHSSWRHG SGAAQGAVLAGFGGVGRQGPGAASVSIP LCPENQGCREPGPSHAVPAPSALPSLRS LTGGQIGGTRAAQAVG
1538	15439	A	1546	2	436	GAPEIKSIIKGYND/RLCTTKFYNLDEM DKFLVRHKLPKLI*E*IDNLNRWITSQE TDW*I*QQSSSSSSSSSS/PSSSSSRPN GFTTESYQSFEDKLIPIICKLLKKIDKE \GHFPLQL*GITQIPKPDIYH/IENYRP ISLM
1539	15440	A	1547	54	419	PATWEDHLSQGGRDCSEPRLHHCTPAWV RE*DPTSKKKKEK/NDQ*LLIP*S*RRL *RSSHQTSHLMDWNSEAGR*EATFLRSY SKL\KEELELLLILDNNDDHNNSD*YLL SIYSIPGTVLS
1540	15441	A	1548	37	339	KRWKCLRA*LLMRPRHAD*LNPDGVGYS EL*SRHCTPAWVTEQDLVSISTNRKNER HTLEYSHQHYSG*P*TG/EESEYPSAL* QREIIDYSFIQGMTDQL
1541	15442	A	1549	477	1	PGSHDLGSYT*PQ/VVSSPEVTSRDAPS HPSAPKFCSNPCRGRWLTSSKQPKLRLT SAVPGAPGARGTFHALGAGAAEAGGHSA SRPEAALCRPLPPLPMTLTSHPLLSGPG RLAWGCNGRR*IKGGG
1542	15443	A	1550	430	8	CWPGSSGTPDLK*STRPGLPTCWDYRHE PLCPASKTFLSPQIETPYPLNNNAHSPR RPALVNYSLLSVSMDLPIL\AFHTNGIT GYVASPAPPVRWGSHSVAQAGVPWPNLG SL*PPPPRLK*SSRLSLLSSWDYSHMTP LN
1543	15444	A	1551	2	419	ETSPSLQGWLGVLFPKRGAKTSRFLIIR PQGGSFKDGDFFNPPGEIKTPPAKKKKK KDSARSPPARLQA*GAGLWDARASFRRP FQAPVPLSAQPRAQPLAVGTSRDGGSSG PTPGQESAV\PWREKHPQQPPPQPG
1544	15445	A	1552	2	387	FRHVAQAGLELLG\SSDPSVSASQSTGI RGMTYRAQPGL*LFNSKNSILSGPKV/L QDYMW
1545	15446	A	1553	393	2	KNPIFFFLKQGFPFFP*LEGRGKFLGPC HLCFPGSKKG\LPHPPQLIGAPGPPPSP GFFFLKRGFS/LFCPGGSFSLRRKGPPP PALPKF\GFLRVTPLAGPGNPSFFFFFF RDGVSLCHPGWSAVAASRLTA
1546	15447	A	1554	1	427	LLLLILYAIVEAVT*TEGAGYPPLPGSY SHRGASGHRAIFALHLTGGCCI*GAMHC

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						ITTMIDIEPPAITQYHTPLLA*SGLIT*GL\LVLSLPVLDAGITILLTDRNLITTLFNPDGGGDPILYQHLL*VFGHPEVYIRILPR
1547	15448	A	1555	3	382	TLYLLFAA*AGGL/GSALSLLIQAELGQPGNLLGNDHIYNVIGTAHALVIILFIVTPIIIGGFGN*LDTLIFAAPDMALSRLNNISL*LLHTSVLLLLASAIVEAVA*TG*TGYLCLAGNYSHP*ASV
1548	15449	A	1556	380	3	EVSPCCPGWS*TPGFKQFACLGLPRCWSYSREPAPPAKACFLDI*VK*WFCK*GSPEVNSRPGLYLFIYLIKQKKGVK**PARYLVLFFCFFVFVFVFVFF*HRIS\SVAQGGVQWCDLGSLQPPP
1549	15450	A	1557	100	254	IPTVPTY*TPIKSFHRARIESSGPGYSWPVDSAK*VPLAVVSLDSR\RDSGNLVHPLMRVTN*MKRHLVTLTQS\CYS
1550	15451	A	1558	2	289	APGVSSTMEDEMGGGLEPQRRGCSKQRSHHCIPAWATE*DCLKFNNNKKNYLLLISLRTQSYLYF/C*VNSY*LKLSIKLAGGTGEKEH*SQKRKSK
1551	15452	A	1559	24	354	PLPSASPGPEGATPVPTS/ACPNKIKLYHLKKKKKKKKKKKKKKKKKKKKKKKKKKKTKKKNKKRKQQLNE*ETG
1552	15453	A	1560	376	2	AARGSGVRDPLEEAVCLFSDLQLRAGRTTALLKALFK\RQGHLSLQRLLLSF\VCLCPAPRGGAYRRRQASLSCGGLHPVRASRLLCLPKQAWAMAGAPPPASLPPCSWISDCCASNQ*DSVGVG
1553	15454	A	1561	3	408	AASTVFLPFLERKGIDFGFLFFFFGEKKFPFLAPGGAPGGLFSFPEASSPGLNPFFWPNPPEK*KKGGPPPPPGFFFFF*KKRGFPGG\PGGAPFPDPKIGPPGPPKGGEFRGGPPPPGPNFFFFFLKGKGGGGPP
1554	15455	A	1562	355	161	FKPGDGGCSEPRWCHCTPIWVIMRDSVSKPKQSKTKKRNVFT/C*D*VF*NNNINYINCFS*RALYILYEKQFM
1555	15456	A	1563	410	1	TPPPPPKNFLGTPLFPKNKAGKGLFPPPLGFPKGGQWPIPPQRFPPLFSPKKRAD*KPKPPPALKIRGPNPGVFPKGFCGFSFFPPPPFPRGGGLIFFLPP/TK*SGG*KKPKKKKKEKCPKKQRGGIDQLTSNLGV
1556	15457	A	1564	2	374	ADRNLNTTFFDPAG/GVGDPILYQHLF*FFGHPEGYILILPGFGIISHIVTYYSGKKEPFGYIGMV*AMISIGFLGFIV*AHHIFTVGIDVDTRAYFTSATIIIAIPTGVKVFS*LATLHGSNMK
1557	15458	A	1565	396	0	IIFLIFLRHGFAVVAQAGMQWCGLGSLQPLFPGFRLFS/CLLSSWDYR*RQGFTMLARLVLNS*PQAI\SASPSQSPGITDVSHCA
1558	15459	A	1566	186	452	KQKCNFKTLNTKYQPLPFFFLERNFCFCPPGGGEGADFTFLEPLPSGAKGFF\CLTLQRM/WE*RVSPPTPLNFGFLVKKGFSLCGSTGF
1559	15460	A	1567	453	37	KTALYWKKTPSSTSIAREEKSVPGFKGQAHFLFRGKHKFKLVSKLIYHFENP/R/ALKNYAKSIL/PYKWNKAWMTAHLFSP\W

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						FIKYFRPTVEM*CSYNKILVLIDTGLDH PRPLIETYK\FINLHVCVLFNTTPIVQP LPR
1560	15461	A	1568	453	39	TALYWKKTPSRTSIAREEKSVPGFKGQA HFLFRGKHKFKLVSKLIDHFENP/R/AL KNYAKS/TLAYKWNKAWMTAHLFSP\WF IKYFRPTVEM*CSYNKILVLIDTGLDHP RTLIETYK\FINLHVGVLFNTTPILQPM PRAQ
1561	15462	A	1569	1	352	FGTRREREREREREREREREREREREGRGGA GHQIPSIEGQHKIVGAIIY\CREC\GEK ISGSTSYIKVWDIRDSAKCIRTLTSSGQ GISGDACAATFTRAITSAQGEH*INQIA LRPSGT
1562	15463	A	1570	394	3	TLDWPQSRGGSTGKPVYPSVCCCCCCCCC CFNFCQEAEKNNAEGLLHNQAGRTKDGS FAPSHDH*A/PRGTEV/DLLESTLQTSI KQVESKPR\EQARTGAGGQKEKATQNPE KSVLTSMYTKSQGSEGRLPGNR
1563	15464	A	1571	399	2	KHQLPVFWQYNKKAWTTRTLFLDWLHCC FVFEVRKYLASKGLPFKVVLILDNAPGH PPRTP*VQY\KGIEVIYLPPNTMSLI*F LDQGVIRTYR/SHYTQYSMQRTISAMQE NSNKENIIKVWKDSTTDDAIVA
1564	15465	A	1572	37	400	RGTITGEAASADQEIADKLSDAINKIME EKG\Y*LPEQVFNLDESTLFWG\KKKPQ RTLLSKEKKRAPGFKTGKDRLTLLFC/A NAVKLIIRTALTYKAENPQALKENVKHQ LPVFCLTTRGL
1565	15466	A	1573	84	485	AGHKDSPRPHQTQEPSWLHLWDPAPGLQ VELPASP\GRALALLSPWVVDGTGRPGA GGGTRRGGSGPTGAHGAGGRLMHGGLQV PSPAPREGS*GPARYQAQRMWARTAGGP STPSAGASRVPSPHCPGP
1566	15467	A	1574	3	463	TPAQGLRDPSNMRKHAYCGCCV/CITLC VGAQNKNRAVCGLYSTCPRLCVYEHEHI CVNE*VCEHVCERESVRVCESTH/LPLC A*TCGPIFGCMSEKHVFSYTPCVHRVCV CVCVHLGCCVC/VCVCVCVCVCVCVCV
1567	15468	A	1575	1	383	FLSFGFAPQAGGQGHNHG*GPP*P/PKA KGIFPPHPPEKREQRVHATPPGKFLDFF FFWKKGGLNLGPKKNLGPGGKKNLLVSP PKGGGKKKETPGPGGVFFWGGIFFFFPP PCSPG*PLSLLKKPKGG
1568	15469	A	1576	35	469	RIPRCHQPVGPLGCREGAKPQGPGPDAA DSHPPASPRAH*/P*SLHRDPIPGFRGP CRRNAGAGPRAHTAGICAPQPNS*SRHH PWAAAPAGDDSPTTSLGSHVPVGRKSSD GCRQRALCTPGSPAPSEAEVGGSPELRS LRPAWA
1569	15470	A	1577	473	62	SLEINPYISGQLIFNQHAKTNH*SMRKE \SFFNKWCLDN*ISTGRRMKLDPYLKPH IKLNSK/LKDLNIRDTTMINLHDLGFGN GF*TMTTK*AIKEKIN/WDFIKI*NFCA SNDIIKKVKRPNVTAYTCNPSTLEGPR
1570	15471	A	1578	59	426	LERRSFGAPLSPFFAPQFEMKKGFGSP* KFFFSPKALNFGGGVVPFFPPPKKRFFS KNPQEGFIPPPLKKKKKTSQPP/YKFGP

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						PKESFKRAPPFFFFKGGPFFPLVSNQWT GKPRLPPPPPKETQNPSSFQIGGQKKGK GGPQSFSFPIKKKKKKGGHSRSRTSPRV
1571	15472	A	1579	2	419	KANKTKNAYFEGINKMDKPQVILKKKY/ REKT*IPSIGEEKGIMSP\NSEDTKRII KECFKQTYAHRFYSLKE/MDILLESHKL PKLTQ/EETDSLNSPV
1572	15473	A	1580	129	403	YMFFIPINCQDHPK*KKKKKKKKKKRGG /RPFKKTLRGPKLNRAEKNKFFF*KGSI KKKCLEILKKKLFFGGEKNCKNPPKKKK PSREKKKF
1573	15474	A	1581	317	76	PRFFFFFPPPKKGFFSPPFFFFSPRFFP PPPFLKPPPRFFFFGPFKKNFF\PPPRP LIFFFF*APPPFFFFFFFFFFFFV
1574	15475	A	1582	259	377	PREMKTYLPTKKLGYEISHYH*WWGCKM VQPVWKTVWQFLKGLNIKLP*DSAVPLV GM*PREMKTYLPTKKLGYE/MFTLSLLI IANK*KQPKCPRMNKW
1575	15476	A	1583	1	415	PTRPITSSICLRQSYLKALIAYSSISHI ALGV\TAILNPTP*SFTGAGILIIA\HG LTCSLLFCLANSNYERTRRRIIILSQGH QTLLPLIAF**LLARLANLALPPTINLL GELSELRTTFS*SNITLLLTGLNILGT
1576	15477	A	1584	216	406	LNLLPLVLGGSSCLPPPCGGN*KPPPPP G\LFLEKKGFSPCGPAGF*PPALRGPPP PPLPRGLI
1577	15478	A	1585	383	3	KKFGYPFYWIG*KILK*FPG*K*SLPHR KSPFFFFF*GRVLLCPPGWRGTTKGHGS QVT\LPAAAMTFQV\K*SSPLRLPSR*G YRQASPWSGNFFF/CLVESLSMLPGLIL NYWAIAIKPSGPPKVLG
1578	15479	A	1586	126	413	NPTLKK*KMKENRMKKNEQSLRDL*DTI KLTNRCILGIPKEERKKGAEGIFGEIMV GNSSNLIR\ENINLNIEVAQ*TLSRIN* KRATLRHVIMKM
1579	15480	A	1587	242	409	GWMIFRFNFFFFLRGSFTLVTQAGG*GG DFG/SLRPPPPGLKRFSCLTLPRSWDYR H
1580	15481	A	1588	2	338	EIEKKGKGKKRRG*RSNKKKRGGRLEGQ KY*SPPCPRLSFFLVDEKGPEVLQDSLG GWWKTP/SGCPEMTDSSQPY/YRAFYVL KN/QRVGFSVDVGEIEKDQDVEKNQDPS CPRL
1581	15482	A	1589	360	0	NNFLEQLKFPPKKKITTDSYKAPRPFFF FPPSQKGVFPPTLFFGFPPGFPPPPFLN PPPGFF/CFWAPLKKFFFPYPGG*TWVS LKGPP/L/RFFFFFF*DGVSLCHPGWSS SAQS
1582	15483	A	1590	75	412	VEGQHCNFCAAQETINRVKRQHTELLET FANWSPDKGLIPRTYKELKHLNRKKHSY *KWADDLDRHFSKETYTPPKTYSCTQYC *P/SITIEN*KLKTSNIKTRLQGGHKRL ER
1583	15484	A	1591	309	1	FSTQGAHMQVCYMDTFHDAEIWTSIEPV TQIVNMLPNR*FFNPCPHFFPPPFCSP/ LVSFLLLLRDRVSLCCPGQSRSVGFK*S TCLGLPKRWDYKCEPPHVA
1584	15485	A	1592	2	415	LSISLSIFSFLP\FSFLLPSLSLSLFLS

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						FFLFLSFFPPSFFFFFHRASLCHLGWSA MA*SWLTAVSTSQ\VKQSSHL
1585	15486	A	1593	3	396	HSAFLFFL*DRVSLCHLSWKAVAQSQLT ATSTLL/VLKQSSHLNLP
1586	15487	A	1594	300	62	KMTGVLKSSCGKSPKQVGWLCVCVCVF/ SFKRQGLAS/VAQTGMQWGDHSSLQPPA PGLR*SSCISLISSWDYRRVPRRAPG
1587	15488	A	1595	1	412	FDRPAADQKAASALKASGVQAQMAKGTY HDWSLQDWKVLWMTH*VS\QQEQDPTNL YISNLPLCMDELQLENMLKPFGQVISTR ILRDYSGTFRGDGFARMESTDKCDAVIE HYNVLLIMTPPGVSAPTEPLLCKFAE
1588	15489	A	1596	428	2	QSESREPENFLLPTSTSSLLLVHCLSRT CVVNSTLSCVPHFFHLTFNSHLLLTSQP RRVHFC*LSLSSIISWKLLNTLPGVPIR \ASEIFGLRTIRNFPFLSHSVLFPFSLS ESHSVTQQGVQWHELGSLQPLPHGCQWL SCL
1589	15490	A	1597	2	442	QGSL*PHPPMLK*SLTSAF\NYRHVSPH LANYFLFFF*KQGLAVLLGLALN*AQ/C HLPALASQSAGITGVSHGAWLFFFFLNQ CYLI*FLILIF\ERRNSPVAHVLVNGGD LGLLKPPPPGLMGFSCLNLLRSGKYKPP ATSPGYIFC
1590	15491	A	1598	419	121	NLGYPRVSPPPPFLNPPPEFYFGPPKKK FY/PPPPPAQKIDPP*TPPPFFFFGTDG SHYVAQAGLELLASSDLPASALQSTGIT KHEPPHLAETIFLVFL
1591	15492	A	1599	45	397	DRVSLCYPGWSAVV*S*LTAASNSW\V K*SACFSLLSRGDYMCMTLHIANIKKNF LGRVRGSHL*SYHLKLCLKK*RTKEGFL SFFWKGKRHFLGQKNILNPRLKVFFLPG PPKGLGY
1592	15493	A	1600	3	397	SRRPGRFSLMLTLSWHS*VCRAALAARE EQWSGCFKSHF*LEVNFWVSGIDREV/C GY/LKTVLGEDLNDYVSTQI*D*LMKPR CPEKQDESLLKEFGGGA*RLNVVHRPGA VAHACNPNALGAKGRRIPRSG
1593	15494	A	1601	244	2	KTKTSFHSLIDSCGYLLSYSNFQI*KKM IFK/YLHLRAVPRHVIVRFTNLERQEKV LRAAREKG*VMHKGKPIRLTADLSA
1594	15495	A	1602	435	2	PQEAIYTPTQHPTYGAICRIARIHGSRD Q/SVEMKWHPQLTITPSGP/LGKSLLPI PVALCFADLEVFIPKGGMLSPGVTIISL NWKLRLPWVILQ*RITPLARVIPPDYQR EIRLLLNNERKKSYVWNTRDPLGHLVVL PCPMVIK
1595	15496	A	1603	288	8	EFPLIREMQIKPTMRYRLTPV*MD\R*W *GCGKRGTLVHCWW*CKLVQSVCERSSK NITIELPCDPAVLILGMHTKERKLRPCG WTRGVGPGYC
1596	15497	A	1604	411	236	LIPSEHFFFSG*F*AFDRSSLAPTPQLR RHRPPTGLLPLSLLQGP\LLTPSVLLS* GGRFKGPNFTPPGGQGKIFFMGPPKSNP GPGV
1597	15498	A	1605	2	437	KCLRISPCAGPRRPWCPSFEPRVCVWPL GVPQVG/PEGP*GEG\GFEGGDVRQLWQ GKKKKKKNTLGKRGPWFPKEKRGFSLTP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						WFGPQGLWEPCLNPGGPLFLIGGFQKGP KVLIGKGKTPGPKKKNNRPRKRGSLGPP GKDDFPL
1598	15499	A	1606	31	467	EFPGRRFRGGGCSELRLRVCTPAWTTEG DSISNNI*LVNEN/HTVNSWKCSDS
1599	15500	A	1607	418	32	VGQVGLELLTSSDPPASAYPK*WDYKR\ DPRAQPNPNILKAQSNRSPPRQR*PASS FSNQNSCMHRCISLP*VLFLIFFKNRP* NNSFGYNSSGWWSGLNILNSC*FWFLFG NSDTEIRICRSFHRGREV
1600	15501	A	1608	379	3	FPILSPSYNPSSTELP***SLQSPLFEP YDFFSVNMFSFLFFNLKSHTVAQAGVQW RNHGSLQPRSFQLK\HPPASASAGTTGM CHHAW/LIYLCVYLFLEMRSHCVSQD*V QWHNHSSLQPETPTK
1601	15502	A	1609	456	99	PFPTPFPPPHSNWGLGLGCGL/EPTMTP SGLGLKGSPS*SPPAHRLSGAQLCPVLR APVLGPSQMPPGRKKKPTARGSPWRKGV FVMSGQSDPLGPSSCQELGPRQSTQGTF PGA
1602	15503	A	1610	1	420	FRFSDGAAGQKCSSPPRPGRGRAEVLLT SQTGRQGRGAPHISDNGQPGRDAP\PS* M*WRPGRGAP\PS*VGWRPGGDAPHF\Q TGQPGRGAPHIPDDGRPGRDAPHFPDGV GAGQRLQTRHFGRPTAAAWKVKVVTSLR
1603	15504	A	1611	426	3	KNPFLLEAKVSFNPKWPPALPPGEQRDS VSQKKKKNLLIHKKAHSKH*FFICRE\C ESALLLHQNIHAGGKSYVCNK*GRGFRN KSHFTYQRTHSGKKAFL*KECG*DFL*K AILTAYQKTHSGKKSFVCKECR*DFTQK TK
1604	15505	A	1612	428	273	HHA*LIFKIF/CVETRVSLLCPGWS*TP ELK*SSLLGCPKCWDYRREPPIRPTT
1605	15506	A	1613	311	4	ANKFKNLNEIKFPEAHNLPKFTQEGGLN NPVSLY*KN*TYSLRLFP\KKKKSGPDD FTGEFN*TSKEEVPSLHKLLQKI*ERNT LPNLFHKARVTQVSKSEM
1606	15507	A	1614	338	88	PNPPPPSKGK\GFPPPTPGRKKKTRPPP PPGKFLGF*KKRGFPPFERGGP\NPAPG GPPPPNPPKGGGTKGEPPSPEGGVFFFF
1607	15508	A	1615	2	162	KHGGTCLYSLLLGRLRHESCLNLGGGGC RE/PE/SHCIPAWATE*DSVSEKKKYL
1608	15509	A	1616	3	399	PEVREYLTSRGLPFKVLLILDNAHGHSE PQRFNTEGINVFYLLPNPRSLIQTLDQG VTRTFKSHYTWYSTERIANAMEENPDRT S*KSRIMTPL/IDAIVMTEKAMEAIMPK TIISCWRKLCPDVVHDFTRFT
1609	15510	A	1617	390	1	KRNCFGPFLTPPPGQRLGGFKFLK\HFF YYRGERGGFFFSPFNKGFPPPPPPFWGFF LGALKF*RGVPPSKPPPPGPGKKFKLKP FPPRKSYGGCFKCFLGGPFPFEGPPPQK KKKKNFTAARDLEPNAW
1610	15511	A	1618	468	0	MKLVNIWLLLLVALL*GKKHLGDRLEKK SFEKAPCPGCSHLTLKVEFSSTVAEYEY IVAFNGYFTAKARNSFISRALKSSEVHN WRIIPRSNPSSDYPT*WP/VALKKKKKK AGV/LPLENYSIITRV
1611	15512	A	1619	421	2	SSRLSLPKCWDYRREPPRPAQPRILKKI

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						S**EPFFLILKCI*LRTQGLGRGHKGKL NSTYVLHKFMD**LGQLMNGLNMLDESS FCNVLKHTKQ\WRDYYFVCLFVCFVRQS L/NPVSQAGVQRRDHGSLRAPPPGFAPF S
1612	15513	A	1620	406	2	GTKKASSNGFINGPGAAKKKSQTFAFLA KPGAFPSILLDEKNRPQIKPPACFP/SI RESQTSYPVFFFWSPSCGFFFFWGKPEP LLLKEAGKVPLFLFLFGFL*DGVSLCQP GWNAVLRSQLTAESNPHASAHAS
1613	15514	A	1621	411	0	PPPPKKKPSGPPPP/PSSSSSPSPPRKF LGGPRVFFPPPFFKPPPPKNFWGPPKKK KFPPPPGGKKFFF*RAPPP
1614	15515	A	1622	2	403	TARCGLNFPCSSSLPFIAS*VAGTTGTH HHAQLILLIFCGDELSLM\CPGWS/PNS SHLGLPKCWDYR
1615	15516	A	1623	298	411	LIINVCWPGLVAHACNPSTLGG*GGRI/ TMRSGVRDQP
1616	15517	A	1624	263	2	DSVSKKKKNFKE*LIPVLLKLFQNIEEE GILPNSLYKAGV\LIPKPDKDT*RKEIY RPISLINIDAKIVSKILANKIQ*FIKKI TDAW
1617	15518	A	1625	3	281	PFSCLSLPSCWDYRRPPPRPANFF/VYF YKKNTRTQCFTVKHGFTVLTRLVLIS*P CDPPSLASQSAGITGVSHRTQPHTVFFL NNPALPKLQT
1618	15519	A	1626	300	20	NPGPRGFPPPGPPKRLDFRGGAPRPGF* YFLKNFLGFFWFQKNFLVFFLGNKTPFP PQFFFFF/RDRMSLCHPGWSEVAQAWLK AALTSQTPAI
1619	15520	A	1627	394	40	PQPAAASLFSPGLFFFFPPVFSPPPFFK TPPRIFFFWPP*KNFFF\PPPAFFFFFF LGAPPFFFFFFFFFFFFFF*DRVSLCRP GWSAVAQS*LTAALNSQT
1620	15521	A	1628	386	3	IFPTRCTHLHLGTNKLPTCSFFDQAKKN PFCS\HHSRGVGLRARLFCERLTIEGAG TPACPAP*FPGEPTRP/PGRVRWLTPAI PALWEAETGS*YVARTGLELLVSSNPPL SASQSARITGVSHRTWP
1621	15522	A	1629	401	93	ARGVLPLNPPPWGGRGGGSP*GKNSKPP RPRGENPPPFLKPQKLPPPGGGPPPPLF LGG*SKKTPPPPKGGAPINQKPPPGLPP PGKKGAPFPKKKKKKDKNIRTKKKARRS GSLLQSQHPGRPR/RGGPPLTKNPPLAS PPQEKRGPPFQKKKKKKTKI
1622	15523	A	1630	417	47	PPPGTISSPNP/QKNLKKGPGPGGNPRN PPPLGGQRG/RGLWAKKSRPPGPPRGNP PLFKKKKINGGGGPPPVVPPPRGARAGK SLYPGGGPPQ*PQMGPPPPPPGAKKGFF PKKKKKKPKKPRKT
1623	15524	A	1631	416	54	EYWCKGR*IDQWNRM*FKMDQHLHSQFI FN*ATKAIQWGKESLFNRLCLKNWLTIR DK\IYLDACLTTY*KINSSWHSGAFL* SQILERLRQEASLSPGI*VQPRQHSKTP SLKKFFFKFFS
1624	15525	A	1632	2	373	LVFLDNMLKLLRHSALASACFPEDLAKI MDEGGYTKGQIFKVHGTAFCWKKMPSRT FVVREQSVPGFK/ATD*LLLGANAAGN\

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						KLKPMPIYHSENPRVFKNYVKPILPALY TWNSKA/QMAAPLF
1625	15526	A	1633	3	383	NIWN*KAWMTVHL/FIT*FTEYFKSTVE NC*EKKKILFKI/LLLIDNTFGHPKALM EIYKEINVIFMPANTISIL*PMDQGVIA TLNSYYLRNTFHKTIAFINYDSSDRCGQ SQLKNFWKGFSILDAIR
1626	15527	A	1634	2	182	GACTQLIGRLRQENRLN/SGDRGCSEPI LHLCTPPWATE*DPVSKKKKKNPCPKLK KGPPP
1627	15528	A	1635	331	1	LFPPPPVLKSGPGPN*N*PPLKGKSFGP LKKKFFFFFF\FRDWVLLYCLGWSQTSG LKRSSCWDYRCEPPHLTPNF/SYF/CRD SVSL*PRLEGSGSIIALCSLKLLDSSSP H
1628	15529	A	1636	80	381	KLSKCHAHHSRGFYKYSLFQLGASQFPQ VLRITHPHKGSWAAPRS*G*SQC/SHFF SFFFETKSHFVVQAGGYGRNFT*LQPPP PGLKRFSHLSLPSSWDYS
1629	15530	A	1637	381	38	SKRQGFHHVGQAGLELLSSSDLPTMALH PTCPLQKCWDYRC/DATAPNLSSTFFMQ EKCLAFL\PLFSSAPHSL**PKAVIEKD CPGL*IW**VARSQRMNVFNFIK
1630	15531	A	1638	3	295	PGPDGFTAEFNQTFKE*LIPILVKLF*K IQEVR\FFKFSITLTPKSNKD
1631	15532	A	1639	48	380	ILGKAISFTIE*KGLKYLGIYLTKEAKG LHTENYKMLLKELKKDTNIWKGILCQ/W TRRLNMVKISV
1632	15533	A	1640	343	23	SWLTAT/FCFLGSSDSPASAGVELLTSG DLPALAS*TAGITGVSHRTRPALSINTS TLLCSSPYCPPHLQSLQGTTQPVPFLKA QRTGCLLQGVILTSQAENFCNKH
1633	15534	A	1641	3	397	LELFSSAHCCPSLTVMQYYPP\RPTSHD CQREKSPHRTKKKKPLEGVFLG*KIKTN LENPPPLPFFGGGPPPKGGGPFKIV*GG WPWPWGLKIPTLPKGPTPRPPWGPLGTF GGEGKPLRAFPLQRFFRGPE
1634	15535	A	1642	2	308	NKWR*GNWISVKIDNFNFYLMPYTNLS* IRDDLNAKATTIKLVGENIGENLGIGKN F*ERTLKA\LRGKKMDKLDFITIGNFCF SKDRIKNKNKARRGGSRL
1635	15536	A	1643	16	386	EKKKLSLFTENGIPYL*NPKESAKRLLS LINDFSKV*GYKNN\DEKSVAFLNTNK
1636	15537	A	1644	533	3	PLSLSLSSLFLSFFL*DRACFVAQAGVQ WLDLGSLQPPPPGIK*FS/CGGNVAVTP RLSPLTLPAMTEVRLPSSKIQTNKEKNT VMSEIYQSLM*MGWG/M*VRMCVKFKKP WVDN**VSVMGCLLPSFLPSFLSFLFLS PSPLSFFPYFFETESCFVAEAGAQWLDL G*LQPPPPAVP
1637	15538	A	1645	341	19	GIGGRPP*FQLLGRLKQEK/HLERGKGF NEPKSRPCISAWATKGDCFQKKKKIHMT LQQIQPKQSWKTDISQFRTDYKTTIIKT VGHGIWIDIFINGIELSENLNQCS
1638	15539	A	1646	279	3	TFYHNEKDNNKCWLTI\GKI*MLTGCYW ECKMVQLPWKTAWQFL/R/DVNI*LPYD LAITLLSIYTRKRKTYVYTKTCIQMFLA VLFTTAKRWKQP

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1639	15540	A	1647	392	1	QKLEIMLREEGMLKAKTGQKLGLLCQAV THLVNAKEKFLKLNVLLQGTHKW*ESET AKSLILFNSMKAEKGE*AAEEKFAASRG WFM/RFKERNCLHHLKVQGEAASAVVEA VANYIEDLVKKIDKGGCIN
1640	15541	A	1648	425	148	SQSLI*SKALTLCNSMKT/ERAEEVAGK KLEASNF\LKFKKRSCV\RNVNMQGKVA SLDGEAAASSPEDLVNFIDEGGYTKQQI FN*DKTSFFF
1641	15542	A	1649	271	462	RRQKKRHKRCILSPLLFDIVLEVPARTI *QEKKIKGIQIGKKEV/KIISLFADDVV LYL
1642	15543	A	1650	70	398	RPEASLRHMCLNAGQLLSKRAKLGALSL SFFFWKKSLAFAPQPGGQGGNLG**KPP LPGLRGFSGLTLLRN/WE*RWPVPPPT\ NFGPLIKTGFPLVGQAGFDLRTLGALR
1643	15544	A	1651	425	3	FEGFPKVGFPLGPRFPSRVPPFGTLPPP PKRGPRCFPQPGAPPPKIWTPPGALPQG GVGPALPG/ALQKFGPKNPGGFFSGPPQ MAP\GGFPGGP*RPPRGGAPFFFFLRQG FPVAQARVHLPGSSDPPISAPQVAGTTD VC
1644	15545	A	1652	385	2	KGNNPSPPEIKFFFFFF*KGLLPLPQGG GQWGYFRSLQPPPSRLKLFSCPNLPSNW EYRGP*\RLL*LITGRGTSGSKTKVPTP CGPFNLNQLGLGTQARNFS/RLVFFFFE TESPFVAQAGIQLRDLHS
1645	15546	A	1653	242	3	KNKNFGINRGFFFTFKVPGFFFFLGKVK LFFFFRNLKFFLKAKPP*\VFFPIGPSF FFFFFFLDRVLLCCPGWNVVVQSL
1646	15547	A	1654	3	285	HFIIYTKDLNRRFSKEDI*IIIKHV/KK CSPSLAVREMQIKTTVRPGTVAGTCNPN TLGGQGRRIVQDQLKQQSKTSSLQKKIL FRLARHGGTCP
1647	15548	A	1655	1	373	KVSLFFFFEQGLLCCPGWSAVVSSLQPQ CPRVKQFSHVS/LPSN*EYSCTPNTFSL QVCVSIHKYI*YIYIYIFKFF/CR/DRT LARLHRLVSNAWSQAILPPWPPKVLGLQ
1648	15549	A	1656	189	2	VQPGQQERNSISKTKNKTKQKLPTKKSP GPD*FKEELIPILHKL/F/HKIEDKGTL HNSFYVVTI
1649	15550	A	1657	385	13	GGPPPWGARSPPKL*NPPPPRKKPPGPP PPPGGAPPLGGFFLFPPPPGGPPPGGGK /SFSPRFFFFFFFLGGGGQIFLFSPGGG PRGVFSPPAPPLVPKPAFFSKKKKRGSS GGEKPEADGYFIK
1650	15551	A	1658	352	2	HLSLLSNWDSIRAPP/RPCVIFKNVPLN IFFL*RGVTMLPRLVLNDPPISASQVAR IIDVSHWAKLRRSV/CYVFETGSGSLSQ AGVQRYNHGSVQPQPSRVS*SSHHSLWK YRYPPPRR
1651	15552	A	1659	265	3	HSGQRDEGRMRCGEWLESHGVVRARSCM TLKTSFLFTMAKI*NQLKCLFMDEWIKK MWHIHTMEYYSAIKR/DEIPSFVATWME LEVIM
1652	15553	A	1660	1	163	NQQNENRKTIEKIIGTKT*LFKKIKKFD KPLARWT/RGKKNIQITNIRN*RRDVI
1653	15554	A	1661	56	320	KFFMYSAGESTKIRCLF/SCLFLFLR/Q

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						ESRSVSQDGG*SEPRSCYCTPAWATE*D SVSKKQNKNKPKKNLNKCFASSLLITLP PARHKA
1654	15555	A	1662	3	421	GIITDTFPNLEKGINIQVKKV/RRPPSR FNPKKTTSRDLIIKLPKIKDKGS*KQKE KTSKSARLPQPHGLLGLGLGKSASSPIK KERKQ\QITYSGAPIFLVTDFSVETLQV RREWHDVFKVLKEK/DFYPRIVYLVKIS F
1655	15556	A	1663	362	2	VIFADEAQILKKEDKLDFIKMKTSVHQK TLSTEYKDNHREKIFVSQISDKELISRV YKGLLKLNNTDKNLILFYF*RLGHSVTQ GRVQWCNHSSLHPQTPGLK\NPPTSAS* AAGNTGVHL
1656	15557	A	1664	79	355	IHLPSLIGDFNLFTGISLLICLVLFVFI FETGSCSVAQ/S/GVQWHNHGLLQPRPS GLRQSSHLSPLSSWNHRHGPG*FIYF/C VEIRAHYHP
1657	15558	A	1665	47	384	KEKASGPLINFFFFPKLCKLAPFFFLPF FLWGGGGGKFSRNPQKHFPR*KRVFVNF FFFFFFLRHCLTVSLSHCHPGWSAVA*S QLTAGSNFW\VKQSSHLS/LPSSWDHRH APP
1658	15559	A	1666	163	601	IFCKGGVLPCCPGLADLHFSTSNSISFY YSSGLLRMTNKTETPMSTIPKGVGVAWR FGNSECIFQELPLTLHHLLSTMLASFIH SHEASANALVGRSLTVGWGCRGVGVSVD PAAWLWRDLKGCF*DKSHSVTQSGGQWC NLSSLQP*APRLKRSCILSLPRSWDHWH VPPFLANF*IFCKGGVLP\FAQGW
1659	15560	A	1667	418	3	SVCLGLPKCWDTGRKPLCPAPSFFY/EG SITLIPKSEMHLPRNENYRSGFLLN/M/ DAKILNRILANCISN*I*NH**KVKFT PGKKDWFNNRKPTDIIYPH*QNREEKSL VSSTDMAKVFNKIQPVLRELTIEIKGNF LNL
1660	15561	A	1668	411	1	LRLHVGRTTT\LFKAVSQGHLSLQRFLL PSVEICPAPRGGVYRGRQASLSCGGLHR VRASQLLWFLTQASAMAGPPPPVLLPPC SLI*DCCANNKGGFIGVGPFEPCVGYNL LVSHLLRPSEKPSIRVGVT*FSRC
1661	15562	A	1669	151	1	PLEKEAEITGP*PHAWLIF/CFF*TESR YIAQARMKWHNLGSLQPTPPGFK
1662	15563	A	1670	1	389	TFF*KLKMINLSEEGMLKAKISQKLGLC \TVSQVVNSKEKFLKEIKSATPEST*MI RK*NSSVANTENV*ERSRTSHNILFS*S SIQNKDLTFFNSLKAWRGQEVAEEKSEA SSGWFMRFKERSHLHTIK
1663	15564	A	1671	1	363	ECTGPKIAKIILEKKNNVGGLPI/PNFK I*YKAPVI*FWLKVPVIPSSSAILMKTV *Y\YFKDRNQDEWYRLRVWKINSHIYGQ LI\FSKGTKTIQW*KSLFNK*CWNNWLF TCKRMKLD
1664	15565	A	1672	203	2	ALNKRTDMPS**IRRCNII/KCLFSPKM N*VFNVIT/IQCPSGHFFTETDKSILKF IWKSK*PRLAKRTL
1665	15566	A	1673	15	378	NYHHNQNNEHMYHSLPNFFFFFFGKGAP PG\PKGGGRG*REP*IPGGKGNPPL*PP

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						KEGGPPGGTPPPGKPGKIWDFWEKGGFP LSPGGAGTPGPKGDGPPWPPKGGGKPGG TKQPGPKKFF
1666	15567	A	1674	2	349	LFLTVLARLVSNS*PQ/CDPPALASQSA EITGMSHRAQPRGIR*I*CGSYTTCHPL LLLT\YLFIYFSTESHSVIQAGVQWHDL GSLQSQLRRLT/CILTLPSSWD*PHVTL PG*FCLF
1667	15568	A	1675	348	78	LGPWVPPVIPAPLGG*GGRSPRPGFLTN PGPKGKPRVFLKIQNLPGV/RGRPPLFP /GSPGSGGPKSP*PLGPSFPLT*NFSPP FWGPPGGPK
1668	15569	A	1676	2	385	TSRRDYRP\GHHNQLIF*/SFCRDGASL CCPCWSQTPGIKKSSCLVFPRCWDYRCE PGL*I*MGKNPT\LFSNGL*CDCIPLIH SIADIRKKPHS*LQGL*LCHQQNSQTES CSVTQAGVQ*CDLGSLQP
1669	15570	A	1677	386	1	KSTRPVLYKWNNKA*MTEHLFTA*FTEY FKATIETFCSEK*IPLKILLLICNVPSH PRALMGMYKEINVVSMPTDITCILQPMD QGVISTFKSYYLRNTFDKAIAT/DSDSS DGSGKNLLKTFWKGFTI
1670	15571	A	1678	2	193	EGGRIFFNSFFEVILTLI/PKPKKVVER K*SYHPISIMNGDVKILAQTLLNQIQQY LKRIIHYDS
1671	15572	A	1679	561	830	TLLLGT\NAVVDFKLKPMLTY\HS\ENS RGL*KSWINLGLTVFYKWGTNNAWGDDR HHLVYRHGFTGIF*GSQLKTYCSENIPF KILLFIDN
1672	15573	A	1680	415	2	TSCAWLSLYPVYLYRSSSLPRFIFCHFK HLWYKNITKKAAEINTNFCCYINRVLLC HLGWS/ATVVSS*LTVTSKLLGSRDPHT LSLPSS*EGRCITPRLGDLLNLFSRDGG GIRGTSTLPRQVLNAWPQAILLVRIT
1673	15574	A	1681	1	78	RPRIRHEVGQAGLKLLTSGQTPASVP*C WDYRPEPPCPALHISYK*NHAMCGLKCL AVSA*RHVLGFIRG\WHVECCFPFCS*A GLKLLTSGQTPASVP
1674	15575	A	1682	414	162	GGPGGPIPGA/AGLRPPPPPLGNPPPP* KAKICPGGGAPPVFPGS*KGGGESP*PP RGRGPFIGVQPLPFGLGHKRGLFPKKKK KI
1675	15576	A	1683	378	129	QPFGPRNFYQIFNFPG/PPV*HSPLFGP KFPPFSPGGGQWGPLGNPRPPGAKGGST LRGPRTGGSRGGPPGPGKFFFFLKQSLA L
1676	15577	A	1684	3	374	GISVLPGIGAPGNKPELFEEVKLYNNAR EREKYDNMAELF/AVVKTMQALEKAYIK DCVSPSEYTAACSRLLVQYKAVFRRVQG SEISSIDEFCRKFRLDCPLAMERIKEDR PITIKDD*GNSLS
1677	15578	A	1685	2	373	PFIRPETIKLLEEIPGGKLLDLGLGNDL LARTPNAKINTWDHIKLKSFCTIKETIN TMKKQPTDCEKIFSRLISDKGLM/SQMC KELVQLN*KK/TDDSVKGWAEDLDRHFS KKDIKMANRPGKVL
1678	15579	A	1686	378	201	HATCLANF\CSYG*DRVSPFCPGWS*TP ELKRSTRLGLPKCWDYRCLGRSLLFPGA

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						PPDH
1679	15580	A	1687	1	404	MCVNPGGGACSEPRSCHCTPAWVTERDS V*KTNKKKVKRRKKIFHANS/KLKRVGM AVLISDKIYYKLKKVRRDKEYIIKGSTY QEDISITNTYTLNT*APKYMKDTLTELK EEIDIYAIIVGDFNTLLLIICRGT
1680	15581	A	1688	307	33	DEGSCHDAHAGLKLLDSSGLPASASQSA GILGVSHGARPLISSYNGTSHGGLGPAL VTSFNLSHLFKDLLSLQI/HVTF*GMGL GFAGAKLSL
1681	15582	A	1689	11	394	IFILEARTRISSRTFFKS*INIHAPYNS AI*LIGIFPREKK/STCPYIYTQMFIAS LFVTAQTRKQPKCPSTGE\WSKNLWN
1682	15583	A	1690	20	391	SEGKGWYSCTKWQSMKLGGITFFFFFPP PKNPPPKKSGP/QKGPFF*GKGPPWPPK KRGHKN\RGFPKQRARPPKPVFFLIFGK RGFLLGPKGG*NPGEKRNPPPWP*KGGK NPGNPKGGPHLTL
1683	15584	A	1691	72	392	IKMIGSLFFGFAFFFFFGKKTPFFPQPK R\GGKP*IT*TPPPGN*RNSGPSPPQKV GIKAPPPLPK\NF*FFGKNGVTPFPPGG FEPPTPKEPSPPVSPKGGKTNPAP
1684	15585	A	1692	389	161	HGGACLRSQLLGRLRREDCLNQGG*GCS EPCTPAWVTE*D/SSQKNQKSKIKKSGL DNSFSIG*GILGLSTCDRYS
1685	15586	A	1693	286	363	DGISL*PRPPGLRQPSQPS\LLSNWGCR STPLCLAGFFVFVETGFLHVAQACLRQG FTMVAQS/ASQKIHIT*GAFETIQVLFY WGGVGFGQWRFFFFFETESHSVTQAGVR GCSLSSLQVPPPG
1686	15587	A	1694	1	356	ELLEPRGRGCSERRPCHCPPVRVAEQDS VSKKKRERKYLYFLRFNWRSLRIFIYFC */HPLQHNIQNISFTLQNSFGFFSRQYC PSPLEIIFLTPLTENLLGLFMKGIIQNW FFGVGLF
1687	15588	A	1695	3	298	KYFETNENKNIQYQNL\AVKLVFRENLT VVNACVKKEERFQVNNLALYPKN*EKSM LNPKGKIIKVRSEKNDIE*KNDEENQ*N *SWYFEKITYWQTLD
1688	15589	A	1696	3	405	RLWCGWRNRHLGS*NRVENPETGLHRYA QLIFLTKVQKQVGEGQPFNK*CGGTWAP TGKT/MEQPPKASSSSSSSSSSSSSSC KM*NIVFFKMGENLWDH*AKSYEVRTKA *TIKGKVDKLDFIKIKHFCYGKN
1689	15590	A	1697	6	392	LQRTLLVGLFNAAGNLKLKPMLICHSEN PRALKNYAKSTLPVFYKWIKIAWMTV*T VAAWLTEYFKPIFENYCS/EKKIPFKLF LLTNNAPGHPTGLMEMYKTTNVGSLPAN TTSVLQPMGQRVISTFKS
1690	15591	A	1698	390	3	AIIESDFLTTSREVAKKLRVHPFMVLWV LEPIGKVKKVNKWGP*KLNK/NKKNHCI EVSSSLFLCNNEPFLDGIVTCDEKWILY HNW**SAQWLNREVAPK\HFLQPNLHQK KVTVIVWWSAAGLIQNEH
1691	15592	A	1699	1	245	GGGGEYSKIIAIKTALKNTTYLGIYLIK \DVPDLYTKNYGTMLREIKYLEK*RARP CS*TERFKIVKMSI/LPNLIYRFNTI
1692	15593	A	1700	2	324	GTSGTSGTSGTSQTCRISRVRSTSSWTS

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						GRHLQCHVSKAESSWFVLSASSCSTGSP ISLSGS/GSSLSNSSKNLTLPCLFSSLL S*P*ANPVDSAFKIYPGLSSVGSCL
1693	15594	A	1701	183	372	PGVLLCWPGWSAVTVHQCDHSALQPRTP RLK*SP\STWDYRYTPLCPA
1694	15595	A	1702	29	382	GKRFPCSWEPKFPLTQGGFPPLHPGQKK KPGSKKKKDKSKCW*G/CREA/GTLTHY RQELEMVQSFWK/TVWQVLRKLNVELPY DPAFLLGLHPTSTQKR\DTMFMA/AITL /ISERWKQPRCTS
1695	15596	A	1703	1	382	KKVKIIGEAAVEFPDTIKKIIEEKEYLP L*VY\NADESGLFWKKKLQRTFISKEEK \SMDRLTLIILCKCSWVYEQDGP*ALKE KGEHQLPVF*L*NKKAWTVRTLFLD*FH QCFVPEVRKYVASKRL
1696	15597	A	1704	2	330	KLNNLLLNNS*VNTEIKAEVSSSLLEIN EYEDTTYQNLWDAAKAVLKGKHVAPRHF LQEVKK/RLKRFQINNLTLYLKEL/EKE HINLKASGRK*MTKIGDLFGLYFVLNG
1697	15598	A	1705	100	342	APKWSIVCPELVGSWSH*/PSRMKPWTL TRQGFTMLARLVLNS*RRDLPALASQSP GITGMSHRTQPLLINLMEIFTEILS
1698	15599	A	1706	600	211	SCSVARLEFSDVIKAHCHL/RTPGLKQS SHLSHLSS\WD*GRVPHDLANF*IFCRD RVLPRLLQAGLEL\LASSDPPS*ASEKC WNYRHEPTVPRQNLGLLKTTYGWVFLKK YILTVSVFSLMCLDHCLLM
1699	15600	A	1707	409	1	RGPFFFSPGKAFLKLGSNSFFPIKKTRA PKKPIFSPVSP/LNFPPKTGFPPVFPPQ MGGFFF/CFPSFLFFFLPPPPPFFFSFP PPFFFFFFFFFFFPLFFF*DRVSLCHPG WSAVALSQLTAALTSMDSSNSPTCV
1700	15601	A	1708	154	2	IGKPLAGLTK/RKRENT*INKIRNEKGD MTADNTEIQSIIRDFVS*RTAHQ
1701	15602	A	1709	263	37	SAQLHPLNIQNHRQSILLHDFFLKKQD/ G/WPGAGAHACNPSTLGGQGGWITRSGD QDHPG*HISV
1702	15603	A	1710	390	42	YAGGFRAIFFFPLPREGAKNPNFPVGPP PFGGPFFFFFAPSQKKEPGFFGKKGVF* GGAKGFPNARGPFFF/G*KKKKGPKNKT PGFFL/MGPPNPGGPPPRGEGGKIGAKK KKKSIRL
1703	15604	A	1711	3	167	YTCVFVCLCLCDCMC/CVCACMYICVCV CTRVCM*VCVCMCVRVCVQALTVLCKSV
1704	15605	A	1712	116	391	KRNFFFGPQGGGEGPKFN*RGPPPPGVK GIFPPSPPEG/GKKKGAPPPPGIIFWFF KKKGVPPCGPGGV*TPDPGGPPPPGPPK GGAPRQGPL
1705	15606	A	1713	401	47	HHYATKPFTHAHTCTCIQDTCNTCMQHT QVHT/HTDTHTHTRKVSSVCVLIMAEQE RPCPHC*GGEAGAECGVCAWLGLSS*TW RNRKGPAHTVRVVGQEQSAGCAHGLVFP RSYLWT
1706	15607	A	1714	1	400	CVESCEVDIEMVSCCV/CSG*SAVCSGT ASAHCSLPIPGSRDSPASACQVAGTTGM PH/LYPGVPLKPREGLQFTELPSGQLEI QPTCENKR*HVPCAL*VQLTDIRPN*RY QFRVAAVNVHGTRRFTAPSKHFCS

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1707	15608	A	1715	413	3	LNTFEPQRSPFIVNSSEMILLVECLFVT SGWIYHERFLNPGREIDWATCYSETGPC PVTQDGVQWSNHGSL*PQTPRLK\HPTT SVFPVA/RQGL/NSVAQAGVQWHDLGSL *CRLPSLKGSSHPRLPSSWNYRYAPPPC I
1708	15609	A	1716	421	144	RLECSGGITAYCSLNLPGPSSSPASAS* VAETTGLLHWKKKIVETGSHFIVQTAFK FLDSSDLPALAC/SWDYRSELLCPACFY NFCLFINIPC
1709	15610	A	1717	3	384	YSACVCVCVWVDVSVHRCMSISGH/ARI IRVGPAHKAQSSCRPVPAGCCTSAQTPP WCSAATADPPPR*GESLPGAYPGSHSTC CPGCCLDW*HSLPSTEPAACRAGAPGGG H*AWLGCGGRAGGRPG
1710	15611	A	1719	3	615	PVGSWARSSGAGWPPGSPQSVSDGEAGH SIPAPRGQCSRHRAEGRTARVCLSHCSF SGPRPGLVPIR*SLGRPDAVQAIVPDSQ EGRKTGIHAEAVMFPLGPGKGVKGCAGG RLCPSSPPSRCLDLGRRGMPPSSGPAGP RPSGVGSDLGRPGAGAATSSSSSSSSS SSSSSSSSSRDGEGP\TGSVEAPGSLL GPWLPSQPS
1711	15612	A	1720	320	3	GLKWLNLKDNSLYLILAKVVDDCLDEK* YADKMLQYTKSVWVSRSRGCQGQVGEKK QATEAAQEWELRK\RLYWRKECDALRAA REEQKELRDVRKAKKVYVCVRV
1712	15613	A	1721	44	373	KAMGQTLWKTVWQFLTKEEIGPM*QSCP T/DLALVFLGICTIDLKAYIHTETCTQM IIITLLIIAKNRKKASCSSVGE/WNKKL YYIRTMESYSSLR*NELSSYKKHWGGGS
1713	15614	A	1722	135	396	AQGLFCTSVKLASEQPLRILFQLDKRNK \FEIYGTSG*L*SIIICQNNLQSKFQMY HHKIMSSLGAVAHACNPSTLGGQGGQIT RSGD
1714	15615	A	1723	4	383	LNLRAKAIKLLEENIGIHLPDLGLDDLF LDITPKSQATK/AKIGN*GFIKLKHFCA AKNIIKKMKRQYKEWKKIFGNHVSDKKL VFRIYK*HLPLIIKNSSS
1715	15616	A	1724	2	405	NSRTSLILNQNLE/IKLSEKGTWKAKTG *KLGLLQQK\ISKIANAKEKLLKEVKSA TSMNM*MMRK*NNFIPEMQKVLVVW/I* NI/PLCQSLIQNKALTLFNSIKAERGEE A\KLEATKRWFMRFKESCLHNVKVQDEG
1716	15617	A	1725	90	400	SQLLRRLKQNSLNPRESSSKTTTRTKVS HWHKNRHVNQ/YNKIENSGINLHIYG*L TLNKGDEASQYSS/DILFNKWCWQKKKK \YLDPYLTPCTKISSTWTISGFL
1717	15618	A	1726	390	1	TFFPKI\EKKIL*FIWGPRRPKIANVFP *QNKPKIEGIPLPGFKIYYRALVTKTAW F*HKNPPIGQRNKVENSETNFHPPSELN FFFF\YKGAKNIHWGEDSLFNKWCWENW ISI*RRMKLGPNLTPYTK
1718	15619	A	1727	3	365	HASAKSNLRWIIKLNLRAKTIKLLEENM GENLWDLELSRGFLDRT/PKLYSIKLKL RK/WNFIKIKNFCFSRDT*KS*MAGKNI LSGKDLYSEYLKK*CNLIIRQSKTST*M FIAALFIIAKH

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1719	15620	A	1728	368	2	RNCLNSEGGGCSEPRSRHCTPAWATEPD SVSKMK*NKKINK*IMFLY\EQQSETEY FKLPLTLA/SRNMKFLGINLSKGVQDLE TENYKILLQEIEEDLNK*RNKTY*WIKL NTVKMKSILSKR
1720	15621	A	1729	326	30	NPFGGPKKGGSQGREIKPPLPPMGKPLF F*KTKNKWVGGAPPVIPPS/SGVLSQKK TFTLEGGGPNKLNSPPALP/ARGPKKNF FQKKKKKTKQNPSQREE
1721	15622	A	1730	1	374	IFNADKIA\FWKKF*KPQGTSVGREEKQ APGFKAGRNRLTTI/L/GASAVGFMIRA ALICKAANPQVLKGRDKHQLPVFRLLYN KKAWTTRTLFLDCFHQCFVPEVRKYLAS KGLVFKVLLILDNGPC
1722	15623	A	1731	389	1	FPPKIFFFSTLFFFFPRFFPPPPFL*P/ SPPIYFF/CAPKKKNFFPPPPGKNFFFF KTPPPFFFFFFF*D*VCLCCPGWSAVAQ SWLTTTSVFRVPVI
1723	15624	A	1732	118	422	DITTHLFKWLKFKK*EKGLNILFTKEDM QMEKNLKRCLT*FVVKELQIKMRYHYPP IQMAKI*KN/STISIAWQGYRTIGTLF/ HC**EQPFW*FLSKLNMILPYNPA\IML LSIYPNALKKHVHTKTCM*MFIAALFII TKNWKEPRCPSICEW
1724	15625	A	1733	407	1	NIKGPFRGPLIQWGLLIWPKDSFPILGY PPFPSPKISFFFLARSCSGAPNHFPLPN QSPCFPQPSFFLGEEKKEFLPGYSLAFP FN/RFGGS*RVRKGNGGPIPMGESFLFF F*DRVLLCCPGWSAVA*SRLTATC
1725	15626	A	1734	322	362	TAIYIYII*LFTDNIPSHPRTWIEIYKE INIFVPANTIPIVQHRNQGVICTFRKTI TVTDCDPANGSGQSKLKTWKGFTILDAV KN/IRDSWEKVKIG/TIN/GVRKLIPSL KNDFKRPKT
1726	15627	A	1735	49	395	RGGPGFFFFFFFFSKKSQILPPGWKGRG EPRVNGTPPPRGKGNPPAQPPQEGGKTG PPHKPG*FLCFLKKKGVQKGG*GGPQ/A PGPKGAPRPGPPKGGEKREGPPGPTRPN LYYAH
1727	15628	A	1736	417	2	FLFFFFFLFFFFSFASGPEILFTCL*HT HIHFLFFYSKST**PPVFAGGMFQDPQW LPETKMVPNFKKKRTTLT/YIP**KLCE CDLSNFFCFF*DRLLLCRPGWSAVA*SR LTATSTFQAQANRTRG
1728	15629	A	1737	316	338	FFFLSFYFETESYLHHP*GFIVKLSKVK DIEN\LKKTARGNYQVTYKGASIRLAAD FSAEISQAWREWDNMFKVLKEKTNWQPR IYKTLFVPHF
1729	15630	A	1738	197	379	QKRAQIDKAIFICRDIAL/P*FQ/MYYW ATVTKTAW*WYKNRHIEQWNRSW\PPEI KSQSYSHL
1730	15631	A	1739	4	401	RGYRHAPPSLANFCIFSKD/MGFTVVLN S*PQ/CNLPASTS*SAGITGISHCTRPQ MATFLIGPHKIIPWSVLWPNL
1731	15632	A	1740	94	117	KDRPMVPPVGAGEDQADEPCRGHASLWS QLVSAPTTPIPLPGRDVPSRATPFPAAL AAQQPP*ASPYPLPPGLGAGHASASPVT VPFSPISESTGS*ESAL/PAPRPGGSG

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1732	15633	A	1741	3	390	VDQFLISHDLSKLTEDEVHNLNSSTTIG \EVEFKVKKL*KKKSSGPDGITGKFY* TVREEVTPIL/SYLF/HEIEKEETLVNS FYEARIIL/IPKPDKNKP*TNIDAKTTS KVLPNRIWQYVKIIIQHN*VGFV
1733	15634	A	1742	3	442	DLHSRVEPRVRPSVRKQ*VVLLKVLICA SKDTLKRAKRQPIGWEKIFVNHMPDKDL IPEYKINMQKSGVFLFTNNSYSSTTDND INKWAKDLSRHFSEEDIQMANKHM\KR* SVSLVIREIKIKTTGR*LFTPKCWQG*G EIITLVH
1734	15635	A	1743	411	2	LPPFKHPPPEIILGAPKKKITLPPPRPK KCISLKGPPFFFFCRYRVLLCCPGWFST PGLKQSSHLGLPKWWDYRHEPYCTQSSF SLSFFLKQTGR*WFDLSNFFFY/CYCFI YFSRDRGLTLLPELVLNSWPQAILL
1735	15636	A	1744	1	393	RPGGPPKGRSREQGREGERSRRRRPRAP WARSHMWGARVFSVPRSFDQRPQEKCVQ SSYKQQLPARARDGTGNLIRGAPLFFF* DGVLLCRPGWSAGFKQFSRLSLPSR*DY RRTPPHPANF*ML/CLRRSLT
1736	15637	A	1745	395	0	PSAPSFFSTRL*LGEPPGFPPPPFLKPP PRN/SIFGAPKKKFFLPPPRGKKFVSLK GPPLFFF*DGVLLCCPGWSAGFKQFSHL SLPSS*DYRRTPPHPDNF*MF/CLRRSL T
1737	15638	A	1746	397	1	CGNFLKREKNFEARRFLQK*AARFRNIR *VTPEITAFCPL*HVASFLVFLTPNFPT IPQLYCLEPLGEMGGSGSKLPPFPTSKT PNPLISVNLCFP\AIKWENFFF*DGVLL LHPGWSAVAQSRPTATSTS
1738	15639	A	1747	392	2	FTKKGGRGGNLSP/LPPQKIF*KKKTLK KPFFWQRVWFFSPLFFEQKGQGPFFFKK PFF*KRPPDTPQPPPPSFIFFFLLFFFR /HLVAQAGMQWRHLGSPQPPPPGLTQSS QLELPHTPPHPDNFCIFGRDR
1739	15640	A	1749	33	403	IKGFKKKRGKGGAPQKKGGTGAKPPPPP PQGF*K*QKRKNGSPPNVFFPNPGGPPP PPPFWGDKRGGPPRGGGAPPPRGKRENP FFPTLA/HGKKEKKK
1740	15641	A	1750	3	396	KRQTTNWEKVFA*KN\ADGLISLIRRKC LKVKK/W*R/DMNTQFTDKGILMTNKHM KRSSTSLIMEMQHKAGVIFHPSDWQKC* STDNTQS*QGHEEMYTIKHSW*TFDYQQ PF/SESNL
1741	15642	A	1752	30	419	NEGIGAGHEVSFAANKCRSMRKNVEVLA LNRRLDGELLSGLTSTQALPGWAYLHLL SHHAVRPLFLCFKRGWVLLCHPGWSAVA QSQ\FELLGQVILRPHLPSS*DYRSIPP CLANFKNFFRERARYACR
1742	15643	A	1753	16	410	VGPKKSLQQVWAAVQATLPLESYDLAHP IILKVSLADRDAI*NLWQIPIVAS*YIP LGF/YSKAMPSSVDIYSSFEKKKTHFFL TGGGGPPLYSNYLGRLGGANHLTPGVKN QPGQFGKPPPLQKVQTLAGRG
1743	15644	A	1754	2	17	NSSLIKHRRIHTGERPYQCSECGRVFNQ NSHLIQHQKVHTR*RMYI*SR/CGKDFT QKSTLI*H

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1744	15645	A	1755	138	380	XPXXXSPXPPPCPXPLSSLFLTKCSAY* TPAHRPPPPGPFVPPPKPCCPPPPPLRP WPPLPLLTNPIPPPTLSFHPGPALS
1745	15646	A	1756	194	3	WLCIPIRHTTEQQPGFPF/LIIWSQPYS PLFCLFVF*DTVSLCGPGWNAGVQSGLT AASTSQAPSL
1746	15647	A	1757	2	403	RVLFSPTLAYTYLLFYLGATILMGVNIW KQPNCPTK/GQQKIKLQYIYRMEYYSAL KKK*ILLFAIR*VNLGDIMLSEVSQ\SR KKNIVLSHMW
1747	15648	A	1758	398	65	FFFFFFFFFP*TKGLGCIHRCDHGSPQP RIH\GSSNAPSLAS*VGGTTGAFHHARF TLIQSSSVHVSTHTLHPYPSSLP
1748	15649	A	1759	456	31	FAKRITDKKLLSLIYLAT*KGEITKALI KQ*\LKAQAKNSLKRHTIVLNHMKL/CL ILLIIKEMQIK/STLRYHFFFITLAK\I *KLGNTFCWQGL*GTLIHCWWECK*HNS YVGGIWQ/FSNKLYVQI*YNSAISNLDG RVGRPG
1749	15650	A	1760	3	378	QFQYFYYNGSVIKAVWYWSKNRK\IDQ* NRTESPDKNLHKHMQLIFDKGTNTPQWR KDDLFKKWCWNN*TSTCQKKKKKKGGGP *KEQNLTPPGWEDIIFLFGAPKNMPGAG VKTRWGGKNPGFPQ
1750	15651	A	1761	69	384	YTSASWGGARYTASAAGWKTLLLLFLFI *DRVLLCHPRWSALTQPRIIAASTFQ\V KQSFWLMHIGDWDYRRCMPPCRANFFNF LCKKKKTLRRQEVNQTPALVRV
1751	15652	A	1762	390	1	KFSTPGNKNLFFLKAPPFFFFCRGRVLL CCPDWYSTFGLKQSP/CFSLPKCWDYRR ESPPQAFFVFFGLPSLPFSPPPAPSLSQ SSSFFF*MEFHSFAQAGVKWLN\LFGSL QPPPPGLK*FSCLSLPPTRP
1752	15653	A	1763	2	390	PRVRGFFMRKFVDSYLVPYTKSNLKWTI DLHVRAKAINLLN*NVRIHLYDRELCNG FLEMIKKTKAAATTTKLDFIKIKNFCAQ QMSS/MKVKRQSTKWKKKCSYHISDKGL VSRKYVKKAYNSSIRTQSH
1753	15654	A	1764	334	3	WSKRSGPPLSKNQTKKKNATKPQT*KNW INEIGPII/NTSPSKEKTGSNGFTD*FY *TLKEELLSILLKLFQKTEKSVIFPKSF YVKDHSSCLSGIHPKDANMEQHMQINQC
1754	15655	A	1765	259	1	KSTLFLMKKYWKGSFLKKHFFLETRSLS D/SPG/GVQWRDHSSLQPRTPGLKQSPH LSLLSSWDHR*APPCPANFRFRLKTRIG RDV
1755	15656	A	1766	402	386	FKKKSRLRKI/KVQDEAASTPDLAKTI/ DYEGHYTKQQIFHVDERAFYWKKMPP/R TFIARKKKSMPGFRASKDKLTVLSGANA AGDLKLKPVLTYHS/ENPRALK/HYAKS TLPELYKWNTKAWMKIQKFPS*FT*IFM
1756	15657	A	1767	2	406	PRVRPRVRKLITLLNVSQRWSSEKKKKK KKTKKKKKKKKRGGGRL*KKKKKKPRRG RVNLFFWGPKKSTPPRVFKHRGGEK/PP PPPPKKPRERKPSLGVGSTWHGISPIKH SKKTKSTK
1757	15658	A	1768	14	409	IASGFLFFIYFGVIGRPPKRGGVFFPGG GGAPHPPQGGC*KKKRGGGGGPPPFFPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						SLGGLGRPRPMSKIKTPPSAGGKPP/PF LRNQN*TGGGGPPQ*PPLFGGPGGKNFS PPRGGGGGGPKTPPPPPPGGE
1758	15659	A	1769	305	1	TKTGPFPSNRAKKKKIVFQKKKKEKKIN CFVTAPFKGIKTEATD*EKIFAKHLSVK G/LVYL*YI*ISKIYKELLKLNNEKTTI PIKK*AKDLSRHFTRYTD
1759	15660	A	1770	148	402	FSPVSLG*GRGNIYAGMSNV*EVPPEID FQHEVKRALQTSFQVKLVKIIFFKSTI* KSLAK/WLAVVAHACNPSTLGG*GGWIT RSGVKSEPGQHGE
1760	15661	A	1771	250	2	KKKKEKKIICFVTDTFKGIKTEATD*EK IFAKHLSVKG/LVYL*YI*ISKIYKELL KLNNEKTTIPIKK*AKDHSRHFTRYTD
1761	15662	A	1772	407	1	KKIRRGGGQPPLFPLIGGGREKKFFFPG KRGFY*TKAGPFPSSWAKKKKFVFKKKK KEKKIICFVTATFKGIKTEASD*EKIFA KHLSVKG/LVYL*YI*ISKIYKELLKLN NEKTTIPIKK*AKDLSRHFTRYTD
1762	15663	A	1773	1	406	KKKKKKPTTFPGLPFFFSLSLPPRVPGA RGPPSSFPSKPGLGC*IKKSGVSPAPKK KKPRKTNPKNFPRPNPKGGGEKFFNLPT HPPGGTPPFF*RRRENPPGFAPQKG/EV FSPGGRNSRGEPRGGPKKKKKKGG
1763	15664	A	1774	2	378	AAGEWLHQGSLQSLPPGLKQSAPLGVSK W*NPWHDPPPPAPRFVVVVVGGVVLRWS FFLGAQAGIFFFF*IEMGSHYVAQAGLE /PPRLQGSS*LNLPSSWDYRPVP
1764	15665	A	1775	1	431	QQMRDKRNLFEHNK*GIRGIYLNIIKAR HEKPTVDTILSGESFSSKIKTMLISPFL FNTVLGVLA*ARKRKDI*VGK*EVKSYM FTNDMI\LDNPKDSTPKKKKTGYFMGGP GSKPPPQRGGAFLSLTRDPLEREFPKTA LFTLGQKKIKGPKFFS
1765	15666	A	1776	334	402	KGGGGVGG*QGPWRLAHCTDK\KEERKR ERERKRQRKKERKKERKKEKKE*MKNNK KKNDK
1766	15667	A	1777	406	3	SPSSSSSSLFSPPPFFWGGPRF/SPPPP VFKPPPPFFFLGPPKKKFFPPPPAV*FF FF\LGPPPPFFFFFFFWEAGFPFFSPG* GP/SGPMAGFRSLPPPGNSLSKKKKSEG LGEGGNSVLTRVLLISSYQIPGNPR
1767	15668	A	1778	70	409	LISFLVSSLIVRLYRPLLCLFPDPSKGH CIPCLLPLFWILLHIFLFMHSFIYCLIN DRVLLCLPGWCAVVRPRLTAASATQ\IK RSGSHLSLPSSK*\WDHRRCPGFFFFFF FF
1768	15669	A	1779	390	31	SHLSLPKCWDY/RL*ATTPSQKILVFTH G*VLSLLSLSFLIPPD*TF*KMSLMRPS LTQKSSIIQHDLLDKVPITIFLRQSL/D. S/VTQARMQWHDLGSLQPQPPGLKLSSQ PQAL\SSWDYR
1769	15670	A	1780	357	1	LTLFWGAQYLPKKGKGPFFLLSLPSPSV WGPLPQKKKSPPLCFFYFLNRVLLCHPG WIAVVQSWHSSAHFSL/VLTRFK*SSCL SLLSSWNYRCTLLHPPNFLNFWYRQGNA VLPKLVL
1770	15671	A	1781	122	254	RKNE\WSGAVAHACNPSTLPGPGGQIMR

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						SGDQDEPG*HEPPRPTDSFFLYPSH
1771	15672	A	1782	45	387	TQTPKLRRFFHFSLLKSWHYRCSPL\PQ HNGYFLTNLDIATSMFFFKDRVSL\LAQ AGEQWCDPSSLHPQTPGLRR\PPASASQ EGETTGAHHHTWRNLIYFFYYTYKF*GT YPMA
1772	15673	A	1783	1	401	FATLARLVSNS*PE/CDLPASASQSAGI TVSPAHLAISPSFPAMPSSGLGLSYPAY HPGLGLRCHLPVLTSPWTSDTGPSSVLP DAGALHCPPEPQHICPL\LSGWLQTP
1773	15674	A	1784	432	1	FLFLFFFIKKKTPFFGAKPKNRGF*KPP EFFQIF/S/CPVFLGRFPKPQKEFFFPE REMGFFFLFSPQGGGPARGFPPPPLNQG EAPRAGHKKKGPNLGGRTFFFFFFEMES \FSVTQAGVQWHDLGSLQPLPPPFKRFS CLTHAS
1774	15675	A	1785	15	434	RLSLSCCGREEHSTLPGAPWRCTEIAWA DSPDPAPSPPSALPSLLPFHVYRDVCPV LCLRGWP**MVERGRLGISPTWLLGWPF PGGA/PHIKPE*YFLFAYTILRSVPNKL GGVLALLLSILILAIIPILHISKQQSII F
1775	15676	A	1786	1	258	CWPETPVLK*SHLDLTKRGEDRREPVWA ASTTIFFFETGL/NSGAQAGVRWVHLGS LEPLPPIPSLFMTP*GPCPGLGSSWPLR EF
1776	15677	A	1787	399	63	SLHNQVVKSTPTLKTSKKISHI*STWPG VVAHACNSNTLGHHGGRTA*/RSGVQDQ PGHHSETSSQRLRNPYIKRCIKYLAHSK CCINDSFTVSVTSRKLIGKREVSPNNIT FR
1777	15678	A	1788	3	474	MSISPVRWNSKEAGRAANRQFPSFSPWK DDSRDASPPEPASPTIG\PIRRLAESSW TWGSPCAEHPRARAGRRKAATDCPWAAG SQWRGPAGQGAPRSCLFPGSRTAARAQH PRVAPPPPPAPLNTRASALRSQLPRNPL *VMTPRPPAAAPRSPVGP
1778	15679	A	1789	66	395	LVQPLFDFIWHSRLSLWSGRDLLWSGKE TMNPCLNHSIGVLQEWQGSDVKKRRRLM ESLTGPAADVIRILKSNNPAITTAECLK ALEQVFGSVDSSRDAQIKFLNTYQNP
1779	15680	A	1790	413	1	PSPRALITDYS*EEGPRFWQV\EKKGQP LKPHPGLGSPHQESPRVGPPKRGGYNPF *KKRAKFFAPGENKGPPFWTGRDPTF*G KTKKKTNPPKKGGKKGPPPKPGQFFFFF LRRSLAWSPRLECSAAISAHCKLRL
1780	15681	A	1791	314	1	KTKPFFLKKTPPKKKNKKKGSC*DKARY QTRKG/IVNLGH/HPSFLFYFILFFETE SHSVGKAGVRWLRANSLQTPSPGFQQFS RHSKPSRKDYRHPPKRPQECVQ
1781	15682	A	1792	104	409	EKQSFAFDWHFDLYFDNVK*KEGEESKA GEFNASTGWFGNFRKRL/RFKNVRVTGE PASVTQEAADEFPDNFKKITEKKGYLHG KFLMYHEAAKYLNFWCPTK
1782	15683	A	1793	392	2	GERERDRL*RERERERERERERERERAR ERERARQGTSTVESRF/HSYCRRDQDVA RPKAKGEVAAGRGSPDGLQVGRGQ*PGP SLRPGPWREWGFATYLACGGPIPTGEVE

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						SGEEWAQQGEWGQALGPP
1783	15684	A	1794	405	119	IIKMAIVPKAIYRINTISIKVPMAFFTK \LKTIIKFI*N*KRARIAKAILSKKNKA GSIPLPDFKLYYKAIVSKPTWCWYKNRP IVLVHSRTARKK
1784	15685	A	1795	455	3	CSVTQAGEQWCNHSSLQPQPPGLKWS/C PSQLPK\WNYRHVPPRPALTAHPALTAD F*RRKEYKLMRHRGKKWHDFTLRSKKMK AMRHEYHSFLTYPNGHLYLHWQFFFFDT ESHSVSQAGVQWHDLGSLQPPPPGFKRF ERVGPGGNSGAD
1785	15686	A	1796	2	134	PRLQHCTPAWATPQDSVSKRKRDMTTDP AI*KG**ATTTNIYIHKFYNLDEIDQFL KKHKLPQLTWYEI/DNLNSPITR\IEFV ILNSKKKYPGSDGFTGEF*D*FCLETKK RYDYRPCNLKRIISDYNKHLHT
1786	15687	A	1797	1	404	PTRPLTGSSASGMMVEIFPKTYLISSAC WVKISKIDLKLFSPFFFFGFLEGGFYFC PPNSRGGSPGGKFGLIEPLPPGLKGIPP PPPKRGGEFGPPPPTPAYFFFFLWGGGV /PP/AVGGGGKPPI*GNPPPWPPQG
1787	15688	A	1798	2	383	SGWLWACRSPDSEPLACPAGPRQ*GAYH PGQQLWMVR*VSQQCWPTPPALHSIS\P RP*LPPRRAGLGTCSPP/VPESPLLPPW APAWPKPPRRALPPA/PPVPGPIDRPRA EECRRMVRDWQAAPPAAP
1788	15689	A	1799	35	410	ATGPSLGKVCS*AFSFL*PKLDFWHLYF QASGFLL/CHNSPSQTNSCSSFGKHYGM VLRVNSL*PDHPWNEFYFLNFFIFYRDS /SLTILPRLVSNS*AQTILLPLP/PKVL GLE
1789	15690	A	1800	65	415	KKGVLKGGPPPQPLGV*GPPPEKGGPGP F\GAPKEKPPLALGEPKGKPF*RGPKGF FFKKGLEPGAPPPPKPRGEKPPVFKGPH PFCKKGGGDKREKNGGL*RKKPTELGNG PPPPG
1790	15691	A	1801	417	3	NLGPNIFPPRAPQNWGPAPPLFFFLKKN FTWGGGSTPLFP/LNLGGLGGPFPGLEV YAPPSPHG*PRFFFKNQKLPPPVWGALY SPFFGGWEN\RKAPPGQTLFFFFFFLK* GQDLPMLLQLVPNYWAQVILPPWPPKV
1791	15692	A	1802	1	431	QPCTPGLK*SSCLSLPSIGDYRC/RTTV PS*FFFFFLEKGVGFIPRGGIKGLDNC* LGPHPPELK\NPPPQNSQEVGTTGPPPR PG*LFFFFETFFFF*KGGFFILAQP*MK WGALKKTPPAFSKRGGYRGGTPMEPTHC FLKEN
1792	15693	A	1803	256	399	AIKNIHDS*EEVKISTLAGIWKKLITTL IDDFDGFKTSVEEVTVDVME
1793	15694	A	1804	407	2	FEKANLFPFLFKNSGPPNVPGRGMAGVP KFCCPSKRKVPGPIFFLRRLFLFYPKCR RPPLFWPAFGP*KFFLPQVFAPAF*KPS PKKKRAPVFFFFFFF/RDKVWLCHPPWS AMA*SQLTVTSVSWAQAILLPQR
1794	15695	A	1805	429	116	LLTKKKRKKKPLACGESGLGGP*GTVTG V*QAEDTHVIW\VLSSAPSLSSEEMTDS MPGHLPSKDSRYGMEMLTDKKWTWDGGA WDSSPQGANGKRGARQASGFS

SEQ ID NO: of *nucleotide* sequence	SEQ ID NO: of *peptide* sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning *nucleotide* location corresponding to first amino acid residue of peptide sequence	Predicted end *nucleotide* location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
1795	15696	A	1806	2	408	FVIFVFLVETGF\SILARALACAISNS* PRDLPTLASQGAGITGVSHRTWPRRSCV F*EAFLTMLMVLHIPPSLLWHSVFTHLL ALSS*CFLFFLRGPWAVTQAEGQGHDLG SLQPPLPGLKWFSCLSLPSS*NYR
1796	15697	A	1807	1	196	FRLGASLDLSGGCSGVSWTPAPPLPPPP PPSAASGIS/SGSTSAAAGL*SCRTAFF SFLSSFFFFFLKKINPFPFLGGI*PFKG GPRLV*GNI*PPPQG\DFLGGTRGGKKP WGGGKFGQGGNFPLPLKKPPGPQKNPPP \PPPPPPSAASGISMAAHLQLPACDRAA QLSFLSSHLFFFFF
1797	15698	A	1808	395	3	LGKKMNNPKFWQGCEATGTL/M/HCWWV CKFVQSFWNTDSIY*G*AAATHDSAMLL LGMHSMPACTFVHQKT*TKMFIAALFIL PLNWKQV/RCPSVI\DGYIPTMDQSTAM KMNKLHAKTWMNLRNLMLNEKPR
1798	15699	A	1809	7	454	IPGSTISLQPPPPGFG*FFCLSLLSSWD RQPAPPR/LANLRR*T*LQSA*LWR\RG PILDEMKSFMCNCNSLTEGVKGRVEMMS QNGRLLTKFCHVGQACLKTPDLK*SARL GLLKCWDYSCEPPCLTQMPFSFFLFF*D RVS/PLSPGWS
1799	15700	A	1810	20	355	PQCAHGCRAVAPVCVCFCFCVCVCSHCV SMCMCGEVSAGWTLLCLCLST\CSGAYA CDWGCG/CYSACVCARVCACVCAQLLTC IGMWE*GQAGQGEVLLDLPLCLCSCWAP Q
1800	15701	A	1811	3	414	SSKNDNNSLQEFMDKIAGMKKNLGNLTE LNNTV*EFHRAITSINNRINHAEERISD LENWLSEI\NRQT*KIVTRNEQKLREVW DYVKRLNL*IIG\VFEREGGKAYYLQNI FEDIVHENFPRFARDANSQIQEMQRT
1801	15702	A	1812	1	443	AGKSPSPKKFKKGPGGGRWS*FLGGAGG GVPFRPGIQGSNYRFF/SPPPPPLGEKK KPPFKKKKKTPQKLQNGNPHPYFNPRVH GCREQQPWEKAPDATRQPHYADKHVEAG EPREPPKPHSEPLFSSPRKRPLFTRSST /SGASPP
1802	15703	A	1813	411	66	WKNNVFNKECLER*IF/IIQKKKLDP\F LTRYIKIKSK*IKDLNIRLEIKKTPGKE SVTLAKWLIRSPYLSFP*QIQSKQ*INS YVLIKITKEERWSTSKEYQKPWRERKAM YKIK
1803	15704	A	1814	369	20	QEVRPSIYLSSSNRKYVKDSNARFTKEA IQIANIHMKNCPTSLIVGETHIKTSKGY HYVPIRMAKILKD\CNRRCGETGTLIHF *WEWKMVQPFQKPF*WFPKKRKIH*QFD LATRS
1804	15705	A	1815	2	675	GLAILGRRLRGEACTRSPFSSILIFMVS MGEWPGVP/GIKGTRTGAEAVPTRRRKS SIWPQTGGAGESSG/PLRGLPRQGKPGS PRGPSGPPQNCARWWHPQAAPLGACCFS GPEPSRLPPWRQGNWCLPSTPSSSA*EG WR/PVLQPGFL*SPSSLASICPGAERGP PGSSRP/GLRGAPGG
1805	15706	A	1816	273	2	MESHIMWPFTIGFFHLVQCLHGPSMLQC IAVLHSSYLFIYLFIY*DRVLLCHPGWS

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						AVVQS*LTGASGSW\LRRSFHLSLP*C*DFRHEPR
1806	15707	A	1817	40	404	GLHE\PGVQGCSEL*SHDCTPAWVTSETLTLKKLKIKKSKKKKRANPRGFERPTFGEAGPGGLLKAIISKPRVIQGTQKSGALLGFNSNGGENHPPQKQPYLCGLYAKAHSPRGGGPPSPCG
1807	15708	A	1818	392	3	EKYNMSYDIKSTNHRKNCKLDFIKI/RNCCSLKDTINKMKMQASNLEKIFAIHMPDRGLIFKRKNSCNLVRR*QPPFFKEAKDLNTQKSQ*TNG/HGSKETSLIIREMQIKTT/MNYTTSIPT*MLKIKKMNI
1808	15709	A	1819	311	431	EVVGRAWWLTPVTPSLWEAEAGESRDQE*KLCTTVEK*KTISN/HDVPIRSSWTGMVAHACNPFTLGGRGG*ITRSGVGDQPD*HGEGL
1809	15710	A	1820	68	410	AKKNQGPGPMVFGFGGIKPPPKQKKVRGGFFAICPKEQVFFFFFFWRAVVQSLNHCSLQPQPPGLKQFKQSSHLSLLSS*GYKHVLPCPANFILFSLVETGS\SIYFPGWSQTP
1810	15711	A	1821	408	1	TPFFFLRVLRLTPPLLGNFFGPGFPPWGGFSPGPLLKGPRP/CFPIFKPIFQPGKWGLVFFFFPPFFFYPRGSR*NLKKIFPNFPFFFPVFF*ILNPPFFFFFFFFFFL*DRVSLCRPGWSAVARYRLTASSTSQ
1811	15712	A	1822	362	76	SEIAPLHFNVGDRVSLHLETNKQSNKQTKKTLIFRDRVLLCRPGKNA/VEVQ**LPAASN/FLRLKQSSCISLSSNWIYRHAPPHLATVFNFLIIFE
1812	15713	A	1823	314	2	VISKPCPRELTCITYGVSLTQCSMFGRMKGLLLIWPPVCEVRRASGRPPLMGSEEPLCPAATPSGRCTQQ/LH*ERAMMTMAVLSNRKGGNVGKR*RNQIVAVS
1813	15714	A	1824	57	389	NLHLLQLPTYTDADSTGPTLSGMNVKNLHWSYEYKYRSITGVQWLILGSLQPLPPRFKCSCLSFLRRWDYRCAPPRRATF*FLVETAFLERLTSCDLPTSASQSADITGV
1814	15715	A	1825	410	70	VPIMSATQDYRHEPPRPAGRFLKKLKMEPPHNPALLLVGI*PKNMKSLHKDVCTPMFSGTLFAIAKIQKKPNCPSSMDEWINCRNY\MHIYDGICYSALKKNEILARRSGTRL
1815	15716	A	1826	2	411	FLVEMGF\SMLVIAGLKLPTSGGAPASASESAGITDVSHRAWPVFFFLKRCLVLVGRS**A\WPHTNLIPPLPSGIKGDLCPNSAGGWEKGAPPPSPGKF/CEF*GRTGTTNFARG/WTKTPD
1816	15717	A	1827	276	3	GRPGPADFRVRPQLLQRFLFIYLFTEMESCSVTQAGVQWCNLGSLQPLPPGLQ*FSCV\K*FSCLGLLSSWDYRHMPPHLDNKSIFSRNGVS
1817	15718	A	1828	1	391	LEPRRRFLQCVQDCATALQPGQQSKTLSQKKKKKKGGPP/S*YQKGQGCPSGKKGRGVAGKGAFGPGFGGENKTPPGGGPTGEGPFPQKGVVGPSQGPTKGPNLWGPGGPKLGGKGGPPGPTKGGGGPSSF
1818	15719	A	1829	2	134	DHLSPVVWNQPGQHSEAPSL/LINIWKL

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						AGCGGAHLSSHL/LREDHLNLEVQGCSE P*LHACTPAWATE*DPVSQTKLN*NIWK LAGCGGAHLSSHLLGRIT
1819	15720	A	1830	427	107	VQHQPGQQRESPSIIIIQKLARGGARCL *SQLPGKLRLENRFN/SGSERSHQCTPA WVTDRDCLKRTGITRASSQRLSVGIKQS CLNPRTAQLQVSAQSPSTVSTNL
1820	15721	A	1831	3	540	VQFPNFKIYYKATAIKTVL\QHKQR*ID E/MNKI*TPEINSYVYGYLNFNKDAKAI QWGNDSF\FKKWC*DNWISACKYSQTSV SASSASSSSS
1821	15722	A	1832	385	2	AGRQSETPYHNSTIMKVSLQVCVDLSCL LGPGSLVQDSPNIPAQRKRFLRLGSFWL PLSRFSRVGWPLPHWGQRSSGFSLPR\P P*SQIPAPRSPPPAGPVPARSWVCGPRP QTRPLPAERPSPRPRRL
1822	15723	A	1833	7	399	RISRSYLSEYGGSGKEHPTLGASYARIM VFG/VFIIYF*RQCLA*AQWYSHSSLLP QTPGLKHPP\AQAS*GAGTIGTHHHT*L TFAF/IFVLGCFFL*NKISVTQAGGQGC NFGSLQPPPPGLKRVSCLTLPR
1823	15724	A	1834	2	306	LARLVSDS*PQ/CDPPASASQSAGIICV SHRAQPAEEILKVFGTLCLEPQRPTPDI FIIPYLFC\LFEMESCSVAQAGVQWRIL GSLQPLAPGVKRVSCLSPP
1824	15725	A	1835	12	400	KKGMVPKQLKVGKKPPFSCWGPNMKKRD SPVFHHQDPIFPIPFFFFGNGFLFFPP/ LAGGQGGNLN*PNPLPWGLKEFPPPTPR GRGEKGGAPPPPINFVFLKKGGFPLGGR GGLEPPPLGDPPPLPPKRG
1825	15726	A	1836	220	401	KGSFVFIPQPEGEGPFLG*LKPRFPGLK QFSCLTLLRSGNYGPLPPPPVIF/CGFL R
1826	15727	A	1837	12	357	GLLGGQMNGSLGTQTSYEDLMSSS\FKP NSPPPTPS/VRTGHLPK*PLESSNGPPP PQVSHSFQGQWARGHPSPPPQWNTPFSP PQQYTQCSKTDP*PPPSPPYLGQEGSNA PSLA
1827	15728	A	1838	8	380	LMKTHAKLLNKRVAN*IQQYKK/HH/NQ MGFILGVQIYFNF*KINLIQLINSVKKK KN/HSSSSSSSSSSSSSSPPVLIKSLC NLGKNKRNFLCLTKGIYKNKTE\NSMKI ILNGEQLNAFPLRLGTK
1828	15729	A	1839	2	444	VPGDAKWFSVLHLKDAFFFIPLVPESQY PFAFEWENPNTREK\TWAVLP*GFWDSP HFFAQPLERDLRGLQLEDGSILQYVDHL LVYSPTQEASDQNTIKTLHFPADRSYKV SKKKAQITLQQVHCLGYILTPGTCK/LS PERVQAI
1829	15730	A	1840	1	642	EIKGIQIGKEEVT/SLFADDIDYLRIDS TKKLLEVICELNKVG*KINM*T*IVFLY IGNEHLELEI/R/ELMPCIKTSSTMKYL EINLKKDV*DLYTENYKVFPREIKIT*A NQ*EILCLCSRRLNTKM/STFPQVFCVY YAIPVK/IPSRNFLVLVDKLILKFI*KY RGPRTAKTTLKKKKKVVRLTLLIFKSYY KTIVITIGWYGFQDRQVD*WNRIE
1830	15731	A	1841	3	423	HRITSE*DLHLARELIW\SMYGSLDHKN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						YDAELDRMAMPCLCAIAGALPPGYVDAS SSSKAEKKATVDAEGNFDPRPVETLSVI IPEKLDSFINKFAEYTHEKWAFVKIQNN WSYGENIDEELKTRPMKR\PY\KTYSEK D
1831	15732	A	1842	33	179	YMLGGRGCSDLRSHHCTPAWVT/TA*LS KKQYQRQQNRLQYHLQEYERKK
1832	15733	A	1843	349	10	LAGGLNSMEGER\LR*EREECTQQQMVH DKYCKDLMGFGTKPRHITPFSSFQAVQP QQSNALVGLLGYSSHQGLMGFGASPSPA KSTLVESRCCRDLMEEKFDQRK\QWVLK CR
1833	15734	A	1844	15	856	AAEQLSFIYKLPQNPSPSTPGSSLSGTH GMQTMLGSTHLPNLTDMLGPELGVQGIP SPGCACQRGRG\GGGRECCSPPGVSPQG \SAVGRGAEGPGGLTRSGSGAASALVRP GEKGCWCRTASGAGPQRRQRTRGPGSWG LSFSQTSEEKCPSPAGSAGAGPVCQRRQ SSFAGGCGTGAGAPGST\GDAHPAQGGS GGPLRSLPAVGGPRPGPSFLKTSGSGSV PQGVPILWSLT*RALAAPGSQGPAGLAV SCTGGRGYRDPQAPGTGAG*HGNSTRLR GP
1834	15735	A	1845	402	2	SKARRQGRPLRQG*APG/AARIPEQKRI GGP/EERRRPSARGPRATRVAGEGPKPK GQTAMAGGGHDPLPLPPARSRSQESIGA RSRGSGHSQEQPAPQPSGGDPSPPQERN LPEGTERPPKLCSTLPGQGPPPNV
1835	15736	A	1846	446	32	TSRKIS*KTGNQFLMKECSCNSHHKAAF TKKDVLNI\LAVVKHVNTKASETFHFFQ SGQAKVQQGFVKEGCELINEALNLFNNV YGAMHVKTCTCMRLLDRLQYIMGDYAEA LSNQQKAVLM\TERVMGTEHPCIRPL
1836	15737	A	1847	440	4	VDGRHVEVSKKGGQVNYQAG\KTVEIWA DKLGCNMLGTADMVECLKSTRYKELIQQ AITAGGAPIAFGPVIDGNVIPGDRQILM EQGEFLNYDIMLGVNQGEGLKFVDGIVH NEDGVTPND*KFSVSNFVDCMRPRRGPN YSRFQ
1837	15738	A	1848	526	0	PRRDPPPKRQTPIPTHVSPVWEKGPWGP APLRPDHPSLSPCPAMG*K\PGLPRGCP QTQISPLFNRSPASPLICHHHPPSEP\K PGPEPPPTPSSSIPSLARFTRPGESSPL PPPQTPSGPP
1838	15739	A	1849	417	31	QATGQECGCHRGGPPPGPAGETEPQAPL RLPGGTGIPWGAGILCPS*LPGPGSLSP AAGRG/SGPSAGPGAAWFSSP*/PACPS SSRSAVPGGAGSFRRAGPGLFYTLPAPP WCGRGASNKIIQMPGLVC
1839	15740	A	1851	3	285	YTVCECVCVCLCVCLPVSL\SLCLSVSV CFFPSLCGFVCVCPCACVSLAECALCAT KRFV/CMAACLW*ASFCVSTWVMRPAVN RFRRGGSALGA
1840	15741	A	1852	128	524	KIPGLGQRSEGVGQGKDDLHVTAPVPTH GWGEGAASKPTVLPPPPP\PDAPTVFFF FFFFWEKKYFFGPPPKGAGPQIYLLGPN PPGFKPFFPPHPQAAGI*YIKPPPWYKC PLLKKRGVSTLAP\GFPKPPP

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1841	15742	A	1853	1	1648	MTVPLHSGLGKGVKPERKTTVRRPFVSA GKKYACPFKKAETPQWRRLRMRPKAPAA SLLATFPISQRLIPLTPARKHCPSESET STWVVSKAPATPRTRGAGPTSPPRPTRR R*ACSLQKLFAVEEEFEDEDFLSAVED AENRFTGSLPVNAGRLRPVSSRPQETVQ AQSSR/PAAVTPHCSLRGFGPARLGP/P ASLPPARPVLTA/GPSCIGAAPLRPVST SSSWIGNQRRVTVTEVLREPARPQSSAL HPLLTFESQQQQVGGFEGPEQDEFDKVL ASMELEEPGMELECGVSSEAIPILPAQQ REGSVLAKKARVVDLSGSCQKGPVPAIH KAGIMSAQDESLDPVIQCRTP\DPP*DL VLWVTFLFQ/PALTVPTQQLHWEVCPQR SPVQALQPLQAARGTIQSSPQNRFPCQP FQSPSSWLSGKAHLPRPRTPNSSCSTPS RTSSGLFPRIPLQPQAPVSSIGSPVGTP KGPQGALQTPIVTNHLVQLVTAASRTPQ QPTHPSTRAKTRRFPGPAGILPHQQSGR SLEDIMVSAPQTPTHGALAKFQTE
1842	15743	A	1854	235	223	IHKFIHQIWLAKITCQRTKV*KERSVLL PTSFSPVPSQGHYTCKQ\LCSLASDLSQ PDLVYKFMNLAVLHAMWNSRKVSCYPWT MIYFLHANRT
1843	15744	A	1855	373	3	IKDGIYRYFYKALDSFCLCCEFMNQFFS CMDRELSQRCFLNSAY*FPSNL*CYLCY LFFFF*LKKYFLTFFLFLRDRVLLCCPE *SAMVHS*LTVPLDFW\VKGSSCHSLLS SWDYRHALPHLY
1844	15745	A	1856	378	1	RQRHSPAGNTGRPQVTPCG*ISWPSITK DRTSMSSVTSGALGHTAASPHARLLPLA LPSVRTQHGSPPPGQEQPTIICPSNLPT HPSLPLGMHPSVRASPPLCK/P/SPPSI PASVHASKHPSPPVY
1845	15746	A	1857	3	379	YMVRKVIEVWFLLLLLLFFFFRGGFLGQ GWGPPAPGFSFGKKNPQGLGSSNLRGPW *TNP*PVPGGALFLVGPPTPAEFPFKNF SRGFLLV/ALADF*TRPRLVSPHGG/RG AKGTPAFLESMPPWMP
1846	15747	A	1858	452	1	GTHGLLLGSGPF\RQVFKPDNFVFGQSG AGNNWAKGHYIEGAKLVDSVVDVVQEE* ESCDCLQGLQLTHSMGSGMGTLFISKIR EECPDCIMNTLSVVPPPKVSDTVVEPYN ITLSIHQSVENTDETYCIDNEALYDICS RTLKLTTRCI
1847	15748	A	1859	1	385	NTSSDYIFPFFFLFRNSIHSVTQAGGQW HNQGSLQPWPSRLK\CPTASASICLHMP PFLANFLIFFVEIGSPYVAQAGSRDPPA LASQ/SAGITGMGHCTQP*VFLFFFFFF SFRKKCSPWPPGGGPPIF
1848	15749	A	1860	470	17	IEMDSRRVPRDKLACITKCSKHIFDAIK IT*NELASAD/DFFPTLIYIVLKG/NPP CLQYNIQYITRFCNPSRLMTGEDGYYFT NLRLGTHCSWLMMTMWTCFRAFRIFSSQ WMSYVLRFRNGITGVSHRAHP
1849	15750	A	1861	3	790	CSRPEFPGRRFVEAVRSKPYLSLPF*SR *SFFNVPAE*TSAKDILASSEFIKQNND VSS\LQKFMPQEVK*LDHIHTA*ADGSW

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						KAELERGPDGSAPSPFPQKPAASRQPEL GELATFLGRVDPWYQSNVNTLCPAIHKL AEMPPSLDTSRTVDPFILDVITYYIRMG TQPIYFQIYTVKIFFSDLSQDPTEDIFL IELKVKIQDSKFPKDGFSPRRRGVAEGP GAELSLCYQKALLSHRPREVTVSLRATG LILKAIPASMY
1850	15751	A	1862	192	3	SSGSHSVTQA\GVQWHEHSSLLP/LLT* PPGRK*ASHLTLASS*DYRRAPPHPANF *IFCREGV
1851	15752	A	1863	82	370	SLCQKRAFVGEKLVHGLLVSPSGGRVPS CPDPWGCRPRFHAIAVYSFLKLRVVIPE VSILPEDLEELYDLFKVRSSGKMRGSRP *AGLSRG/DPACP
1852	15753	A	1864	2	325	IQVYSISHLSIYLF\IYHLSRGSMHVSM SLSI*SIYPCMDV*MYLSNLCMHVYIYL FYGSIYRFYLSICLSVYLSIYLSIYLSI YLICHPSIFKTVIDEHAIFATWRH
1853	15754	A	1865	3	377	YSPWCKLFRELCKINVFD\LDSPLLSGK EFNDTTHNTFDHMWRTKEHNEAGWLLLS SVDKVMKENDELRDSNSWLQKQV*PLK SAKTALSGSLNSCREKAEIVEKQTQSLT M*VADLQRKMHVQP
1854	15755	A	1866	10	378	GWKNGEFIDAL*KVYGHKAPNKSAVYKW IT/*FKKGQDDIEDEDHSGRASTLRKKI HLVYALIDKD/*RLTAEAIANTIDISIS LAYRILTEKLKLSKLSTQWVPKQLCPDQ LQRRAELPMEILK
1855	15756	A	1867	346	1	DILVVKLQKPQPNGKMLKAAKERKKFAF KGVPVRMNADFSIAAMKA/RRRWNSIFS F*KENNCHLRLLYSAKNIFP/EIKTFSD REFVTIRSAVKEILKDVLWAEERLSHVK SRNV
1856	15757	A	1868	1	377	GTFFQRTQCKGIKQ\YVVGLIIKASSDP TCVEKEKVYIGKLNMILAQMLKQEWTEH WPAFISDIVGASRTSKSLCQNNMVILKL VSEEVFDFSSGQITQVKSKHVKDSMCNE FSQI*Q\LCQF
1857	15758	A	1869	90	384	QWLLFTEYSSLYHPVLFFFFFFPGGRTG PNPPAGGEGNETG/PNGPSTPGGGGNPP PLPPGGLGLLSMPPPPRQILLMETKKRP PP*TNKCCSPGYSPP
1858	15759	A	1870	2	578	FVVKHALLLGLDFLPGKMAPWSGQGCSL GHTEGGTSWDFAVGGASWRLKVVCVKGD SHKGPATPIASCKGPLGRPCPLLAQSKA *GS*KRG/VAPGSP*LALGMGGG\DRLT LISQVHGNQVTQIIPFSTEGETKAQRSP SLPPRDLIRGRHSWNLDSTQLLGYCPLL PPPLHPAGPLPVPFTNGEIQKENSRE
1859	15760	A	1871	1	382	SGQDAGSCLLYGAGSGAMVSGAYNPYIE IIEQPRQRGMRFIYKCEGRSAGSIPWEH STDNNRTYPSIQIMNYYGKGKV\RITLV TKNDPYKPYPHDLVGKDCRDGYYEA*FG QERRPLFFPNLGIRCA
1860	15761	A	1872	490	1	ADSLSKDPGRPLHPPNIWGDRGRQ*PGE TPQ*HRRSCASQDPGRSQ*PGKILPSPK PGRPPPMTGEDAGPPK\HGNPSPNDQKK NPPPK*/PQGNRIHRDPGRFPPQ*PRKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						SFPNNLGDSNDQRSRFPVA*KNLPQSSS GTRAIGRELYLPPQPGSSAFPNSTT
1861	15762	A	1873	373	1	GGGVPGALFSHKKKSLFFFPPPPFFFRK GL*NF\KIKGCGSPFLPLLFFLEKESCF VP\RVECGGVILGPCKVCLPGSPPFSAS AS*VSGATGAC/RPRPGKFFSPFFFFYF LVEMRFHRVSQDV
1862	15763	A	1874	3	374	YMLGKEIVSKTKIGQELGLLNQ/TSQVV NAKEKFL*ETKSATPMNT*IKRKQNSPI TETEKALLVWIEDQTSHNILLTQNVI*N MALTLFNSIKAERGEEDTEEKLEGSRYW FMRFKKKKAISIT
1863	15764	A	1875	2	364	IHSGKGESLWDLGLDTEFLDLPSKA*HI KAKNDKLDLIKM*NFCSAK/ET*/IRMK TQAIHWERIFVNNI*NRKLVYKELLKLR N\KKNTIRR*AIDMDRHFTK/EKMPMTN *YTKGCSISLVIL
1864	15765	A	1876	41	461	GFLYLCSSEIDPYPSPSKKIKSEWIRTY WMKLLSENATIMLKDSDLSQV\FCVNIP FVQAAKAKIEE*DYIKLKWFCSAKGAI* KAKRQPTE/W/DRIFANYPCVYGLITTT CMEFTQLTSLITTPTITLPWNPRQSYHH NPT
1865	15766	A	1877	2	185	VRPTKLDPLERTQYTLPLLYKWNNKAWM TAHL/FTA*FTEYFKS\SVKPDE*VREI DYRMLYL
1866	15767	A	1878	1	491	IHRLLWPPLSAARPPSRESGLRCRAPRR PASAAAATAASPS\PTAPQGPPR/RRRL LIQPPLYPRGLFTPGVPPL/APGGSREP S*SLT*DARTLPLPVLGPRRARLLGACP AVQAEEGVDPVGHLSEVLAAPCKQP*TP PPACHCLDGEGRPSGVQAPLHKAKLYP
1867	15768	A	1879	24	449	LQPPLTWALLLQPPQPKSRAAFFFFFFF FGKKSQFLFGPPGGGEGEKLG*REPPPP GTKGMPPPPPRERGKKRGGPTGRENLGI *RKGGVPPGGRGGGQTPNPGGGGAK\PP KGGK*GGGRLPPPQIKGPKRGRPKKRKG RP
1868	15769	A	1880	190	2	PLYCHKVGQVGLELLTSGDPPPLSLPKC WDYRY\DHHAQPSF*LFLSVQISGIKFN HSVVQPCI
1869	15770	A	1881	1	458	FAIRAGRNLPDKEFRYLRTVIVTAAVYW GLNSKLRCLTS\LLTFQHRAGVSPYTSP FGFA*TCVFAKQLLEPILC/RPCFHRAP LLPKLRGHFAE/FP*QCFFR/QALGFSP /RSTCVGLRHG
1870	15771	A	1882	3	392	YMMRYHYILIRMAKVKI\SSTNDDTQ*L KLIHC*QECRMVQPLWKMV*QFLIKLNI *LP*NLAILLWGIYLIEMSTYEFR/RKI CIQMFMTDLIVIAKYWTQ/PQCPSVAGW IKQ/IRSIHTVEYYSAVKRNQL
1871	15772	A	1883	2	473	IQGGIAAYRVDRQERSNGRQGNRRNLSG TNMRRNKQKGLRRCKPRW/RSRGMAWKV DKPRDAR*KSDRDRQ/RGETDG*RVSGG LTA*EAYRH\HRGQ\EAASQSGRSRQAG RQTP*QEQAGNEAEIRREEEKSRGQERE RE\KDRDADRHKG
1872	15773	A	1884	138	444	CYLTLIKCRIIYINDKVIVLTIVWY*HK

SEQ ID NO: of *nucleotide* sequence	SEQ ID NO: of *peptide* sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning *nucleotide* location corresponding to first amino acid residue of peptide sequence	Predicted end *nucleotide* location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						DRHID*WNRLQSP*LNPSIWVQLILLNN AKNTQWVKDTLLDKWYW/ENWIYQCMRM PLGSYTIPMNQFKMNYGLS
1873	15774	A	1885	27	470	TICCYIFLFFSFFSLFFFFFGKGVSF*S PGGENTG/ANLG*WNPPPPGKGISPA*P PKEPGMEGAGHPPGTKS*PGKFGPGPGG GPSFPYRGPNKTWGKPGPKWFPGGIGYP ATIPQKKQPEGKRGR\PGGPMSPYNGPP KTPTHGKGPG
1874	15775	A	1886	478	1	KNVQENSALQAAMCRKMLIVCQTQCVII SGESGAGKSVAAKYIMGYISKVSGGGEK VQVRRGKQKDKLGRPHLHGSAAPPICTP ASV*LLPTPPASAP\HVKDIILQSNPLL EAFGNAKTVRNNNSSRFVSLCRPAWSSC SLRADLSTHTPTHTHTRV
1875	15776	A	1887	1	402	HSLERPHYIG*LFKNIFSRD/RVFAMLA HWSRTPGLKQSTPLSLPKCWDYRCEPQH PAGSFFFFFFLKNGFWGCSLGGRAGGQQ *LKS*WRPNPLG*GNPPC*PSKEVGTTG AHKKIANREIRTRACGGTNFSL
1876	15777	A	1888	511	124	GTRRQHFAGAHVPPEGP*S\MLDPKLK\ DDRPARDMWIREPGLLLPRAPAQDAGKY YCHRGNLTMSFHLKITARPVLWHCLLRT GGWKVSAVTLAYLIFCLCSLVGILHLQR GESCPQWVCPNPTPSSPG
1877	15778	A	1889	667	310	QLKP*ATKSV*KDTAFGIDVGNDFLAMT PKAQAMKGKIDKWGFIYR*SICTAKETI NRVKR*PRK*EKIFAKPTWQKGQIS/RI HKEFQQLN/KQKSNNLIERQTKDLNRFL SKECSKDL
1878	15779	A	1890	462	3	KWFFPLGPPFLPPP/PPPI*NPSFQKNK KLTRGGCARYFPPLKSPRPRIPFPFFEK GEGSPNSKHSPAPPFWGPKETFFFRRTP PPPPPPPLCSFLKNNLFSYIPKGFLGGK GQNFHSFLPSFFFSIKKKLLGLGVHVRF YCRVNSCTGFFVQMY
1879	15780	A	1891	1	455	NTCLGFGNGFLDATPKA*SMKKIINKLD FNETENFCSVKDTVKGMKRQATHWEK/V RKTHILYKDLILKIYNQLLKHHNKKTST IKQ*AKDLNREDIQMTNKHMKRCSGWGR WFTPIIRALWACKVEGSLELESSLGNIV RPHRKREREIHCY
1880	15781	A	1892	1	537	RGGIQAPKEVSPEGRQEPARKSLI*TA* ETPP*SQ*/PIPEEP/TGVFMKKPVSVS LETGKHAVVVPKVNGKELPDNPTIKWFK GKWLELGSKSGARFSFKESHNSASNVYP VELHIGKVVLGDRGYYRLEVKAKDTCDS CGFNIDVEAPRQDAYGQSLESFQRTSKR SLYALALEDPGM
1881	15782	A	1893	2	514	VRCQRRCHE*RACGSSLVNAKKLYEDAL MARKVKQSLFSLDVETDEDKFQMMSLQ\ CSLAYGTLTKILSEKRSAKSYGMSSVRM RSAGQTSKAHLHQPRRVSQVLQVPAVNL LPFRKKGQTKDPALNTSLPQKVLGTTEE ISGKKHTEDTISVASSLHYSPPASPQGS
1882	15783	A	1894	473	2	VMGESRGFSPPPTFTGGNFVFFWKQGVS LFCPEGFKTLCSSSPPPPPPQKAGVLGG SFHARPPPFFFFQI*IPFFFGIKKP\LC

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						SPPP*PL*KKRGIFPVPKGIFCEMESCS VAQAGVQ*YDHGSLQPWPPGF**SSYLN LV*LSS*DYKCVPPHPMY
1883	15784	A	1895	613	11	FRPRSPACGLHAVSSPKLPGAQALSSPG LNLVFTAGSWDAG/LLRLSPRANNPRVA LPRVHTGPSST/DLSPSCPLGLACGFGT SQPACL*SPFLLLAPARPSGCAWPGLPP VCSLHLRGGWGGADPTGCLDAWAMALAS LRPCLCPALPLSREPPSPLLNDLVLPRM PRRAPVLPLGRTPHSLLLCHVQSPSEQL PSKGPERL
1884	15785	A	1896	20	449	KFGYSSAAARRQQLGWEAWL*YSFPLQL EPSAQTWGPGTLRLPNRALLVNVKFEGS EVSPCVACGIQAALSMGSTSSVKLLSHP QAPLPQWHQMVFARCLCMCGAQLNVPP\ ESFTFQVSTKDVPLALMACALRK/KATV FRQPL
1885	15786	A	1897	393	3	RPTAQSKGNI*VRVAS\EALSPKLLDFL PGKVLNGEKVDVRPATRQNLSQFEAQAR KRECVRVPRGGIPPRAHSRDSSDSADGR ATPSENLVPSSARVDKPPSVLPYFNRPP SALPVMGLPPPPIPPPPCI
1886	15787	A	1898	395	217	RER/CKSFR/PPA/HLQAKIKGAQ*QVN QAAAAQAAAPAAAMVSRDISSLLVSSQK SKVSNYM
1887	15788	A	1899	1	375	NTVLVQ*NNKAWMTVHPF/TAWFSEYFK ATVEIYCS/EKIPFKILLVFARVHSHPR TLIEI*KEIYAVFIPANTPSILQPMDHG IILSSKPYYLRKASRAQRLTPVIPALWE AEAAGSPEVGSSGLA
1888	15789	A	1900	47	326	VKSIIQFNSKNEPGKHDKTPSPEKTQIV WWLGSELRSPSYSGAAGGAEMGRSLESW RSRPQRAETAPLHSSPGSGSEMLSL*RQ HLTPTAWAGVQWRGLCSLRPRPPGFK*/ FCPSQHHPQPPSSWDYATRCQATKQFVF FLEMGF\VMFARLILTVELNN
1889	15790	A	1901	181	837	AGRVDRREPGMGTGICKELETGSRETRS ASRWGRGRWRLGQACRVPQGLPLSTFHL GAQAKARGGTPLACSSHLPNSHVGSLKA QRDEAMVQSGLAPAVSSTCTRWT*GSEW **GLHIVAARRQQGREEEPPRTTAAPET LCFQQTSWASSCSLEHSAQPSEVQVRAL SVPSHSPMWV\PQLSLPRDHRKPPGE
1890	15791	A	1902	1	385	YTWGFRGKKPLIHCL*EYKLVQPLWRAA WRFSK*LRVEL*FNAAISPLGVYPEENK LFYQNSTCTCWFITALFITGKT/WNQP
1891	15792	A	1903	207	3	FREMEFLHLGQAGLELSTSGDPPTLASQ NVG/HYRREPLRPANTLQS*PLGLKQPS CLSLPSSWEYRHMY
1892	15793	A	1904	2	391	IQPLISQRKYKTLGQNSLS/CCAHP/PP HFFFVLDSYFHSLLSQLKNAPFT*G*CP YWYSKSYSLIHSWGSSSILPCPLTSSGF PSLPPSYQPLPCPSLFLL*NSLSTLCLL FFSLLSQPSFSNRWPSQVYL
1893	15794	A	1905	3	424	YRAGCLQSLLPPPLLLFLLPCDVPFPPS S\LP*VKASCGLIRSQQNVGTIPCLQNR KSNKPLHKLPSLRHSLRAMQNRILPILR IGKFF/IFFS*DGVSLCHPGWSAGVQLQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						FTALHLL/VLKRFSCLSL
1894	15795	A	1906	2	389	IQRGLDKSCLITDNIPSSQSLIQKKGVN PSFKSMKADRGKEAAEEKSEASRSWFMR EKERSHLHN/IK*VQGKAACYPEDLASI IDEGGYTKQ*IFNEDY/MWKKM*FRSFL TREKLTPGFKASKDRLTPLV
1895	15796	A	1907	458	13	AKEETQSVVVDFPM/VPQGVYVNFPVSR NANLSTIKQLLWHRAQYEPLFHMLSGPE AYVFTCINQTAEQQELEDEQRRLCDVQP FLPVVRMVDCEGARVNKLLSSQISLFIG KGVRELDSLSDPEVSDFSTKMCQFCEKS AAL*DQATS
1896	15797	A	1908	409	3	EKTDGLYRASQRGKDLRRLCAQSFHASW KDGMALCALIHRRRQ\DLIGYAKLRKDD PIGNLNTAFEVAEKYLDIPKMLDAEDIV TTPKRDEKAIMTYVSWL*IVIAGAEQAE TAASRICKVLAVNREKKKLMEERV
1897	15798	A	1909	116	379	HSGPRREGALLLPKCLPHAKRCLLLFKM CSDGATALCCPGWSSAAPS*LTQSP/AS TSQAK*PSHLGLPSCWDYRCIPPHPANC LDYYY
1898	15799	A	1910	418	3	QD*YATANRWFICMLSQACFLPSL*PAH LL*L*QLMLFSFPGTPVFSYGDEIGLDA SALPGQHMEAPVMLWDESSFPDIPGAVS ALMIVKGQSEAPGSLLSLFRR\LSVQRS KERSLLHGDFLAFSAGPKLFSYIRPMY
1899	15800	A	1911	394	3	ILEAYPEVKDPAVKGASSKKEMYGH*/A AEQALPVASEQEQQRHERSEKKQPQVKE GNNTNKSEKIQLSENICDSTSSAAAGRL TQQRKIGKTYPQQFPKKLKEEHDRCTLK QENEEKTNVNIMSKKNREDV
1900	15801	A	1912	499	141	PGLGERDWTSKYGQGAGEGSTREWASRC G/IRPGGDAGQQQPRPE*SVCPRGAHSP GPGSWKASPAWHSAEPGGRCSGLGVQKE GFPGHLLQPGCRTPGPGIRKERFSGYLQ
1901	15802	A	1913	127	387	ISFVFPPTLPKMPQLKPETISMTGLNLF QHLCNLARLATSAYDGCSNSEV/CDLDL LY*AALFLKLDYQIRFPNYFSTKYRIYY LCLY
1902	15803	A	1914	504	0	PGPGQRKHSTAPMCLLNIYAQILRFVLA NQIYKCIKRIIHHDQVGFIPIMQSWFNI QNQ*\INLIHHINRLN*KNHMIISFDKT HHLFIIKTFIKLGIEGNLLNLIKNIF/S KNPAANIILNSEKV
1903	15804	A	1915	46	415	YTSNKQLQIQILKITYNSTKKYKILINW IKDVKDQYTENQKILLREIKDLNK/YRD TSCSW/NIVQMSMFS/KLIYRFSEPPNK NLSTL*ILTTSF*FAWKYTGTGIYKVTM KNRVGRLSLPNFQNY
1904	15805	A	1916	420	1	ENADCVERARKSPDSIP*\RGGQISVTM VSPNEQEKAGQLAIGVRAVRYNGV\LLA KMWRKKLHLTLSANLEKIIAIGLFFSNF ERKPPENTFLKLTAMATHSESNLSCFAQ EDIAICRPHPAIKMPEKAEQYKPLTASV
1905	15806	A	1917	384	3	TRTITSGQYSTHVIRASRVPTRS*VPVF RSCTSNRRFSQAIEPRVMH*KVHIRAST VRYDSGGHVAVYPANDSALVYQLGKILG ANLYVVMSLNNLDEESNKKHPFPCHTS/

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						RRTALT*YLDITNPPMY
1906	15807	A	1918	405	105	KAEAQRRREICSGPHSQADSAWHPLVTW WH*PPPVARSSQEPGVHSPVP/HVCRKI LLIRPKMALANEGNYRELRWFTPWSRSR *VGCLTTPGMCVKHLRCV
1907	15808	A	1919	409	3	GGQEEGVFRVLNSKEFETERGKP*IPPV KDQEIIH\PTKFNHVAHMGPGDGKQVLM DLPLSAVPPSQEESPGPAPTNLARQPPC RNKPYISWPSSGGSEPSVTVPLRSMSDP AQDFDKEPDSDSTKHSTPSNSSNP
1908	15809	A	1920	9	470	APARNPLPRPCTWPTGP*CLRPARPPVA SACLCGGTWNLALWLCSPGT/PVPFLTP PCS/SCEVQQPASHSVASNQSKEPAKSA AVAHECPPGGTGSADPGWPPGATCPESP GPATPHTLGVVEPGKSSPPTMEEEPWAP QGSPCWTVRQRMTMMM
1909	15810	A	1921	556	1	IQLWAALGGILRRVGRDPPSHRIGKEPS AMAGQAGGNGDGEEGSS\GGLAAVPHLP *SQHAAHPLLIGPPGQQNLGDSKV*GFP SPRLEENTLENGGWGSKQLHGSPGSQHA GGSWKNGETSLKG/PH*ADGAGRHTMPQ SPPSPPFKPHSV*HNPPAS/PPPHGSPA PSGTSPLPMSAVSLLPPGSL
1910	15811	A	1922	567	41	GGWGETFSRLGNDLQAHR*SRFNAQAQE ETSR\VLAVSLINEALDKGSLEKTLSAL LLPAAGLDDVSLPVAPRYHLLLVAAKRQ KAQVTGDPGAVLWLEEIRQGVVRATQDA NTAQRMALGVAAINQAIKEGKAAQTERV LRNAAVALRGVVPDCANGYQRDLESAMA KIQRPAAV
1911	15812	A	1923	2	405	IQGCGITSSSVLHGMVFKKETEGD/VTS VKDAKIAEYSCPFDGMITETKGTVLIKT DEELMNLSKGEENLMDA*VKAIADTGAN VVVTGGKVADMALHYANKYNMMLVKLNS QWDVRRLCKTVGATALPKLTPPCL
1912	15813	A	1924	510	37	LLGHAFHVQSSSGRPQLAEASGHSHLKK GECVQQRTGNVGLSPNTARWGTPLGPSI SSSAPPWSFSAFPGPPGSGK*AAKDGPG CSLKSGLKR\RSQGGLR*TRGSGPSPMP PSPSPS/ERPPPGDEGLLPCTPRGGLPG PKINTACVCAADISPGLEPV
1913	15814	A	1925	74	429	ATIPGHELLLLFFFFFFFFFLGKGAWPL G*GKG\GGPIRG*GNRAPRG*REFPPPT PGKRGNTGGGQPGQPIFGFLKKKGAPPG GPGVPKTRGQIEPPPWPSKRAGVTGWTL GPGPKV
1914	15815	A	1926	515	304	ALAASLALALNGVFTNTIK*IVGRPRP DFFYRCFP/GMG*PHSDLMCTGDKD\VV NEGPKETSPSGHSSPV
1915	15816	A	1927	1	433	NTVGSNKKSKKLYFAEIEKSYLNFIWNL KGPQ*VKIILKKKSSVTKCTLIHSKA*Y KV/LKIVWYWQRDTHM/DHWNSIKQHMV KQFFDGDTKTVQWAKDCLYNNWCWEK\W ISTSNRMKFNIYPTP*ANINCHQDPNSK ELYRYKN
1916	15817	A	1928	316	356	GGT*PPQAATPIS*LYLPITSSL/TLPP APSLPLQIAPIPSDSPSPRYS/TPTPPI SLGLAPPTTLLIPVPSLPVSPRPLNSTA

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						PP/TFLTGSGAAVTVVSLAVSLSPAPAS AMDKAQNM
1917	15818	A	1929	490	11	PTRLTCPGSHVPGPVTFPPYETHSMP\P PCHVHPLVQPPGSSHVPGPVTSSPSPPS ATHIHPLVQPPGSSQLPNTWVHPSQRMR TWLQQHPPLPAPPQP/PSPGSICSSMTH LTEYLASFPAPQ/PREQAPQGGVPTSLP QW*APQPTAPCRATQSQQLLDG
1918	15819	A	1930	1	552	RNPRKRAFPSPPIPAPPS*NQENERSRH PQSLL\PFVKSRKRAFPSP/LSPCSSFV KSRKRAFPSPPVPAPPS*NQGNERSRHP QSLLLLREIKEMSVPVTPSPCSSFVKSR K*AFPSPPVPVLLRDHTFLPLPEPRQPS TVPVGCFGFSRIPRRWNHTGCAFLLICH SARLLCDPRVSSCVVRHS
1919	15820	A	1931	414	3	RVPGESRK*ERVLDSRHKD*EGRRRGNI \MGKRVDYTT*TVITDVTNLSIDQVGVH RSIAANMTFAEIVTPFNIDRLQELVRRG NSQYPGAKYIIRDNGDRIDLRFHPKHSD LHLQTGYKVKRHMCDGDIVIFNRQCI
1920	15821	A	1932	521	103	ATEPAGVRLKEGGNITESFVTVGNVISA LADFSQDA/SRYS*KKKQVLVPYRDSVM TWLLKDSLGGNSKAIMMATISPADVNYG ETLSTLRYANRAKNIINKPTINEDANVK LIRELRAEIARLKTLLAQGNQIALLDSP
1921	15822	A	1933	1	490	NTGWVVRKGEGNGTLMVRRLPCVPLCSS AGGLTEEDEGELCAAGFPLLAEDFGQAL QQLQTAHSQAVGAP/KGGDQVLGGGTGA PPTAYPNHALSIS*IPSVSWHDEGALPA VKIEILGIIHLLPERHALLSLVQARSGL LLHGPPATGKILLNKAGTTECCLT
1922	15823	A	1934	383	151	EVAFLENLIKDDIERGRLPLLLVANAGT AAVGHS\S*LGRMKELCVQCVNRPKMEG YMHVSQHPVPESHKMRAKAIF
1923	15824	A	1935	379	1	YVPVVSKDKEYFFNSQ*GLTTHQILPYI DGFRHVQKISAEADVKLNLVRIAIQILL *VGLQSYLGQGHQPGKS/CRGPGCEGWE GMVLRS*AQLSLSGTTAL*HWCPSSRKL IQFGIIKNLIRRLCI
1924	15825	A	1936	376	2	GCLFIYMKPTAMSSSQVARSGEVSPFTA VPA*S*K/QGHGAVLGCHITSEACFQAC FPFLRPGRSTCFA*SGC*DVERSSSHSH GTAHSP\HGTAHTPMEQHTHSHEQHTHS HEQHTHSHGTAHMY
1925	15826	A	1937	426	1	KHGEIIDDLLKVYRDNASKKSAI/YSKW ITHWKKRRDDVGEEVHSSRPATSVCEET IHLVCALI*ED*LIAAETIANAVGIPRC SAYTILT/E/KLKLSKLSTRWVPK/P/L LPAQLQIREKRSMAILNKWNQDHEAFLH IIIAGLY
1926	15827	A	1938	2	469	KRRKLVSSIAAAIHPALSS*TRQRFLLL LFLFHIVREDLVQLRIKKKHTIQIGNVE VKLL*PTDNIILCGKLYRFHRSTQKVLQ LI/NFSIVAAYKINMHISLVFLYSNDE* LENKTKQTSSFTIALKRIKYVGSNKKSK KFYFAEIEKSYLDFIWN
1927	15828	A	1939	468	920	IPLSTHSPGMGTSTHLSTRHHLSFWTYH ERLLNPGRETDWA/IMLFRWGLLMLPRL

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						VSNS*AQVIPPTSASQSAGITGMS\HAS GHLIFNY\CSM*WLHLRNSQ*KRCTGQE TGPCPVTQDGVQWSNYGSL*PQTPRLKQ SYHVSLPSSWDYS
1928	15829	A	1940	448	474	GIPGG*GSTTRNALYHVMNGEDVVILTT CKHGKDWQKHKDSRCDRDNTEYEK\YDF GEMLHNATFCLVHRGRRHGSFRFLEAMQ AACVPVMLSNGWELPFSEVINWSQAAVI GDERLLLQIPSTIRSIHRDKIIALRQRS QFLWESCIATAIEDPNLIGVVR
1929	15830	A	1941	1	423	NTTLIFAGGM*NVCPGPLCARLLHRSLT HATPDPPLLTLP*IPTPTPSSRCAPKAP PHLICPTSCPLCSKPHPWPP/CSSCQ
1930	15831	A	1942	48	417	RLTMYQVLYRLHCTALQPLPPRVK*FSC LSLPSTWNYMHMPQCPTNF\CIFTRDEV PPMLP\SWWRTP
1931	15832	A	1943	450	2	VHRRSNRQNMDTSR*RGAMQSVESV\GV PY\EQ*TIVDGI\NSGVWEGIAYA*IEE RYPEEFALRDQEKYLYRYPGGE/AYKVE TIKLNVEAVNTRRDKPTNIFAKNQAPVR MRRNSFTPLSSSNTIRRPRNYSVGSRPI KPLSPLRAQECI
1932	15833	A	1944	451	3	GRITRHLPRRAEDDREREREPSPLPSRH PMFPPSVTPKASSDWP/PASSIPCQACH G/PPPVSLPRKPAHRSC\PVFPP\ASGG DTSIHSGKTVYVKRKSQPAWPVLPPGGL *APSHGAPSPSPPDQHRHCPEI\R*DLL PAPAPSPFSIPPLY
1933	15834	A	1945	402	3	VRLLVSWKVMYP*SRSKASL/HPQITAS LTGSCVNCIVILILNFFYEKISAWIAKM EIPRTYQEYESSLTLKMFLFQFVNLYSS WFYVAFFKGKFVGYPGKYTYLFNEWRSE ECDPGGCLIELTNQMTIIMAGDV
1934	15835	A	1947	1	405	NTGWRVFAILCSLKGRPRGIERV/GGKK KKKKKPGGPLGPAQGKTPKTQKGGGAQG NRGKPPLFSGGNFGNGRIFGNPLPAPGP GGGGGPR*KTR\KRKNGNWDLLKGGGKL VFCPMVGKKLSGVPGV*QKNFKGGW
1935	15836	A	1948	443	1	LTPGAANASLLG\CCMEDLSVNG*RQGL WEALLTHNMVAGCRLEEVDNAYGHYEAF STLAPKAWLSVELAEPCVPEPGLPPVFA NFIQLLSA/PVVVTEGGTAWLEWWHVQP MLALMEAELRKSQVLNRVT*GAHYSDCI AAALRIKIT
1936	15837	A	1949	396	2	GNGRGGSVPPNSLNEDGISCAI*/RHIN WLNG*TPTIYCL*ETHLICK/DH/HRLR VKGKKKILHPNGNQKPAGVALLT*GQTD IK*KAIKSNKEGHYEIKGSVKQENITVG NIYAPSTRAPRYKKQLLDLKGVN
1937	15838	A	1950	419	1	RWQ/PSARPPTPSGK*GASLPARPSSGT *GALLPGCPVWKVRSASSWPPSRLGSEE PLCPA\PSHLGSEER\PSRPPSHIGSKE R\PARPPIA*DVGSASAPP/LPSGM*ER PAAPPSGR*GASLPGRPSPEMWGVPLPR RPVWDVRAPSRAPVWEVRSVSAWPPHLR REKTLRLATAPV
1938	15839	A	1951	422	3	QNHVIMSE/DAKIAFGKIQYPFKMESLN TL*MKVNFLNLIKITQKNPIANTMFTGE

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						MLE/AFLLRQGKRSC/CSLSPILFIILL EVLPS*VWQEK*/IQG*EREE*NCDFVD DMIVYVEN*KKPLYNLL*IIS*VARFKV ILDTCI
1939	15840	A	1952	2	409	CAHYSKNPPQRPLRTDARLPAV/DFWSL GAILFMVGCGQPPFQEANDSETLTMIMD CKYTEPSHVSKEGKDLITRTLQIDPRRR ASLQ*IENHPWLKGVDPSPATKNNIPLV *YK\NLSEEEHNSIIHRMALGDITDR
1940	15841	A	1953	2	367	IQCVRL*VHVCLCASSCVCICLYVHATL CVSTCL*CVAVCM/CLLCACATVSACLC /V/CGCVSTCVCVCPPVCTCDCVCMSAC VCT/CLCVCVTVSTCVCERLCVPTCVCR CPCICSSLNGNEWMG
1941	15842	A	1954	374	2	EAPWLLRAGRGALPPCWSKTPPSPLLF\ PPLLPGTLVYQPWVPLPPWNRLACAVTL ST*ARAGTSNPSWHLPPVSTAPQHPSTW QSPGAGTMGDPSLSPWTSHLLPGCCHNP CHCPFPHHKPTRV
1942	15843	A	1955	1	411	NTPSPELHPC*PGL\PPLPSPPQQPPTW APPRTSTQQKLPILCLLKPSAHTDAPCT QPGSTLPLHTPHTQQAQGTAYQIHTT*A APPPGAKPG*RCPPPPPSRQPQRMQTPA PGNPQPCPRLTTLTRVLVPAVPPLPI
1943	15844	A	1956	33	451	RGRNTFGPLQSPPPRFK*FSCLSLLRSW EE\RDYRCMPVHPANTMLASLVLNS\CD LPALASQSPGITGVSHPTRPHLS*FLMP LE*GHHHLLLVLLSQPPNMPP*FQRFST GQLECSSFRTNLIVPSPSLNFHSDFPLT S
1944	15845	A	1957	3	399	YMQVRTTMSDHSSHSISKINTDNTKSCK G*GSTESLFHDRWEYKFVQLLWETVWHY VR*TFTILYNPEIILKR/IFRHTYKNVC
1945	15846	A	1958	47	399	AANPTLPAVFFFFFLETEPPFGPPGGRA GPQSRLTEPPPSGVKPIPR/PPPPGEPE KWPD\QGGGGGGDPKPPGGPPP*ATGQN SAGKKKKKKIPRPGAHGADPLLPGKAGG EEWLDPA
1946	15847	A	1959	407	238	TQAFALI/KDGGVIGGICFRMFRTQGIR EIVF*AVPSNEQVKVSGSPRRQPQCTAH S
1947	15848	A	1960	106	1854	NEAVKSKPNQTRNHKEKNNYVHLPDAGP SQPASAGGSSSACRRSTKATLHKRWVSS PAGPGVQPLSWQHPPMMA*GLQGNPSPQ AAAPPARPGLVSGNCLT*EMAQAGA\GT GGSLSASLGKRCPHIPVPCE\PVL*GLC VPGRSSLGELGGNPVTVQSFPGPGAESD PW*GDAECCSLLQASFGDRAGWSIR/RG SVGRPAGVPRGKGRKPTLSGA/SGPGSV LGGFCCPEPLSREAESGMVQE**GRFWT GQERTPTGR*GCKVAGYLHSSATVGHSG AGAGGSPGKTSATLDVGQGLGGT/PSGP AWDRTNGYMEKAALPLCNGKVTGNTQCG AQPPASGPSPWVWQPLLLRQRLRQSTGL *LLFPGVGGGLQPGEG\GQPFPLSPWGS LTGRKNSNKARPGGNEGTEG*GARNGAS LTWVWTVPNGGYCPQAGRDFWLVDSRFK PSLGLRAMV*NSRKAPLSFEDGRMGTV*

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						PQGQEGRASHRKGDSGLSPHSGKG*DP*G/PGGKERSISPPLPRGL*GP/VGERGRNGDWPW
1948	15849	A	1961	76	427	QRQEPTPGHTTSGTRHPPGPGGRGPIQTHSHSHLFPWLETSAGSSPPNFLCSLPPYTPLLRLLPSPFLCPSQTTQRMPIPAPHPSPASPCKVP*DARGAPAGGAPSTL/RGHHPPHP
1949	15850	A	1962	375	131	FLVGRIRLLYCLRELFVYLLREQKAKRNSQWVHTLPISSRHVDAVPCSPSINRNRMGRDKKRPFPL\CVDA*LHSPSVVIQP
1950	15851	A	1963	89	538	GLILLQKWHPGAVSSMVERG*LLHSGLFFSFPDKVSSVVQAGVQWHDLSSLQAPASGSKRFSSLGDHRHAPPHLAHFCIF/M*TQDFAMLARLGTSFIYLFGCCC\FETGSHSVAQAEVQWHNHSSLQPHSPRLRRSFHLSIPGSWDHRNAP
1951	15852	A	1964	402	42	CCHYPGTPGLQGRLSASHQAS/SGPQLPAPLPLQVLPFLALGIGVDDVFLLAHAFTEALPGTPLQVGPCP\QGSSEAAQLTG*EPLGSSDLGLLMNLGASCPHL*TGEIIVLCPKGYCLDQ
1952	15853	A	1965	8	14	SSRAAACPPRPALSLPRPPVFTRRMGPQGSGLPKLPVSAPSSRMGSFPAPSPLLLASGDRHLCPDAAALPLLAIETGCDS\PPGH*PPPSPGGLHPCSPPS*PLIL
1953	15854	A	1966	521	2	YELYGIIKRHRREVSNNQQVRYKEHSIPPDYVSSVPTDPTWGPERREEESSGHFMVDHTGTAAGGGGGMILASPKLGATPLPPE*APA/PPPPPPPPPPPGVGSGHLNIPLILEELRVLQQRQIHQMQMTEQICRQVLLLGSLGQTVGAPASPSEIHGTGTASSTKPLLPLTV
1954	15855	A	1968	111	395	YLMRGFLLHHNMVKGKEDERKTKGARLILFFFFFFKKESPSPPRVEGRDP\NLGT*NPLPPKVKKLSRPTPPEKWEPGAVPHCPNNFLFFRKNGGS
1955	15856	A	1969	413	101	DVNRHFSKKNKHCQ*LVIKEMQIKTKRRYHFSPTRMGKIKN\KKENKFWQGYGETGIFTHCWWECKMVQPIKKTVWQFFLKVK*LLVFGPACKELGSYYSLVTKS
1956	15857	A	1970	411	1	NLTPALCTKVHFKWVMDIKMKGKTIRLLENNTRKYLHNIKIWKGLNRTE\KP*TIKKKTDKFDYDTIKNLSSSKNKTRQTIDWENIL\YLQYITDK*IISGIHKAFLKV/YK/KKTNNPVGKWARDLNGHLIKNDIHMACI
1957	15858	A	1971	3	828	GQACHFIFRSAQAGGSRLRIWRAKQLGLWRVCALIMPALEHSFPTRLLQGNSVPGPSISLDTSCL/CNRCVWEGGRG*TGPGLPSLGKVLVEGIPSESPGPTASHPCCSPRPDPDQ/LSCISAPSATPTVH*SHLTLPMGWPGPQ*GLHLSDQPGPRKP*PGCSGLGGGDAAPRGMEKP\PPPQLP
1958	15859	A	1972	398	3	GPGCYFSVRLQCP/RKIPAWKRAVCSATLI\SLQGPSLSAPHVLGLAALAVHLGESRSALPEVDVGPPAPGAGLPVPALFDSLLTCRTRDSLFFCLK*ALLPQSRLLSSLSK

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						SDTCSFDKIRRDRHADIPPLY
1959	15860	A	1973	2	433	QDPTKMTKEELNALKSTGDGTLG/RASE VEVKNEIVANVGKREILHNTEKEQHTED TVKDCVDIEVFTAGENTEDQKSSEDTAP FLGTLAGATYEEQVQSQILESASLPENT AQVESNEVMGAPDDRTRTPLEPSNCWSD LNGGS
1960	15861	A	1974	373	580	TIFSRQVLRIQNALSDKPNVSTVYSNNG SELHGTSEASV/YHWKILISTEYHKTL
1961	15862	A	1975	47	413	KWKHLRGSEHWRPQENQVHQRIAELRKA GLWSQRR/PAEAAGGPRPKSHWDYLLEE MQWMATDFAQERWKVASVKKMVRAVARQ LQDRTRREAGARREEPSRLRQTSPVLPE KSSVPGLVLRR
1962	15863	A	1976	444	3	GYERSRGTTSGTHSSRDYDGIFGQATVK WAMLDQFRMLSPCSKEVMHQPFYLKRVE IMAQCEEWIADIQQYSSDKRVGRIMSRH SAAIKRRTGQLREELLKLPCPEGLDPDS GDAPEVCRAATGAEETIMHDQV\QPSSS KVLPSDFQ
1963	15864	A	1977	281	567	PRSSLQGQELSRPWGRKGNFPGPPVPPP QRMFYDSELFSGISDPSCCF/RSAPTAD QVYGDQDMHEVVRKHCMDYLVRKWRPLG KGQGGKISSPHRP
1964	15865	A	1978	357	2	KQILGPPHPQAQPGRVVPPPHGPKDAPL WSSRAAPPGRGLGRAGPAAGVEAGATLR DSSPSTWTREGLHVQAQRKRPSHVHKG/ SGPGCLEDGEFPTSLRLQAQLAEIGRGN GLSVRRQ
1965	15866	A	1979	29	434	VQAEAEGLPGDTEHPQPQLMSRSLEGQS DVTIKHVACGDFFTACLTDRGIIMTFGS GSNGCLGHGSLTDISQPTIVEALLGYEK AQVACGASNVLALATERELFALGRGDSG RTGARTKESH/YLPQQVPMP
1966	15867	A	1980	3	2082	SSEGYLRGNMSENEEEEISQQEGSGDYE VEEIPFGLEPQSPGFEPQSPEFEPQSPR FEPESPGFESRSPGLVPPSPEFAPRSPE SDSQSPEFESQSPRYEPQSPGYEPRSPG YEPRSPGYESESSRYESQNTELKTQSPE FEAQSSKFQEGAEMLLNPEEKSPLNISV GVHPLDSFTQGFGEQPTGDLPIGPPFEM PTGALLSTPQFEMLQNPLGLTGALRGPG RRGGRARGGQGPRPNICGICGKSFGRGS TLIQHQRIHTGEKPYKCEVCSKAFSQSS DLIKHQRTHTGERPYKCPRCGKAFADSS YLLRHQRTHSGQKPYKCPHCGKAFGDSS YLLRHQRTHSHERPYSCTECGKCYSQNS SLRSHQRVHTGQRPFSCGICGKSFSQRS ALIPHARSHAREKPFKCPECGKRFGQSS VLAIHARTHLPGRTYSCPDCGKTFNRSS TLIQHQRSHTGERPYRCAVCGKGFCRSS TLLQHHRVH\SGERPYKCDDCGKAFS\R ASDLIRHQRTH
1967	15868	A	1981	2	188	LPETNFAELFLPYISQHNLIRKYKK/WP GAVAYACNPSTLGGQGGWITRSGDQDHP GLHEEWP
1968	15869	A	1982	3	424	EGQAIVERMNLCLKQQLQKQKGENRYYR TPHKQLN\ALLTLNFLSLPKGRILSAAE

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						QHLQKPAAKTEAEQLVWWRDLITESWEI GKIITWGRGYAYVSPGL/NPSRHLKPYH ERMLRKRFREDPEDPPSCSHVKTDAEED PN
1969	15870	A	1983	3	399	YSKLSFKGTLTKFRRIYSSSFYKEFQGC ISDLCHP/R/TLTNCLRGELLKENLVWG AFGCHPHFPCYYNKSQERNLLQALRHPT TVAFGETGFNYSYKCTMPVPEHHKVFKR QLELAASLEK/PLVILCQQADE
1970	15871	A	1984	1	405	RRHIGGGVRLYYIGGEVFAKSLSDSAIF AQTPNCNQRYGWHPGTVCKIPPGCNLKI FNNQEYADLLDQSVNQGLEADY/QLTRM CTILMSLLKGWGAEYRRQTATRTPCWIE LHLNGPLQRVDKVLTQMGYPSILM
1971	15872	A	1985	27	452	QGREHAQGGQSPGAGHLGPTPEPQPEPQ PRPSSQAVPAGRWEPAQE/PTRHPHPRL SPASRPLGSPPAPLVRSSPGRCRLHEHT IWSSTVGTSVEPAPSLGRPQAPLEPGTV TSSVRLQQPHMHTPGKIMPDPSKRNGKF TFT
1972	15873	A	1986	414	220	GAEQEELLSP/GSGGCSELRSCHCTPAW ATRAKLRLTKQNKTKRESYRQGNQNWGR ILGELLGRL
1973	15874	A	1987	52	412	TRERKLFFACDNVWKHLKRYLRKNSFGE NLWSSRNIKKKKKKKKKKKKKKTKNFST PKNFFFFKACQCMGKKNTKHDFHEQNFI EHALLQQLNINFSTNYIEGRVF\HPGAP IESLLLMCH
1974	15875	A	1988	2	143	EKRRGLDKRTP/AQAAFEKMQEKRQMER ILKKASKIPPPFVCMWSVDS
1975	15876	A	1989	3	163	TEFQPSEK/WGEDLGDNTWEYIFAIDLL CCHQKWICHPLFLVGVVRAGAEVSGVF
1976	15877	A	1990	1	439	DKTAAEDAIRNLHHYKLHGVNINEEAST NKSKTSTKLHVGNISPTCTNKELRAKFE EYGPG\IECDILKDYAFVHMERAEDAEE AIKGLDNTEFQGKRMHEQLSTSRLRTAP GMGDQNGCYTGGKDGHWSKECSIDRSGR VADLTEQ
1977	15878	A	1991	1	145	VVAASKAMK/MGDWKTCHSFIINEKMNG KVWDLFPEADPVLLKRLRESR
1978	15879	A	1992	2	425	NISTLKKTLESDCT\KLFSQGIGGEQAQ AKVDRCLSDLAAETNKFRDLLQEGLTEL NSTAIKPQVQPWINSFFSVSHNIVEEEF NDYEANDPWVQQLILNLEQQMAEFKASL SPVIYDSLTGLMTSLDAVELEKVVLKST FN
1979	15880	A	1993	3	449	VAGPAPGAGARPGLDLQFLQRFLQILKV LFPSWSSQNALMFLTLLCLTLL\LKSFD QFTCNLLYVSWRKDLTEHLHRLYFRGRA YYTLNVLRDDIDNPDQRISQDLERFCRQ LSSMASKLIISPFTLVYYTYQCFLSTGL LGPVSIFGY
1980	15881	A	1995	1	410	SSRRPFIALKTKSMRDLNPEDIDQLITI SGMVIRTYQLIPEMQEAFFQCQVCAHTT RVEMDRGRIAEPRVCGRCHTTHSMVLIH NRYLFSDKQMIQLPESPEDMPAGQTPHT VILVAHNDLDDR/VQPVDRVNDSGFF
1981	15882	A	1996	1	154	LFFFRLLVRYTKKVAQVSTPTLGKVSRN

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						LGKVGKKSWKHPEAK\KRPCGKN
1982	15883	A	1997	2	475	KKLRRQTRREAQKE\LPDKV\RWGLVTP SETPVGISNLSPFLGPRCL/QNPAELKP PWRFPWAQRPKAH\ERANAGPKTPAEQR KVKKIKKLKEDISQGVHISVYRVRNLSN PAKKFKIEANAGQLYLTGVVVLHKDVNV VVVEGGPNAPKTITRLMPLRI
1983	15884	A	1998	3	431	QLRTRDRGWPSRRPEREKRTSQSARRPT CTESRWKSEEEVESDDEYLALPARLTQV SSLVSYLGSISTLVTLPTGDIKGQ/SPL EVSDSDGPASFPSSSSQSQLPPGAALQG SGDPEGQNPCFLRSFVRAHDSAGESSLG SSQA
1984	15885	A	1999	1	400	ALDLRGLQILVGFPKRRVTTCSYPTALQ SPIEYQRKERSTAVMRTEPDSAYQASPR PYSAGPADSKKPTKGYCYNPTLP\RLEI MTLEGTTG
1985	15886	A	2000	1	372	QNIDLVISFFSSRLLQAGAELSVERVLE IIKQGVVALPKDRL/RGSCAPTLSAAGR SSGGQSPCMPGLCVCSFWVLTVSWLVCQ KFPELKFKYVEEEQPEEFFIPYVWSLVY NSAVGLYWNPQDI
1986	15887	A	2001	393	1	GGIGRGGGAGGGVGAAGSASGGVGRRGA GGVIADSGAPGGGVEGGVGASGGWRE/G RGTSGGVGGSGGACGSV/GGSGGAGGGV GACGSTSDGVGRSRGTIGGLGGSGSAGG GVGACGGASGYVGIRGAGGG
1987	15888	A	2002	2	362	WVTFISLLFLFSSAYSPGVFRRDAHNSE VAHRLKDLGEENDKALLLIAFAQYLQQC PFEDHVKLLNEVTEFAKTCVADESAEDC DK\SL\HTLFGDKLCTVATLRETYGEMA DCCAQQEPE
1988	15889	A	2003	2	358	EANRGWFIRLKEGSQLYNIKVQGEAASA DVEAAASYPEDLAKITDEGGCAKQQIFN VDK\QTAFSWMKRPCRTLIAREEKSVPG FKL/SKNRLALLLGANAAGGFKLKSVLI CHSENSRTF
1989	15890	A	2004	190	1	DQTCFLSFTVKAVTFNGWVWWLTPVIPA LWDYRH\RPANFFVFLVETGFHHVAQAG LKLLGS
1990	15891	A	2005	1	132	GMCHHAQLIFVF/CSRDRVLHGCSQTPC LKQFSCLGLPKCWDYR
1991	15892	A	2006	2	134	PMTFFTELEKTTLKFIWNQRRIQIAKAI LTNQK\NKARGITNIC
1992	15893	A	2007	315	127	SEIAFFFCSFLKIILDTR/FSFFARAGL KLLASNDLPSSSSQGAGITGVSYGTQPV CFEYNVG
1993	15894	A	2008	3	325	RCSMLAVREM/QKATKRCHFLPTRIALI K/ND/GSNKCWK\HCWWECKMVQLLWKI VWQFLKKLNIELPFDPEIPLRDIYPKQL KTYVHTKTCGQMFIAVLFILNVPHLMNV
1994	15895	A	2009	369	3	VGQAGLEFLTSGDPPASASQSAVITGMS HHTQPIFCIFGFA\GCPDWSQTPELKQS AHLSLPSSWDYRCMPPHLANFYFCRH/R VCCPGWSQTPGLK\YPPALVSQSVATTG TSPRAWQDTILPV
1995	15896	A	2010	114	287	APLCLCLRHLRLLIKRLTVLGTEAHTL\ NPITTRGRGGQITWGREFETSLANMVKP

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						CF
1996	15897	A	2011	218	346	IMKFNLLKFYFIYLFSRQSL/SSVAQAG VHWRNLGSLQPLPPKF
1997	15898	A	2012	310	1	SSSSSNTHFGIPKYLINPDTCFLA/KVN NSSLTGLEYTETLKPGIK
1998	15899	A	2013	3	301	SDCCASNQRDSGGVGPSEPARKHTLCV/ CNSLDLIE
1999	15900	A	2014	332	3	LRDPLEEAVCPFSDLQLHAGRTTALFKA VRQGHLSLQRLLLSF\VCLCPAPRGGAY RGRQAG\SLSCGGLHPVRASRLLCLPKQ AWAMAGAPPPAWPRPCSLISDCCASNQR
2000	15901	A	2015	2	325	LLLHHAPPVNLFLRDRVSLCGPLCGPGC SQTPGLKQSSCLSLPKC/WDYR\RATAP GL
2001	15902	A	2016	373	3	WAHGLQPGKPKVDSLSKKRKKKKGKKLN TFPLRSRTRQACLLSPLLSNIVLEVLPN EIRQ/QKKEIKGTHTGREELTLSLFTDN MIIYVDIPKQSTKKNQGSYSVARPGAVA HACNPSTLGGLGG
2002	15903	A	2017	343	1	EFPFVSGSRATGKSSDIRATKYIWRVLE YLRAWPRGQRRLKSS\HTSLLGSYHPGA FRGDKWSCCHQKDETGGRGEDEVLLCCP GVLGCSALCRSGVRTKFGIRGRPWKERE R
2003	15904	A	2018	139	2	NSISTKNTKNWSGMVAHAFNPSTLRGRG GQI\RGQDFKTSLANMVKP
2004	15905	A	2019	3	322	ARELVFFFGAYRKGFFHRDMKPKNLLCM GPKLGKIADFGLARELRSHPPYTDYGST KWR/YRGNPALLRPTPMAKFPYEGWLHI SGSSIWNIKTSDSNFIFFKESKG
2005	15906	A	2020	205	377	NIVENIVFCWPGVCFLQTCTVCINPETS DE/WPGAVAHACNPSTLGGQDGQITRSG DRE
2006	15907	A	2021	3	324	KKWGKR\LNRAPNGRRYPETRWALEEDQ CHICKELHIKTVRFHCTPIRMAKIHTTD NPQSWPRCGTGTLIHCRRGCKTV/R/PL WKTVRQ/FL/RKLNIPLPCDPAVLSLCI Y
2007	15908	A	2022	2	382	RVSQDGLNLLTSRSTRLGLPK/CWDYRC EPPSP
2008	15909	A	2023	1	421	RWNPGGRGCSELRLHYCTPTWVTERDSI SKIAKNK/NNKRPRNNCR
2009	15910	A	2024	339	3	SWDHRRVLIFVFLVQTGFCHVGHAGLEL LTSGSQSAGIAGVSHRA\GQKHQFRPEH RFLKFGFVFRDRVSLCCPGWPQTPRLKQ SSRLSLPKSWGPATALDPDSSYLEEMVL S
2010	15911	A	2025	2	146	NTFGRSRQEDHLGPGGQACSELRSHHCT PAW\VIEQDPVSKKKKPPKP
2011	15912	A	2026	3	380	RLECSGGISIHCNLR/LPGFKRFSCLSL PSRWDYTRLP/PFVFLVETGFHHLGQAG LELLTSGDPKCWDYGC\DHCTWP
2012	15913	A	2027	32	296	DYMNSLMYFHSLVLASTDEGFLPKTVST QSAGITGISHCARPWIPF/CFFFFKNRK TRFVAQAEGQGGNFGSLNPLPPGFRGFP CLSLT
2013	15914	A	2028	2	187	FTLLPRLECSG\MILVHCSLNLPGLRWS SCLSLLSSWNYTCVAPFSIFYYFIFLTW

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						GGTLNC
2014	15915	A	2029	197	3	AAGLSQAGMQWGDFGSREHLPSRFQRFF CLKVPNNWDYRHGPPRPVGIFFFSF\LV ETGFHHPGQ
2015	15916	A	2030	88	362	KFGINLKKKEKKGPQKNQNFFPTFLFFF FFETESHSITQAGVQWRDLSPLQPLPPG FKSLPSSWDYRCLPPCPANFCIF\IPDS VSLCWQGW
2016	15917	A	2031	7	131	GTIMAWAPGEGGCSEPRSCHCTPAWVT\ SETPSQKKKKGVLL
2017	15918	A	2032	1	343	LECSEPRLCHCTPAWV/TGDSVSKKKKK KKKK
2018	15919	A	2033	243	14	QKLAPWPPQSAGNNRRVPPHPASMAFLT KIEKTALKFIQNHKRPQIAK\TILSKNR VGSITLFNSKIHYMTTVIKTI
2019	15920	A	2034	238	3	FLALPKVLGIIGCVPPHPASMAFLTTIE DTALKFIQNHKRPQIA\KPILSKNRAES ITLFNSKIHYMPTVIKPLRVTST
2020	15921	A	2035	345	2	LVKIQKEMNVFMTANPISIPQFMDQGVI SSCKSYYFRNKFLYV\IAAMDTD/SSNG SWQSEWKTFWKGFIILDGIKNTDDSWEE VKISTLTGIKKKLIPTSTDDFKEFKTLV EDVT
2021	15922	A	2036	1	140	GRCC\HELRSRHCTPAWATRAKLKKKKK KKREKKTQKGKNGLGFWAF
2022	15923	A	2037	199	348	RSSNEGGRDCVFCFGDRVSLCLPGWSAV AQLWLTATSTSQ\VKSLSHLGL
2023	15924	A	2038	3	193	NGLNAPIKRLRLANWIKSQDPSVCCIQE AHLTCRDTH/RCYLKG/WYKAF
2024	15925	A	2039	116	337	SKLLKILPRLCWGWWQAPVIPATQEVEA EDHLNPG/RSRPAWATQRTPVSIKKKII LRPANGK/CHGPSW
2025	15926	A	2040	368	252	VFFFFALFYLFFFFFFFFFFFFFFFFF QFLGFYFRFKF
2026	15927	A	2041	204	399	VSSHKINGLTVCSTSPFFLSLLPPSEES ACFPFAFCHDCKFPEAS/SVMLPVKPVE L
2027	15928	A	2042	103	356	WHFSPPQPLPPP/PLPNPPPPPTPPPP\ PPPPPPPPPPSPPPPPPPSPPPPPPPL PPPPPPLSPPPPPSTPP/PPPPPPPPPP PLPP
2028	15929	A	2043	3	344	LYKWNNKASLAAHLFAAWFTVYFKPTVE TYC/SGKKKIPFKILLLIDNTPCYPRAL LEMCEEISIVFAPATTTSS/LKPMDQGV IVTFKSNYLRNTFQAGGGEKKEKHERKK NIIS
2029	15930	A	2044	2	349	PRVRKSPGPNGFTANFYQTFKELISILL KLFQKKKKIKKGENPPNSFYGAIIPRIP NPNMDLSKK/ETYGPVSGRNMEAKIFTK FLAGHFKQSFGREIHHDQREFIPGIQGG FNIGN
2030	15931	A	2045	280	462	CXFFLVVVLVWCVVLLFXVVVLWLCFFG FVVCCVVFCXCGVWFFVFFVVCVLCGVL LGCWC
2031	15932	A	2046	3	284	PSPSFSLLLPPSFSLLFPPSF/SPPPPS FSLLLPPSASLLLPPCTSLLIHPPTSLQ LPPLPSFYLLLPTSISHHLPTHNLPTTS IQDPSTPCSIK

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2032	15933	A	2047	95	1	GRVDAILAHCKLR/LPGFTLFSCLSLPSTWDC
2033	15934	A	2048	211	1	EPTTMTGAKWGSSQTTTNYHMLQSLRINVRVDFFFFFCTDR/SLSMLPRLVLNSWIPAIILPHPPQVLGLQ
2034	15935	A	2049	35	266	EVRRPSTWQPPRLRSEEPLRL\QPPRLGNIGFCHVGHAGLKLLTSSDLPTLASQSAGIT\GHSYRRASEEDKKESSMSS
2035	15936	A	2050	281	3	QSNFKRALLSILLKAIYRSNIIPIK/VPMTFFTEI/EKVIPKFIRNLKRLRIAKVILSKKNKTRRITLSDFKLYYY\IAVFVAAWYWKKNRLSDQWN
2036	15937	A	2051	251	12	ILRFFLPKFLGFQKPPSLEKTHFFLPAFGNSLFWPPEKLGQKKVFFFFFFFFLRQGL/NSVSQAGVQWHNLGLLQSPLPRLR
2037	15938	A	2052	2	325	ADHLRPGVQDQPQPGQNGKTPSPLKIEK\LAGCGGGHPRLREENCLNPGGRGCSEPRSRRCTPAW/VNDSKTLARKKKKKKGVEKNECGRKVMRV/LQGPKAKVKPWGENL
2038	15939	A	2053	3	166	SLLLPRVECNGAISAHCNLHL\HNLHLPGSSDSPASASQVAEVRGSLEPRSSSLA
2039	15940	A	2054	227	3	LNENIGRITGMSHHARLILLFCE/YRVSITQAGV/QHDPGSLQPLPRVFKQFSHFSLQSSWDHRCAPIRLAIFWVFC
2040	15941	A	2055	301	0	QRKSHMFLTINQKLEMIKLSEEGMSRVETGQKLDLMC/QVSQAVNAKEKFLEKIKGDTSVHTQMIRKQSSINVDMEKVGIVWIEDQAP/HNHIPLSHLLMRAR
2041	15942	A	2056	1	109	RPLRRLRQENRLNRGSRGYSEPKLC/HLCTPAWAT
2042	15943	A	2057	313	250	PQPPPPSPPPQPSPPPPSPPPPSPSSP/PPP
2043	15944	A	2058	134	2	EKESRSVA\RLKGSGAISA\HCNL\CLPGSSNSPPSASRVAGSSGA
2044	15945	A	2059	120	326	NSLVADME/KVLVVWIEDQTSHNIPLSQS/LIQSKALTLFNSIKAKRSEEAAEKIFEASRDWFMRFKIKQK
2045	15946	A	2060	102	413	ERTGFRHVGKSGLEFMTSGDPPTLASQSVGIT/VHEPRTRPG
2046	15947	A	2061	311	1	FFKKQRFCKSGCKTPGKPRGPKKLGANQFSGPTPLKNGVGFSPGPKGGFFPPPPGGFPAGRPKWLTRILGKGGSLLRG/RYPKKGFLKPILGDNSPQRAPKRGP
2047	15948	A	2062	229	380	WYDLGSLQPMPLRFKQASRVNLPRSWDYRHPPLSRLN\IVFIVDTGILHVG
2048	15949	A	2063	142	383	PQSCFSTHWQLLQKQEETAGAVSVCVCTS\VCVCVCVCVCVCAGAMCVCAGA/CFCVCVCAGA/CLCVCVGA/CLCVC
2049	15950	A	2064	408	200	NLIQIKALTHFSSIKAERGDKSTE/EKFEGSRGWFVRFKERGHLCNIKVKHEAANAYAEAACSQLSRRSS
2050	15951	A	2065	348	3	WVSPYSPCVCVCVCVCVCVCVCRDWVSPCCPGVCMCVCVCVCRDW/CFTM/CAQVCVCVCRDWVSPCCPGVCVCKDWVSPCCTSWSILKLLSSGNPPTTVSQSAWITGRSHSAWPARA
2051	15952	A	2066	73	286	NLIRGLLESHILISMRYGYCKSYTLSMRDIPEALNKWKS/IPMFCSWSRRLIVSMA

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						VLSKLINRFNAKDVQH
2052	15953	A	2067	329	0	PSSTFLLPFPRPPPSPPPPPPPPPPSPP/PSSSSPAPSSPHP
2053	15954	A	2068	221	3	ELKVILHCLRDFSLQSSIMKVLILKILILSVCCVC/VCVCVCAVCSCVC/VCSCVC/VCSCVCLCVLCVCVCVLSC
2054	15955	A	2069	1	167	GTRENPLNPGGGCSEPR\SCHCTPAWATKSETLSQKKKKKKKISNYKTPFKSYRI
2055	15956	A	2070	2	354	ARACLGLPSSWDF/SVENRFHRVGQAGLELATSGDPPTSASPECWDCRH\DHHTWPLL
2056	15957	A	2071	20	341	CIVTVNTRGENINICWSPDGQTIAVGNKDDVVTFIDAKTHRF/LKQNSSSS/SEVNEISWNNDNNMLYPDTGNGCINILSYPITESRAIYQRPIFHVHVNQDLPHGDVLS
2057	15958	A	2072	353	58	LQLLTTSDPPASASRGAGIADGVWFTQ/SLNGAQAGVQWRDLGSLQPHPPSRL/LLASQSAEIAASARPPPRLGSEERLCLAAHRLGCEEPLCLAAQSGK
2058	15959	A	2073	1	338	GSRLQRVCINYRLSFFPFLSQGWINFTWLFCLCVCFLRDRVSLCCPGWPSTSGFKRSSCPSLLSRWDYRHMPQHLASHTLFKKL/TILPR
2059	15960	A	2074	1	322	GGGREAGEARGGGEGGQGSGRRRRGRGGPRTGGAEGGRGAGETPGGGARPEREQGRGRHSERQGPT/RQTKRPKTKTKQLSQNKNT
2060	15961	A	2075	450	225	TPVGRGCSELRSCNCTPAWVTD\ETLSQKEKRGGVKIGWKKRRTRIISLHLPGSHEKFNNLETVKNCVNHFCRLNT
2061	15962	A	2076	2	470	TPQNKPHPTTKNTQPQPTQKK/PTQTQP/TTPKPKTKKNTTPNPAPPNTQKNHTTKPTTQNPHKTKQKNKTKPNTTQQQNKPTNQNPKTQTQQKTTTQTKPPKKKKKKTADTTSPNPISTKKIKKLAEP
2062	15963	A	2077	304	1	NSATPPCSPTA/KPHPTPPTPPPTSFIPTCQHSPPTKICPQARPRTPPYAHPPRCPRKIIPKGRRHPLAPPQAARRDLNYYHPIIWRGRVCVCVCVCVCARA
2063	15964	A	2078	167	1	TILQTNSTWSNVLLWQGAVAQAC\NSSTLGGQGGRITRSGDRDHPGQHGETLSRA
2064	15965	A	2079	3	364	HETRSRHSCAWCSAALWRAAVASRCPSS/IPVTPPQCLYWP/WKVPLQCPPDL
2065	15966	A	2080	303	2	SKRGRPSGHECPFLGTSSSCRHVASCTIRTPRRLCKSQLDRCSPLKERHKFGLSRSVLSAMTQSGIY/WQPPPPEFKRCFSCLNLLSSWDYRHAPPRRARA
2066	15967	A	2081	4	326	AGITGMSHRAWLFLYFLNKFAFT\YGLVLNFFLHKIQEPSLG\SGSGP/LSCNS
2067	15968	A	2082	1	343	PPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPSPPPPPPPPPP/PPPSSPSSPPPPPHTPHP
2068	15969	A	2083	330	88	ACDRSIISRIHKEL\EQLCKQK\SNNPIKKWPKDMIRYFSKQDVQTVKTMNKCSTSLIIIEMQIRSTMRYYLTTVRTPHPS
2069	15970	A	2084	1	340	RVRSHGTTHLAQLIFVLLVQTGFHHDGQDGPDLL/NLVIRPPQPPKVL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
2070	15971	A	2085	2	348	ARALSLGANAAGNFKLRPLLRYHSQNPR ALKNYAKYTLPVLHRWHSESLETAFTEC FTEYFKPTVETYCSEKD/I/SYKALLLI EKALGHPRALMEMYKDISIVFMPVNTTS ILQPMD
2071	15972	A	2086	369	2	KGLPPSPANLFFLSVY/MGFPMFTRLIL ISCPCYPPPSASPSAGIKGLNPPGWPPF SFFYQKFVRFFVLARNRTFGFVDYFSIL YLIYGCSNLYRFLLSALYFFVSVFVFVL TQGIEAMVPRA
2072	15973	A	2087	314	3	LLESVGPTRNSRPFKGLIGRILLDPEFY PSLVSDDLPASASPNAGRILPFFFFETG SHS\TQAGVQWRHHGSLQ\LKRSSYLSL TSSWVYRHTPPHPANICIFSRA
2073	15974	A	2088	330	16	CPCFFLSALSVLVGWCFAFVVCGCV/WW CVCFVVVFVCVCFLGCVVLCLCFV/VCL VGVCCVVFFGGLCCVCC
2074	15975	A	2089	1	337	GTRTFLPPSYKDPCEY/IWAHPDNPGSS SNCNMLNFSTSD/PPVHSSGNWKVLSSP NRPYYYSYTATPHTDPTPHLPSPNPSSP SPSYPLLSDSTICQTTPTTTPITSSHTL LTS
2075	15976	A	2090	350	84	QRKENKRTRKRATERRDESREEKAGRKE GENQEKRNKEQQGRQRRSRDRT/EEEKE EAKRREHKNPKKKKTKPPPQKKKKTEKK KTDNLSN
2076	15977	A	2091	1	355	SDPPTSASQSAGITYVSHRTWPLLEFSG TSIRLAGKPAGVLVEVTGK/SVCGGGVT KTHWNECHTGYPKCCWSSQAGESSLQPP PPGFKRFSCLSLPSSWDYRLLPP\QNFC IFSRDGL
2077	15978	A	2092	27	345	ASIPCLKKRKKKKKTGGKPPP\GGPKP KRGGGGGPPPTKRTLFGPPQGNQTPGGV S/GPPKGDPPFSPIPPCQRKSPPFEKGG KKGPPPWRGVKREKGHFLKNFQQK
2078	15979	A	2093	3	301	HEHVAQAGLKLLGSSDLPTLASPKCWDC KR\DYCAWPHIFPISGPLYVFFPLPRMS PHTHTHKYTRTFFHYAHKHCACTLNLLL RAQFQCHFFKGVVPDP
2079	15980	A	2094	76	342	WFXXFFFLLFVFFVFWFVCFCVFCGFFF FCFFCCVWFVFGFCLFLCFLFWFCFFVF FGFFGFWFFVFFLVCFLVFVCFFGCFFF LFCFF
2080	15981	A	2095	115	325	MDERKKIRGGGRQGKECKIHCKKKLSPG IRSYPVEN/F/VDTMYDYLQPAYYKLND LTNADPCAVRYLLFDQN
2081	15982	A	2096	80	227	SCLGN/CIHLYSHSPTLSFTHTHTHTHT HRERERERERERERERERERERERERE
2082	15983	A	2097	308	1	NSTVTMENSVNIHYRTRVFTEAQFTIAK SWNQPKCPSILEWIKKL\WIYIYVCVYI CVCVCICVCVCVCVCVCVCIYIYMMEYY SAIKRNELAAFAVTWTRA
2083	15984	A	2098	2	361	ARACLGLPSSWDF/SVETRFHRVGQAGL ELATSRDPPTSASPECRDCRH\DHHTWP LL
2084	15985	A	2099	1	221	LLWRLRHENHLNLGGRGCSEPRLHHCTP SWMTR/GKTPSQKKKTKQPMEWQNLCLK KVFGNTGVREIFNGIKLS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
2085	15986	A	2100	186	2	ERVYVCVCVCVCVCVYQCYLPQIRSL/VASSLKANARVCVCVCVCVCVCVCVCVSLWHPLTA
2086	15987	A	2101	305	2	HNILLSQSLIQSKALTLFNSMKA/E/RGEEAAEEKLEASRGWLMRFKE\RSHLCN\TKVQGEVASADTEAAPSYTEDHSKITDEGGYTKQQIFNVDKKASYWNMS
2087	15988	A	2102	6	166	EQTALEILARAIRQEKEIKGIQIRKEEVKLCFFVND\MVLYLENSKDFLKVDAA
2088	15989	A	2103	53	176	EIKNNRPGMVAHAY/NPSTLGGRGRQISWGQEFETSLVNMVK
2089	15990	A	2104	3	267	FRHVGQGGLKVLTSGDPPALVSQSAGITGVSHCAQPIVGDFNTPLSIL/D/RSTRQKINKDIQDLNSALDEADLLDIYRTLHPK/STEYTFF
2090	15991	A	2105	268	3	PPKEHGSSPATEQSWMENDFDELREEGFRRSNYSE/LREDIQTKGKEVENFEKNLEECITRITNTEKCLKELMELKIKARELRPECRSLR
2091	15992	A	2106	3	170	GFHHVDQAGLELLTPQVIHP\LGLPKCWDYRREPPCLASPHFHQIAISQKRHREAK
2092	15993	A	2107	1	398	SARGPDGFTAEFYQTFKEELVQILLKQFQRIKGEILL/KNHYVKPSITLIPK\PG\RDITKKLLTRSFCVSLCPVLSPLQSLQSRPSSLSMISLHSVCFSVLSASAHPHVHLCPTCPTLVLSGSHCVCCVSLFFF
2093	15994	A	2108	3	370	HENWNNKGWGDSTIYSMKYLYFKPMLRPY/C/SQKKIPFKILLLFDNAPGHPRVLMEIMYKDMEVF\MPVNTTF/ILQPMDQRVILTFKSYYLRNTFHKTIAAINSDYSDGSGQSQLKTFWKGFIVL
2094	15995	A	2109	1	213	HFPVENESAPG/FKAAGDLLTLLLGGNAAGDFKLKALLVYPSENPCFLKGSFKPNLPLVWCSHKKAWVQLG
2095	15996	A	2110	391	3	KKKKKNPHRKKIKKRWKKIFNAERNKKRAGVIIHILDRLDFKQQTIRRDKR\GYYTMINGTIQQEVITILNIHAANTKAVRYIKQVLLKLKTELGPNTIITGDTNTLLLSTLNRSSRQKNQQTLDLICNI
2096	15997	A	2111	188	365	FQNTIHICVCVCVCVCVCL/CVCFCVFFFCLLCGGFMCGCWCDFCILFCFYGVGFFFL
2097	15998	A	2112	3	340	RMESALDRLKQFTTVVGDTGDFHAVDEYKPHDATTNPSLILAVAQMPAYQELEEEAIAYGRKLGGSQEDQIINAIDKLSVLLGAEILKMITGRVSTEVDARLSFD/SDAMVATA
2098	15999	A	2113	11	305	FLFTDFCLFMTHILGHKINYITN/CKRNVIIT/SYFSPHNRIKLKISIRKISRKSSNTWKLNNRLLHYPQIKDEVSREIRKYLELNINENTNF/QNLWDIHK
2099	16000	A	2114	3	387	QTNH/NIPLSQNLIQSKAITA/NCMKAERSEEAAGKFEASRGWFMRFKKSSY\IKVQGEAASAGVEAVAIYPDLAELIDE/GCYTT/QIFSVFQTAFFWKKKPSRTFM/REEKLIPGLKASKDSSSLLLRVHAAGD
2100	16001	A	2115	152	393	VYCPICWLVFFFCFCSVLILFVMFV/CLCFSFFCFLGFVVVFSSFYLFICVFFFIV

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						LGCLFLCVVFDLFLFVLFVLCLFFVS
2101	16002	A	2116	2	373	ARACLGLPSSWDF/SVENRFHRVGQAGG ELATSGDPPTSASPECWDCRH\DHHTWP LL
2102	16003	A	2117	3	449	HEFDHAMLQAHRAHHLAIDAYHEFEETY IPKDQKYSFLHDSQTSFCFSDSIPTPFN MEETQQKSNLELLRISLLLIESWLEPVR VLRSMFANNLVYDTSDSDDYHFLKDLEE GIQTLMGRAEKRHCRTVQNLKQTYRR/F DTNS/HNHDALL
2103	16004	A	2118	146	15	FFFFYFFFLFFFFFIPFLFFFFFLFFFF FFYFIFILFIYSLLVF
2104	16005	A	2119	406	3	LFSVNETGFYSKMLSRTFTATEETSIPG FKVSKDKLTL\LGANAAGDFKLKPMLIY HS/ENPRALKNYAKFTPPVLYKWKNKAL MTTHLFTARYTEYFKPTVETY/ILLLID NAPTHQRALMEMYKEINVFMPANTTSI
2105	16006	A	2120	109	396	YYFYFYLVLFYFFIFLFFYFFFFFILLL FYFFFSFIFFFFLFVYFIFLCYFFLFFF FFFFYLFFYSFFFFFIFLFFFFFFFFFF SYYLIFFLSYII
2106	16007	A	2121	15	413	IVLARNTNFWLSFLFPVALGILIVLKGV KYIFWPLEYCQRLKMFVSYSFHY\FFLG SLLFLKYGFHMYLILLL/CIFIIIMCFF IKYSFFFCCLYHFFFSFYLFFLYFLIF\ CYLVILFFSFLLFLFLSSYCFFF
2107	16008	A	2122	1306	429	SSSSSSSSHVLRIIKDEDFKILEQRQVV LSEKEAQALCKEYENEDYFNKLIENMTS GPSLALVLLRDNGLQYWKQLLGPRTVEE AIEYFPESLCAQFAMDSLPVNQLYGSDS LETAEREIQHFFPLQSTLGLIKPHATSE /HKRGPSMVMILTKWNAVAEWRRLMGPT DPEEAKLLSPDSIRAQFGISKLKNIVHG ASNAYEAKEVVNRLFEDPEEN
2108	16009	A	2123	3	206	LRRLRQENHLNWRGGGCSEPRSQHCAAA W/VSNSETPQKKKKKKEKKKKKKNLPNS ALKKTYSQRGKLF
2109	16010	A	2124	23	401	IASGRPFFFFFFFFFFWPPPPGGYPHFS FLKKKKKRGGGGGKSLLPPGKGPNPPK\ WGFPLFPPPLFPQKTPPPPFFFYKTPPI PPQGPRGGPLKFTPPGGGGGNPPTILLD KKRGVLGPPPFFWTN
2110	16011	A	2125	3	439	MFDVSLLTFTHSLFHFSPQFHRKCELST LCDGGELRDHILLPTSICPITR/DKCSC PGEGC
2111	16012	A	2126	1	213	HFPVENESAPG/FKAAGDLLTLLLGGNA AGDFKLKALLVYPSENPCFLKGSFKPNL PLVWCSHKKAWVQLG
2112	16013	A	2127	104	419	NSFFFEEELYNPFGGLGKKTFFGGGEEF GHTPPENEALGGKNKFFTGEGGQTFSNN GEEKSVSFWISIEKILHRALL/AHALCK NCVVELNFGQKEEPFFPPPEEF
2113	16014	A	2128	399	140	PPPPKNFFFPPKGKFFG/RG/VGPKFPP PKKRVFSQKPPRGFFYPPLKKKNNPFPP PGNFGPPRGFFKRPPPFFFFFFFFFFF FFFFF
2114	16015	A	2129	10	457	KTSWTWCPVPVVPATQKAE/AGGSPEPG RSRLL

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2115	16016	A	2130	409	0	PPPPSPPSPPPPPPPS/PSPSPPPPPPPSP PSSPPPSPPPPSPPPP/PPPPPPSPPPS PPPSPSPPPPPSSPPPSPPPSPPPSSSS SSPPPL
2116	16017	A	2131	317	177	FFFFFFFFFFFFFFFFFFFFLRLQIFFF FLPILIFLFLFFLFFFLFF
2117	16018	A	2132	3	542	EPWSVAQAGVQWRDLSPLQPLPPRFERF SRLSLPSSWDYRRLPAHPANF\QFLVET VFRHVGQAGLELLTSGHLPALTSQSAGI TGMSRTS\RPGFLFKV
2118	16019	A	2133	146	439	LKSVTSIAKTWIQPK/CPTNSEVDKCPS TVKWIKKMWYI/YFTMEYYAAIK
2119	16020	A	2134	95	1	GRVDAILAHCKLR/LPGFTLFSCLSLPS SWDC
2120	16021	A	2135	2	380	THTHHTH/THTHTHTHTHTSLS
2121	16022	A	2136	4	337	KRNNKAWMTVHLFTAWFPEYFRPTVETY CSEKKIPFKIL/LLVDNAPGQPRVLVEM HKEMNVVFRPANTASILQPMNQGGISTF NSYYLRNTFHKAIVAIDSNSSDGFGQNK
2122	16023	A	2137	2	356	PVSSSQVRASVYLKKKKKKGPPPEGITN TAGEKPPQSFRGKG\PPFPLISPKKEPV I\SFLKNFGPCTIGKKKPPHPPAKNGGP LQ/RPPTQGGGRGKKKGKNNQRPLSGLG GNRSPKPPF
2123	16024	A	2138	2	357	FLGSSDPPPSASPVGRATG/RVFFFFFL VEVVSHYVAQNGLELLDTSNPPAVASQS VRITCVSHRTWLLSPLYKIIQVCVSK/S PELEQSEDKSLKK
2124	16025	A	2139	379	16	LLQVRCFVSTVNRGSSCQKTIQVYYVQE AIPPSFLLSPFLM/PYTKINSRWIKDSN VKPKTIK\TLEENLGMPLNIFFTYQLLW LYLHPESQLEICNSFRALQEGNLIIFFI GRVGRPGTTGL
2125	16026	A	2140	73	411	NYLLNNLFFFFFLERGLTFAPRAGGWGG NLTSWNLGPPGPNKPPPFPPKRP\GTPK PTLKEGLFGPFFKTTGFPPGAQKGPELPG LRGPPGLAPPRGGNKGGNPPPGPLKTFN G
2126	16027	A	2141	46	421	AGVSWRDHSSLQPCLTSRARAV\SHLSF LSSRDYGPMPPPPKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKQ
2127	16028	A	2142	26	479	LAYLLPSPVMYKPQNWRTILQSISNKGL ICRIYKETLQLNHKKTNNPIFFKWVKKS KHFTRGAIQVANK\HIKMKLNIISVYGN AQKNTMRYHHTPIKMKKMGCALWLTPVM CQEAGYILKMYPGWTPYPGRVVGRPTAP ALPPRGTFPRD
2128	16029	A	2143	9	166	QNRLLARLTKKKRGKNQAHP/IKNDKGD ITADPTEIQASIREYHKH
2129	16030	A	2144	1	328	LEKESRPPPPPPPPPPPPSPP/PHPGS LPKPLGLQPLPRPEVSFLTEYLPKLKAC EGGGVEIAAASFPRIYLMGMCSRQDRIQ KDIDVVIQKSRAEDCLFAGVKAILKA
2130	16031	A	2145	1	440	KTFLRSLWQLVE/CYISSGLIDDHRRPM ALTPRHPRSGITAPRPRPQPPGRVGIPE PTALSPSPGPPPPPCSTPGRCQVPSLER RRKEGREPPSVGRGCGGHGISPSSDIFF HLNFCLAHPPDLFVFVCSISNQLYIFHE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						KKKKKGGR
2131	16032	A	2146	23	422	IASGRPFFFFWGAPGGEEGKKNFFWGPR GGKKKIRGAPTPRGKGNPPPKPWGKKGG APPKNLGLFGKKGAQRGPPGWFKTPGKK KSPPPGPKKGKKNRGRP\GPPPQIFFKP FFSTGEKNPLGKKTPNWRLLPW
2132	16033	A	2147	3	372	KKNTPFFLTPRGPPPPPRGPLSPPPKRA TPPPPPFKKKKPGFPPKKKNFFPPPGGG PPPP/LPGEKKGGYF/WW
2133	16034	A	2148	363	1	FNCRWFETKSHSVPQAGEQWHSFGPLQP LPPGFK\EFSCLSL
2134	16035	A	2149	2	361	FFFLVETGFHQVGQGGLEHLTSDDPPTF GLP\GGWDYR
2135	16036	A	2150	387	2	KKSFFLVSPARVQWGDPFNPPIPGSNNF PFSTPPKTGVIRGPPPARKIFVFFIKTG \FPQLGRGVLKSLPQ/CDSPPPAPPKGG VSGGNPPAPPFFFFFFEMESHSVSQVGV QWRNLGSLQPPSPGFKQF
2136	16037	A	2151	23	421	IASGRPFFFFFFFFFFFFLGGRGVFFYP PGGGGGPNFFKKTPFPPGKKKFFPPPSP KGGFLTPPPPPPFFFFFLKKKGVINGGG GGVKISPPGGTPPFLPQKGG/NKKGGPP PPRKKKIFLFFFPGAIKQRPPP
2137	16038	A	2152	3	366	VIWAHCIFHLLGYTDRPCLKKKKKGFPG GEKMGLKNFFPPLGKKPPPPQIPNFWSV IEKPPRGFYLGGAAPPKKFFLLKP\GPP FFKEPPPPKKKGGASPPLKKKFFKGKKS PPFFFSDPTS
2138	16039	A	2153	423	253	FFWGGGAPIFPPPKKGFFPKNPPGVFFS PPKKKKIFFFP/HPVNFGPPKDFFKRPP P
2139	16040	A	2154	287	1	KEMNKKKNPKKKKVSKKISTAFYNKTLN NINFF\FAFFFFFFFFFFIFFFFFFFFF FFFFFFFFFFFFFFFFFRFLFLFNYKQTA QLMQHSAPTRP
2140	16041	A	2155	433	2	RRVLFIFPPL/HPFSPPPLPFSPFPPPP PMKFFSPPPTFFYFYKSPPHPP/HPPQV VFSPPTPPMPFITPPPPPHTSPSFPSFF FFFPFFFFFFFPSFFFFFFFFFFFFFF FFFFFFFFFFFFHIISIKGEIGRSSVVR VMSRTRG
2141	16042	A	2156	69	606	LWWPPLSRHAAYRQWPGPTAPRGLGHKV KGPGASPA\PCGAAAGSTAQG\GGGAAC LPGPAAGAVTVVPAGPGGGRATGPVLQR PAGAGQPTQQGQHDHAGRVLWQHGIGRP GAHRPGPCAP/DSAPRAPGGRCG
2142	16043	A	2157	449	0	SSPGSSSSCSPPPPGGGVGFFL/YKPPQ KKPPPPPVGGPGFFPQKKLKSFFPLPPP FFLGGGGPPPPPPPKIKSFYPPPKKVSF PPPPKKAFLPPPPPPLPPPPPSPPQPPP LF
2143	16044	A	2158	241	5	KKFSFFPPGGSQGGFFGSLQNPPPGFTP FFCLNLGKKWGQRGPPPRPNNF/SFFFF FFFFLVETGFHHISQDGLDLLTS
2144	16045	A	2159	434	2	LGSASQLGCSGVRDPLEEAVCPFSDLQL CARRTTALFKAVRQGHLSLQRLLLSF\V CLCPVPRSGAYRGRQASLSCGGLHPVQA SRLLCLPKQAWAMAGAP/PPASLQPCSL

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						ISDCCASNQRDSVGVGPSEPRAGYNLLV RCFLSP
2145	16046	A	2160	448	84	FLGGFFFFFFWFPPPSPPQKEAL\QKKI FFVFFSPESNQKNFFFSFSERGGPPNFL FKGGGR\FSPWFLFFFFFWFFFLVVFF FFFFFFFFFFFFFFFFFFFFFFFFFFF FFLGKCPLKYT
2146	16047	A	2161	3	156	RGCSEPRLRHCTPAWVT\KETVSQKKKK KFLTLGGKTFKNFFFFNRAPGTFP
2147	16048	A	2162	412	37	FFHSPPPPPPPAGGAVFPPKKKKKSPPP PTPLLL/RGGGGPPPPPPPKRGPPPQKP KRGFFSPPKKKKKFFPGPGGPPGPPQKT PPPPPPPFFFFFFFFFFFFFFFSLFFF FLRTLWRKGRGRGI
2148	16049	A	2163	5	370	QSSCVQWLVPVVPTIQEAEAGGFLEPRS ERLQ/CSHCTPAWA
2149	16050	A	2164	437	36	FFFFFSEAESCSVAQAGVQWHARSLPQP LPPG\SSDSCLSLLSSYMCLSPRTRGS
2150	16051	A	2165	3	623	RQGFTLVAWAGVQWYDLGSLQPPPTGFK RFSCLSLPSSWNYRHAPPCPANFVFLEE TGFLHVGQAGLELPTSGDLPASASQSAG ITGMSHCA/RPKVCSYHLFF
2151	16052	A	2166	337	0	PPPPPPSPPPPS/PSPPPPPPSPPS\PS PPP
2152	16053	A	2167	350	156	AEATSKIRCQKCYIMIAGHSGTRLQFQL LQRLRQENHLNPRA/RGCNEPRSHHRTW PTWYISKSFLA
2153	16054	A	2168	1	337	DERSLSQRSRSWSYNGYYSDLSTARHSG HHKKRTKKKK/IKKKKKKKKRGPFKKKG PLKTRKKPRGGLLKAHPFWGGPPPGFFL TGEGAPPPVFFKKKKKKPPLGGKGGFLW G
2154	16055	A	2169	2	606	RVLRAVAAHEEPDKEGKEKPHAGVSPRG VKRQRRSSSGGSQEKRGRPSQEPPLAPP HRRRSQPP\HPGPLPPTNAAPTVPGPVE PLLLPPPPPPSLAPAGPAVAAPLPAPST SALFTFSPLTVSAAGPKHKGHKERHKHH HH\PAPMVIPAPAEPI
2155	16056	A	2170	311	2	GLQPLGLGSVKQCMDLACVPETVCVCVC VCVCARAHTPVCTQGCVPESTQCVCMHV C/VCVWACTCVPVCMHTCVGVGASVCMQ RNELGRWAWENDAIRQQRC
2156	16057	A	2171	78	337	NTPNSIYKAMSLKGPITGTFLPNYPGHK VCVCDTYLCVYQHTHTHTHTHTHTQAFP HI/HIYTHT
2157	16058	A	2172	2	278	KNRLNPGGGGCSKLRSCHCTLAWAT\SE TPSQKKKEKRKRKGRKRKRKKKIVYTKI EKGNAKMTGESFIHFCKKSSSVPQVALS AEYRCSST
2158	16059	A	2173	2	365	FYHVGQAGLKLLTSSDPPALGLPKCWDY RRE\DCAQPNVKS
2159	16060	A	2174	195	389	FRVFSKLKYYYDFFRGRISLSCPGWSTT PGFKRLSCLSLPSSWDYRRPPPCPAN\F CIFSRDGVSP
2160	16061	A	2175	23	374	IASGRPLIFFFFFFFFFFLFCRGGGPPF NPRGKERGGFLIKGPPPPGGKKNFWAPP PGGGEIKRTPPPPGVFFFFLKKKGFSFG GGGGKK/PPPPGEPPPPPPQKGGKKKKK

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						TRGPLF
2161	16062	A	2176	2	158	FFFLKQSLSVTQAGVQW\PVDSLQPLPP RFKRFSCLSLPSSWDYRCVPQCPAN
2162	16063	A	2177	340	120	PRFHFLASPSEMSQMTVKAKTTVPASEC AYPKIEPFFPF\DPRGSES\FDKLGVHH HPLFPLSGEPLMILHKNTH
2163	16064	A	2178	3	256	YLKKDLNVNQKTLTLLE/EKQGK/HLHD MRLCKEFLNKTSKAQYILKKISQY/LIK VQNFNAVKDPVKRMKRQASD/WENIFT
2164	16065	A	2179	95	1	GRVDAILAHCKLR/LPGFTLFSCLSLPS SWDC
2165	16066	A	2180	1	143	ARGERERERERERERERERERERERERE RERVFV/RERAALSRERGDKCERSGLF
2166	16067	A	2181	1	304	ARGQGHLSLQRLLLSF\VCLCPGPTGGA YRGRQASLSCGGLHPVRASWLLCLPNQA WAIAGAPPAALLPPCSLISDCCASNQRD SVGVGPSKPCVGYNLLVW
2167	16068	A	2182	3	163	FQRRSTESCGWDKDARSQSRSPPRQQAH GHHS/HTHTHTHAHTHTHAHTHAWTRP
2168	16069	A	2183	3	205	NFKLFCKGFFFLRQSL/DSVSQAGVQRH NLGSLQPLPAGFQLFLQPPPPGSKDTHP GVQRHDHNSLQP
2169	16070	A	2184	228	88	WFFRIYDSFFLVFLFVFFFFFFFFFFFF FFCVFTPFPVYFIQYVVYI
2170	16071	A	2185	287	3	SLFLAIPQWEFQRKIYLRKQKIVLLACQ PSKGLSIVQVVRGQLNSPVLKSQDPTP\ PRFKRFLCINFLSRWSYRHVPPRPDSFV FLVETGFLHLV
2171	16072	A	2186	252	105	VSISCHPQ\PCLIYTCY/HIDGYSNIHL CTHTHTHTHTHTHTRVELQGPA
2172	16073	A	2187	267	459	KHVPGSSYTWL/IFFFRGNFLKKGANFV PQGVLKGGNLSSLYPPPPRLKQYSCLTL LRIGNYRHA
2173	16074	A	2188	170	15	RSVMKDLNSHFSKENIQMANKRTKECSA LVVFREIK/TTMRCHLTPIRMATIKK
2174	16075	A	2189	2	504	DVTISTCHASAKVGTRLVFDHYGKIIQK TPYPHPRGMTVSVKQLFSTLPVRHKEFQ RNIKKGLG\RRSCFCFDF
2175	16076	A	2190	1	565	FFETESLSPRLECSGAISAHCNLHLPGS SDSPASASRVAGTTGACHHTWV/IFFVF PVETRFHHVSQDGLDFL/NLVIRPPRPP KVLG
2176	16077	A	2191	142	382	NTPPLLFFFVIRDRVSLCCPRWSGVAQF WLSATYASRV\KRFSCLSLP/SNWDYRC VP
2177	16078	A	2192	138	365	KHQYHHCC/LLKKKKKKKKKKKKKKKK KKKKIKNKKHGGPFKKNFW/EGQPRNWA GGV
2178	16079	A	2193	385	21	RGEIFFFKTRRKKFSPQGGRGGVFPPSP PKNFFFPQGGKFFGG/EGGPKVPPPKKG GFPKKPQGGFKVPPKKKKKIISPPGVIG GPPGNFLKGAPPFFFFFFFFFFFFFFF FFFLVRAVKLS
2179	16080	A	2194	415	56	PPPPTTAPVFSPPPPPRPFFSPPPPVFF FRSFPPAPPPPPLFFPPPSPP\PSFPPP PPPTRPCPPPPPTIPPPPPPFSPPPPPF FFFFFFFFFSLLPFFFFFFFFFFFSFL FLFFPSRLW

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2180	16081	A	2195	35	369	MKRPSPPPPTPPPPPPPPHPLLPPFPEK KTGPP/RGFFKGGERGPPPPKKKDPPP QKQKKKKKWGGGGGGGGQRKKKHPQKNP PPPPGRGGGKNFLWGRPRGPPPQGGGGK K
2181	16082	A	2196	2	266	SKPRSCHCTPAWATQ\ETPSYKKKKKKK KGLPLGGPGEKTIFFSLKPGQKAQPKNK IPFKKKIPFFSTPKGKKKKNFQGGPKKK KKEI
2182	16083	A	2197	1	277	ARGERERERERERERERERERERERERE RERERRHP/RPRERE
2183	16084	A	2198	1	285	ARGERERERERERERERERERERERERE RERERERERERERERERERERERGGAPP PRLYRERVLKKQRGRFLPPVRERKK/RS PVQTLPGY
2184	16085	A	2199	346	1	VPRHGLPCFCFPHQLQPPKRKKFNNRKR ALTSHTQFFVFETESCSVA/RECSGAIS AHCHL\CIMRSSNSPASGGAGSSELRFR HCTPVGQQTEIWSPKNKPIKKEEGCPYC QFLSC
2185	16086	A	2200	3	389	HEGMILAHCSLNLPGSGD/ASHVARTTC VHHHVQLILFIFVETK/FSHYAVQAG/L ELLSSSDP/PTSQSSRITGMSHH
2186	16087	A	2201	3	204	HECHCTPAWAT\SETLSQKKKKKKKKK IFPGEKTWGGWNKKKFLFLNRKFFLGKG LFHLKRGPLKLF
2187	16088	A	2202	69	379	KKKRVFFWGPGGSKPPT/SGNPPPWPPK GGGLRGLPPPPGPRGVIFKNFGKRGPPP PPGLKSWGPRDFFGLALQRGGISGLNNG APPFFFGVLKKLPPLFFVSKG
2188	16089	A	2203	81	379	KKKKKPPPPKKKNPGPKKQEGGPLRGPP TFSGGGGGKKTCPQKLKAAGG/SKKAPG PPPGAEKKNPALGGEKKTLGPNGRGPKR LRGLAKKGNPPSSFGGK
2189	16090	A	2204	1	341	GQSLPVSPRLQLSNGNRTLTLLSVTRND VGPYECEIQNPASANFSDPVTLNVLCEY LLF\PVAQATSPNPRSQRPGLSVPLSSK NADSPPTPRNPARHDFLPQANMGRPSLD QE
2190	16091	A	2205	2	370	DAPPRPANFVFLVKTGFPPVGQAGFKLP PPGDPPPLASQITGKG/HCAQPPF
2191	16092	A	2206	362	24	PRGSSSASSSSSSSSPPSSSSSSSSS SSSPF\PPPPVLKPPPPPPKKSPPPKKK NPPPPKKKTFFFFFFFFFLRRGLCPFGR GKRAKPPFQKKKKKRKRESSFYQQVIIH M
2192	16093	A	2207	357	3	AGQALWLARVIPVLWEARSYYVRISWYR NIVAMDSDSLDGSGHSKLKSFRKGFPVL YAIKKTHDSWEGVS\MSALIVWKSLIPS CVDAFEELTSSAEEVAAQVVGIATDLEL LVGCARA
2193	16094	A	2208	280	411	GNDVYFLVFLF/CLFEKESCSVAQAGVQ WHDLSSLQALPPRRMA
2194	16095	A	2209	3	392	PIIYEKYTQQINEMPRKLQHQQLALVSR NGPILLHDNAQLHITQC/LQKLNELGYR VLPHLPYSLDLSPTDYYFFKHLDNF\LQ GKHFHNQEDAENVSQKFVKSQSMDFYAT /GNKLISHWPNCVDCN

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2195	16096	A	2210	248	417	GILANCASIKDLISRIYKKLKQIN/KQK TNDPLKKWAKDMNRYFSQEEIQGVNKHM KK
2196	16097	A	2211	213	493	GKRFYFACPGKIGALQGFFKGGGPFFFF FFFLTPPPNTNYLTNKLKIKSPLCTFYF SNILGFYPSITHRTIPDAWVTA/SQSGP VLMRSIS
2197	16098	A	2212	159	413	LAPRVIFGPPKKPPERPPLFFFFFETES SSVTQAGVQWHNLSS\PPRFKRFY/CLS LPSNRDYKRPPPHPANFCTFSRDGVS
2198	16099	A	2213	455	60	NPRREVGPICPPPKIRVPPQNPQVGFYS PPLKEKTFTSPAPVNLGPPRDPFKRPPP FFFFFFLDFFFFYFTIYKTSAACPRSPP AQPRVARRPLVPSS\PPLPSLCLAPAPR GPGSLCPRGSLEGDNGSSPG
2199	16100	A	2214	2	243	LTLSPRLKCNGMVSAHCNFCLLSSSDS/ RLR/QENCLNLGGGGCSELRLRHCTPAW TTERDSVSKTNKKNSLKIFTCFFVDAA
2200	16101	A	2215	1	286	FSQLLRLFIC/SQGGRLLCCESCPASFH PECLSIEMPEGCWNCNDCKAGKKLHYKQ IVWVKLGNYRQVFPRTKRKYSIIVQTSF ILWIQSDLEIDR
2201	16102	A	2216	173	2	ITIFFFVRQGLTQAGVQWR\DLSGETLV ILPPLEAPCSLQSSWDYRRVLPHLPNFC IV
2202	16103	A	2217	216	4	VYPPSFMVFSQVFLSSTHISLSFSFFWN YLFIYLFIYLFIYLRWSL/DSVTQAGVK WHNLGSLQPLLPGFK
2203	16104	A	2218	14	228	KRSSHLFTDDIILYMENTKHSTK/NLLE LIKEISKVTG/YQKSVAFLYVNNKQAIK KTIPLTIASKRIKNSGQA
2204	16105	A	2219	244	3	EVLNQNSGLPRWPNILRAKASLRVPRQC SRGVVFSANGAGTTRYLYAKEWGGLGGG GCSKLRSCHCTPVWAT\SETLSQKK
2205	16106	A	2220	162	2	INMVGNLFFFGDRVSLCHAGWSAVAPSW PTVASTSL\VKQSSFLSLPSSWNHRH
2206	16107	A	2221	146	3	GRVDGVPWRNPGSLQPPSP\GSSDPPTS ASQESGTTGAHHHTRLIFVF
2207	16108	A	2222	239	2	SYISKPDKFPHDSSPEIKPVTVNWRNSF SFIFPFFFLFPEKESHSVTQAGVQWRNL GVSSYWP\AGLKLLTSGDPPALAS
2208	16109	A	2223	2	159	LNRDLGGGGCSELRSCHCTPAWAT\SES PSQKKKRKKKKKKKKGGRGRNSKI
2209	16110	A	2224	3	345	RFKLFSCLSLPSSWDYRRVPPRPA/NFF VFLIET\GFAILTSSKTERQSRLECIFG FYGLPCREKRASERRSVEG/HERKILFS FDFFFLGGTESCFVTQAGVQGCYLGSPQ PPPPG
2210	16111	A	2225	103	319	FSEEYRNVTNFLMLTMSCSCLTLVE/C/ WSEGYMATPCTILLLLFFQRHCLTLSPG GVQWCSHSSLQPQTPGIK
2211	16112	A	2226	2	110	FHHVGQAGLELLTQWSIHLSLPKCWDF\ RHEPPHPA
2212	16113	A	2227	2	178	IFLIFTFLEMSSHYVAQAGLEFPG/FKL TSRLSLLSSWDYRRPPPRLANFFAFLAK GDAA
2213	16114	A	2228	173	3	FIFIFISLFFIFFLRQSIVLSPSAVQSR LQPPPPRFKQFS\CLSLLSSWDYKRVPP

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						C
2214	16115	A	2229	333	1	HTPPPPPTFHSLCTEGAPPPPQNT/PNP PRNPFIIPLSRSHTRANEPSLSTPRTHP HSPRPPLLTHPHPNPRASAPPGSRYPPR ARHRERPRERPTQRERERERESVCVCV
2215	16116	A	2230	350	3	KKKDIPPVNIYAPNTGAHKYIKQILLDL NRDGP\HTITAGDFTTPLSVLNSSAESR CSRPFIISPSLVVGLRE
2216	16117	A	2231	277	1	QMHPARGHLPQALIPVQKPALISQGMSA SGSTQVSPFLSPCFWVEVNCSNTKVLT\ PFCGAGTGSHSFAQAGAHWCNRGSLQPH PPGFKRL
2217	16118	A	2232	3	335	ETRFHHVGQAGLEPLTSDDPPASASQSV /GITGVSLRARPGES/GSWKTVCCNNMS EPT
2218	16119	A	2233	29	448	CPSLRQAWHEAAIDEVRTGTYRQLFHPE QLITGKEDAANNYARGHYTIGKEIIDLV LDRIRKLADQCTGLQ\GFLVFHSFGGGT GSGFTSLLMERLSVDYGKKSKLEFSIYP APQVFTAVVEPYNFILTTHTTLEHSDCA
2219	16120	A	2234	1	365	GARLILVFLEETGFHYVGQAGLELLTSS DPPASA/FPKCW
2220	16121	A	2235	28	460	DRLIDHISKLGTRGLQGFLVFHSCGNLG \TGFGFTSLLMERLSLDYGKKAKLEFSI YPAPQVSTAGVEPYNSILTTHTTLEHSD CAFMVDNEAIYDICRKNLDIERPTYTNL NRVISQIVSSITASLRFDGALNVDLTEF QTNLV
2221	16122	A	2236	614	84	LAASLAACAQLSALAASHRMWALQRLRK LLTTEFGQSININRLLGENDGETRALSF TGSALAALVKGLPEALQRQFEYEDP\IV RGGKQLLH/SPHFFKVLVASRLVTLEAG HFCPCCAETHKW\AWFRRYCMASRVAVA LDKRTPLPRVFLDEVAAVRVCGHILQLG DTELQQHICHL
2222	16123	A	2237	1	393	GPMLAQLSVFRCGSTSAPNDLWYHFIEL PYHGESITMLIALPTESSTPLSAIIPHM STKTIDRWMSIMVPKKVQVILPKFTAVA QTDLKEPLKDLGITDIVDSSQGHFCQIT KAENLLV/SHILQKQK
2223	16124	A	2238	3	402	HVGQAGVQIGKACWELYWLEHGIQPEGQ MPSDKTIGGGNDSFNTFFSETGAGKHVP RAVFVDLEPTVIDEGRTGTYRQLFHPEQ LITGKEDAANNYARGHYTIGKEIIDLVL \DRIRKLA\DQCTGSQGFLGFP
2224	16125	A	2239	2	478	GRGGLHRIPVVTPLTPSFARGLVPSLAR GVEARNGAGPIKSYPRPGSRLKMQNGSK GSGLQNKTFHWEICDAHVNSKIQLKQ\H ISSRRHKDRVAGKPLKPKYRPYNKLQRS PSILAAKLAFQKDMMNPLAPAFLSSPLA AAEAVSSALTLPPRPFCFV
2225	16126	A	2240	255	2	FLFVKPHQISCPTKKGIKSFLVLCPLNF FLFWRQDLAHPGWSAVTQSWLTAASN\Y GLKQSSYFSLLSSWDYRCIPPHLGGKRP L
2226	16127	A	2241	365	11	EPPPPGGEKKKRGKPPPKKTPKKDGPQK KSAAFFGG\GKIKKKKGAFRKKKKKGGG PPPKKKPPPRKKKKKKNFSPLPPPKHTP

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						SLFQKPPTKIFLFSPPLLFLNILFFFPL SPFIF
2227	16128	A	2242	3	143	PNFLSPRLDCRGTIRGHCGLYLPGSCDP S/CLSPPSSWNYRSTPP
2228	16129	A	2243	132	2	MSAHCNLHLPGSSDSPASVSQVAGIMGA CHIF\VFLVQTKPHHI
2229	16130	A	2244	334	43	TSKHMKRCSISLATREMQNKTTIGGHFV PTRLANIQKPENAKYRQGCLMC/WCWVC NLASPLWKTIWHYLVKCLPYSSAIFTLG \IYPEEVLASSVPGT
2230	16131	A	2245	312	2	PPSKLPEKNFFFFFFFLRQSL/SSVAHS VVQWRDLGPLKPPPPESKQFSCPTLLSI WETQTALSQDCATALHPGGQRETLSHKI CVCVCVCVCVCVCAVCIYIN
2231	16132	A	2246	3	230	RAQAMVETSRERCLLRPPQIETR\HVAQ AGLKLLASSDPPTSASQSAGITGVSHHT WPQPLTFCPHAKSLPFINQI
2232	16133	A	2247	2	214	GRVDLVIQAGVQWHDLGSLHPPLP\GSS DLP/ASDSQVAGTAGRFHYAWLIFF\VF FVETGS/HTQVSNSYDVL
2233	16134	A	2248	3	139	EGVQGCHHNSLQPPTPG\SSDPPTSASI EAGTAGSHYHVWLIFLLF
2234	16135	A	2249	3	160	EGVQGCHHSSLQPPTPG\SSDPPTSASI VAGTAGSHYHVWLIFLLFCFEGDAA
2235	16136	A	2250	319	3	GQKRYKIFLCFFLFGWLVFLRWSLTLSP RLERESVSKKPKSQKPPIKKPKFTPREF KEVLAKYGTKFFFVFFGLFVWFFLRWSL /NSVAQAGVQWRDPGSLQASPRP
2236	16137	A	2251	15	394	FVSFSFFPSFPSHLFFSSSSFPPFLPSF HFSFLPSDRPSVVPS/FLPSFLP
2237	16138	A	2252	60	306	GRERILEEIMAEDFLNLMKDLNISIQVA QQIPSKMNSKRPHRYQHFRSQSQRILKA TREKQLATYKGSSVT/VSPSPGPQTVNS
2238	16139	A	2253	3	351	GFHHVDQANLKLLTSSDLPASTSQSTGI TGI\DHCTQPNFPI
2239	16140	A	2254	150	2	RPRRPDHSRLGAGDQPGQHSKTPS\HQK KTKTSQAWRHAPAIAGTRQAEA
2240	16141	A	2255	357	1	LNLNLSLTLYAKINLKWITGTNVKHKTT KFLGGKNGANLMDTRLDNAFLDLTSKAQ LTKEKIDKLNFIKIQTF/CSIKDLLGNL KRQAPEEKKILRNHISNKELVSRIHKEV PKLNNKK
2241	16142	A	2256	397	1	FSLFPPVGGQGGFFSSCKSPPPRFRAFF CPNPFRKGGNRGPPPHPGKGTLGFFFFF FRQSFALSPRVEYNLCLPGSSDPPASAS QVGGAPGLPPPAWVNFGIFFF/CFFLRQ SRSVAQARMQWRHLGSLQAMP
2242	16143	A	2257	2	132	TLTLTPRLECSGTIS/AAHCKLHLPGSR HSPASAPRVAGCGGGHL
2243	16144	A	2258	214	347	KISLILGVHKICCEF/CFFEMKSRSVTQ AGVQGHDLSSLQPPPPGL
2244	16145	A	2259	347	2	FFSFFFFFSEAESRSVA\RLECSDTVSA HCTLHLPGS
2245	16146	A	2260	333	1	SDQRWTENAFVELRDEGFACPSFSEL/R STPSTSGEEVENFEKKLDECITRITNTE KCLKELMELKAKAREPREECRSLRSRHN QLEERVSVMEDQMNEMKREGKFREKRT
2246	16147	A	2261	2	357	SPRSCSVYGIAILLFLYFLYKLAFALLY

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						GLALNSFLHEIQEP/SLASGSGPLSRNS
2247	16148	A	2262	355	0	PPLPSPLSPPLSLSFFSLPPFPFFFPFF PLF/CPSFSFFFPSPFFP
2248	16149	A	2263	348	35	YFLKKGFSFFPRGEGRGKDSRSLKQLTF GFKKP/SCPSFLRKW\ETRLCPPAQKIF FFFFFLLEMGFCYIAQGDLKGSSQSSGI TGVSYHIWPTFIGHLTMCLAKC
2249	16150	A	2264	270	92	DRPARRKMFFTYSSRLFFFFFFFFFFFF FFFFR\FFFFFFFFFKFFFFLFSRWSLM IFIS
2250	16151	A	2265	1	417	FRPPAGVQWRNLISLQSLPPGFKRFLYL SLPSS/WDYRCMPPQLA/NFFVFVVFDV VVVVVVVLVEMRLRHVLARLDIVVLICI SLMANGMEYLFLCSFAIHLPSLLKCRFT YFAHCLFLYYFLETGSHSVTETGWQWCI I
2251	16152	A	2266	344	427	LIGLCEDTNLGAIHAKRVTLIAQDLQLA
2252	16153	A	2267	310	417	RVPYGTLGSGPLATMAGFDDKLKPHMEG AAAPILVR
2253	16154	A	2268	186	464	NSCLSHNQRQLLFRLEKGMGPISAQEKL VLHTLSGFSGLV\VGWLVFEMESCSVVQ AGVQWRVHPPPRFKQFSWLSFPSSWDYG HVPPCPANF
2254	16155	A	2269	1	427	PEPPSLPPDGAKKQKTQKSKKWRICFLR KKKKKKKRKKQKKKKKKRGGGSQKKSRR GPKLTTETNIIILIKGGLKKMNYREIEK KLLFGGGGVIGPTPTQDIKGREEINYLE AVGREKQRFISLVK/TNVA/HEATRDTI FRGYL
2255	16156	A	2270	399	44	ISFQLLLPITVLPGHVRVLMEMYKEVHV VFVP\STTTFMLQSMGQGVTLTFKSY\Y LRNTFNKAVAALTSDSSEESGQSQLKPV WAAFSSLNASKNI/RDSWEAVKIPALKG VWKKWSLKM
2256	16157	A	2271	19	420	AAGIRHEERERERERERE/QRERERERE RERERERARRNIYHTYRPRPPRVFFFFF FFFFKKKRRGFLVPTPPGGGGAQKKKTS LEGGKGVFFKGGGKKTPLKNPGGWGEPP QKKNGGGGPPPRDPPPPPRPLF
2257	16158	A	2272	463	20	SYNIPLSQSLIQ/SRALTLFDSTKAERN RRGK\RSGKLQWEGSRGWLMRFKERSHL HNIKVQDEAVSYPEDLDKMDALNTKQQI FSVHKIALYSKKMPSRIFIAVERESMPG FQASKDRL/LLLG/ATAAGDLKLKPMLI YNSKNPRVPRAEF
2258	16159	A	2273	474	82	VGVWADFLKNTSQAQATKAKMDKWDPIK LKSFCTAKETISKAKRQPTEGEKIFANY TSDKGLI/SRIDKELKQPYRKNPNNPVL KWAKGWAQWLTPVILALWEAKAGRTQGQ EIEATLALFSGLFCQVFLC
2259	16160	A	2274	152	3	AEGRNGDGIIQKSSI\RTLLSNDKNPQN IHRRPTRFLTMLYQQNLCHLGL
2260	16161	A	2275	32	361	LGASARYEKPTVNLILNGERLNIFPIR/ SKTRLGYLLSLLLFNIGLAILASAINQK KEIQIIQIVKKKIKTQRKKKKNKTKKKK ALFKFKGGPEKEKGPPKNPFKTPPVVF
2261	16162	A	2276	329	487	EFVNITIKIATSLHYKAIVIKA/AMVIW YWHKNRHIDQWNRIESLEINPHICNK

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2262	16163	A	2277	2	466	AHHSCSHLLTTAAHYSCSPQLLTTTAAH TYSPPQLLTPAHHHSCSHLLTTTAAHHS CSPPQVLTAAHH\GAHTCSPQLLTPAHH SSPQLLTPAHHSCPHLLTTTAAHHSCSP PQLANSYRG\SPYCSSWSQTPGFRKSSH VGLPEPWIFHGLQVV
2263	16164	A	2278	4	467	KNVTQQGKIHIRDKLDEMWGNTSVFCTN HMKHQTNFNAKKCNVFKECGK\TACNFQ LTQYQISHANQKPYECQICGKPFRKRAH LTQHNRIHTGGKPYECKECGKVFICCST LIQHKRTHTSEKPYECLECRKTFRRSAH LIRHQRIHTGEKPYK
2264	16165	A	2279	383	3	FLCVCACVCVYVCMCMCACAC\CMCMCG CVCVCVCVCVGLRGLGWGAVVCRSWGPP LCFLLLGILPLKSRLLWLPRRTISICTL PSAQGPLPAPGFGKYASNTTGVKGSSSV FSLLSRITALSHLHW
2265	16166	A	2280	47	219	VCSELKSCHCTPAWAT\SVTLSQKQNKT KQRRTLGSIFFQHTFMHLKKEKSLILQK W
2266	16167	A	2281	294	160	NKTFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFLFLF
2267	16168	A	2282	68	490	RTFAYPKPPVFGSHSGKTTIPKNARGSF PS/PPLPFPCPSPSPGPSPVSCLPPRLP SPSPSPSLSPISRLPSP/SRSPSPSLS
2268	16169	A	2283	3	454	CQSAPLGGASQLGYSGVRDTLEEAVCPF SDIWLCAGRTTTLFKAVRQGHLSLQRFR LPFVWLCPAPRGGVYRGRQASLSCGGLH QVRASRPLCLPTQASAMAGAPPPASLPP CSLISDCCASNERGSTGMGP/SEPGTG
2269	16170	A	2285	1	452	LKDSGRDYVSQFEGCALGKQLNLKLLDN WDSETSTFSKLREQLGPVTQEFWDNLEK DTEGLRQEMSKDLEEEKAKVQPYLDDFQ KKWQEEMELYRQKEEPLRAELQEGARQK LHEL/QEELSP/LGQEMLDRARAHVDAL RTHMAPYSDELRQ
2270	16171	A	2286	3	266	NSSPPSSGHSTPRLAPPSPAREGTDKAV SALKSPQPNRGMGRGQR/PGLPS/DTAT ITPHTSGFPKQPQLSLKVQTQRAKGRLS HWDLEP
2271	16172	A	2287	274	453	IYTFVKSSSKTLRPRHIDQWNRIENPEI KP/EYSQLIFDKANKNIKWEKDTLLNKW CWDN
2272	16173	A	2288	81	487	TVYFKPTVETY\CWDKKKIPFKGLLRRD NTPCYPKSLLEMCEKINIVFAPATTTSS /LKPMDQGVIVTFKSNYLKNTF\RLGEG RKKKKKKGRKKSFHKALAAINSDSSDGA GQSKQKT/FWKGFSIPNAIKNIQDPWE
2273	16174	A	2289	75	469	SRGVAGAPPKPSPSTPSPGPLDVTPGPH SSHHAASPGP\PPPPEPTASSMASAP\P PAPQPTPL\PPATLGPPSAGPE/PSPGS CTSTGWGYSFCCPRCRRWMRWQPPQQGP AWHWWPREFP/PPPRVSGS
2274	16175	A	2290	256	55	PTQPLRVELTTVTLRCDINKWDYIKLKS FCTA\KKRQPTEREKIFPNHVSNKRLIS KIYKELIHRI
2275	16176	A	2291	497	29	SLTHRVAGGAAVTPLAHAGARQIFFLGD PHPTSSLLGWGPAWDPCAFQVSDHPASS

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						RVGKTLLSCPGGGRLPWVTCPGGGQLSC LTQMHLTPAGMCSPCVCVCVCVCVCVPN GMCPRCMCVCVCPCRDVY/ICVCVCVCV CVCMCLCPCWDVFTEL
2276	16177	A	2292	141	392	SCSTEVKQPKIGVREVDFVAAPGIAPSS PQKKQTTSTSSLKSLLRLSKVRFLFNIV LDVLAREIRQEKEIKGIQ/LGKEE
2277	16178	A	2293	14	291	YVGTEGISFISFMRVTNYMTRHLATLRE S\CYSR\VYPRFIEFLRFDIQSTGQ/RI TSRQHPPR/DLRDALLYLNRRITLVRTR CKSVAKRPPGSP
2278	16179	A	2294	110	293	LLSNRSLAIASLCGGCNELRSCHWTPA\ WRQRETVKKKKKKKKKPGWGFLNPPPQR GKLCF
2279	16180	A	2295	96	313	WNGCYLLSNRSLAIASLCGGCNELRSCH WTPA\WRQRETVKKKKKKRKKPGWGFLN PTPQREKLGFLKRGPGF
2280	16181	A	2296	234	2	CCLETTRSLFDKGTKENTQWGKDSPSNK RCWKNWISTCKRMKLDPYLIP/YTNINV KY/IKDLNLRPEITKLLEENLREK
2281	16182	A	2297	334	6	KLFSPPGGGGGPPPPPPKKGWVPPETP\ KRGGGAPNPPPPKGGGAPKPPPQKKNSP PKKKKKIFCPPPKKKGPKGVFLRGPRGP YRVFLKGPPLFFFFLKKSWRPLAMYA
2282	16183	A	2298	467	8	LPGFKASTDRDN\VAGDFKLKQMLIYHS ESSSALKNDTKSTLPVLYRNKEAW/VTA HLLIPWCTEYFKLIAETCCSERKISFKI LLLI\DNAPSYPRALMKMFKINVFMSDN TTSIVYSTDQGVILTCNSYYLRNTFYKA ITAIDSDSCRMPQEGN
2283	16184	A	2299	1	449	SIYLSIP/FNLSINLSIYLSIPIYLSIY /HISVYIYL/SIYLSSIHLSAIICLSIF QSISLSLSINLSTYLSTIHLSLSSIIYS SIIYHLSIH/LSYYLS
2284	16185	A	2300	1	445	QAGLQLLTSGDPRTSGLPQCWDYRC\DH RSWQT
2285	16186	A	2301	241	22	KWVLGTCACVHVFICVYMCLYVCAWV/C VSMCLYVCACVCMNQC/VTVCMCVCVCV CRFVCVGIPPHSKWISIG
2286	16187	A	2302	3	478	GGQTETLLTSQRKGGWPEALLTSQMGRP GRGAPHIPDDEQPGRDAPHLPDGAAGQ\ SAPHLPDGE\PGRGAPHIPDGAAGQRRS PLPRWGG/ELGRGAPHIPDGAAGQRRSS HPR/PGRPGRGAPHFPDGATG/Q/DGAP HFPGIPPDGT
2287	16188	A	2303	440	41	KSHHLSFLSFLLFFFP/TKSHSVAQ/CW SAISAHCNLCLPGSSHSSALASRVAVTT GVYRI
2288	16189	A	2304	2	395	FFLVKTRFLHVGQAGLKLPTSGGPPALA SQ/SL/RITGMSHRTQPE
2289	16190	A	2305	184	2	SIKKPKPLVNLRNH/NT/WQGAVTPACN SSTLGGRGGRITRSGVQDQSGQRRESEF LRLGYGLD
2290	16191	A	2306	86	472	IIKLCKWQNK/RFEAGSLVPEMGFYYVT QAGLELLFSRDPHTSASQSAGITGAAFH QRWSVGTVLLQVDRGTPPVGDCGSRTPQ WPGQAFLRTALKSEAHPPHSSTDVTPVL WSEGSPCLLSPPSLSFTG

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2291	16192	A	2307	133	2	RVIHVVVRSHPAIP\TTREAEAGESPEP GGGGCNEPRSCHCTPAW
2292	16193	A	2308	3	369	LTTAFPDFPGSTHPLTSASQVAWATGAH HHSWLIFVFFVETGFHL/SELLSSSSPL ASASQSAGITG/REPPCLTSPFFF
2293	16194	A	2309	253	365	TDYFYLFIYLRQSL/SSVAQAGVQWQDL GSLQPPPSGFK
2294	16195	A	2310	362	0	TKAQQCVHENHFKLKDANTLNIKVWRNI CHSSPNQKKYGLAILNLDKSGFRSRKDT GDEE/HFIKIKKSVIQEAIIIINIYA
2295	16196	A	2311	167	2	LCYCVIFVFFIFWRQSLTLSQGGMQWCD HGSLQPLPP\GLKRSSHLSLPNSWDYRR
2296	16197	A	2312	67	482	DHLIPGGGGCSELQSHPCTPAWVTA/ET LSQKKKKKREK
2297	16198	A	2313	188	437	AGFFPPENQLTNMKVRKANESDPWGVKP ESDESETHGSLSLSLSLFFLFIFLRQSL /NSVIQAGVQWRNLSSLQRISP
2298	16199	A	2314	41	325	TTTLFXRVRQGYSSLLMFLLPFVCLCPA GRGGVYRGRQSSLSCSRLHPVRASRPLC LPTQASAIAGAPPPALLPPCSLISVCCA SNEQGSVG*DP
2299	16200	A	2315	417	0	SPPRNWDYRCVPPRPANFVFLVEMGF/Y HVARPEFGLELPTSGEPPTLA/FSKCWD YR
2300	16201	A	2316	98	288	LMAVVPATWEAEAQESLEPGGWGGGEEG CSELRSCHCTPAWVT\SETLSHTHTKKK KKNGAAL
2301	16202	A	2317	1	410	LNHIPNLSLTKRKPSPHSLNLKKKKKKK KKKKKKKKKKKKRGGGVKKKPRGGQKKK GGEKKNFPSKKGGKKKKRGEFGKKNFFG GGKKREKTPQKKKSPKGKKKNLR/EERG EKNPKRGGEKKRSSSPRNNNLRGEKK
2302	16203	A	2318	249	3	PLKASSPPKAFNFCREVGPICPPPKKKV P\PKIPKLVFIPPPIRKKLLPCPPPLTL APPRVPLKRPP
2303	16204	A	2319	2	393	AHLGLPKCWDYRHEPPRPAPLFLLNSYF GLDLLT/S/GDPPALASQSAEITGVSHC AQ/PEYVY
2304	16205	A	2320	389	2	RGNSNIGGPGPLRGKKFSPPPPLKNWGT KLGPPPPPPPFFFFFF\GKPGFSIFFKPI LKFKGPKKPPPRAPKNGGSPGPGWFFFF FLSNFTQLPGIKLSKGGKKNFASPPPPF FFFVHYKTGYPSATPDAW
2305	16206	A	2321	389	206	FQWRWGF/NHVGQANLELLTSNDPPASA SRSAGTTGMSHHAQLKNYFLMVRMWRNW IAVGM
2306	16207	A	2322	371	42	SFPPQSGFFSPPPPHEFFFPPPPSFFSW VGVRQIPPPPKIFSSPFPPGGFFSPPPE R/VDFFFSPPPFFFPPPSFFLSPPPPFF FFFFFFFFFFFFFFFFFFSFFGVKKRK
2307	16208	A	2323	82	386	PFLTQKYFFTPPEEGFLKKPNRREGPPS PITDPTLWPNMMKGIVPKAPPIIFMGGG INMTFSGFVTTKAPFPRPLRFNPMLRQG FDLLTLKAS\WGSSASWY
2308	16209	A	2324	1	413	RGSGDNRHGPPCRVNFVFLVETGFLHVG RSGLELPTSPALASQSVGITGVSC/RPP PQASY
2309	16210	A	2325	58	400	SETLVSKKKKKKKKTPPPPKNPKKKKNP

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						PPPPPPGAKKGPGGKF/PPPPIFQKKRGG FKK/SPPKKPPKKKKTPPPLGKKGPPPP RGGPLGGFPPPPPQKKNGPPPPKKKPPF FFPPK
2310	16211	A	2326	462	306	AHHNLRLPGSSDSPASASGVAGTT/GMC HHARPILYLSGDASALLHCFSSAQLF
2311	16212	A	2327	1	393	SRPPSRTEKIRNFFFVETGSCYVAQAAL KLLDSSDPPTSASQSAG/ITGMSHRAQP TS
2312	16213	A	2328	391	2	AWPKETKAGWIIPRSWDRGSWVSQPYSA LTSSPESGFHSVTNGDSMTCLEDGKHSL VAPHGIPQRGSSLQDGVSFCPAPTMKPY LASTKM\RLHEARELGFFSFLSLRQGLA LSPQLECSGAILAHCSLNL
2313	16214	A	2329	2	115	GCSELRSRFCTPAWAT\SKTASQKKKRG KKKKGGVFYF
2314	16215	A	2330	2	406	AAAPSALALRDGWAVRPELDLLPPCGEE VAPGAHCLGCGPSPCLFLSPSHTRQSPP APTSSPGLSTSPPLVPTHVSAPHSSKGP PSIPGAQALRGCGLGGWDR\PSSPSLP/ PDVSPKPLNFAP
2315	16216	A	2332	226	377	KRKSKHITFLFKTLSWPDTVAHACNPST LGGQGGRI/TPRSGVRDQPDQHG
2316	16217	A	2333	3	191	CLSPGGGGCGGLRLCYCMPAWVT\NETV SQERKKERRKEREKEIKKERKKRKKERK KEKKKKG
2317	16218	A	2334	295	81	FFKPFFPPKKTCPEFS\FFWEKRGFPPP PLRSFFQNPPPKGGPPILLKGPPPPPSL GWPPPPPLFFFFFFLR
2318	16219	A	2335	375	8	TQIVPLPSNLGNKTRLRLKKKKRNEQGN IPTDTIDNRIKQIIQ/TYYEQLCANK\N LDKMDKALESHNFPKLKQRESLNI/HSA KEIHFI/ILNISTKKTPDPTGFTGKFLQ IFKEKKMAGHSGSHL
2319	16220	A	2336	399	97	FFFFFFFKQNLA/SVTQVGVQGQYFRSL QPLPPRVKPFSFPNPLSNRGYRGPPLGR VRQENCPKLKSKRFQLNKIPRLGKKKKL RFPKKKKKEKEKKIVKT
2320	16221	A	2337	411	57	KKPRSFSSCSSSPPFFFFFSPPPKKKIF PPPQIFWGPPFFPPPPPFFKPPPPPFFFS PQKKKKI\SPPPPKKKFFFKTPPPPFFF FFFFFFFFFFFFFFFFFFFFFFFFFF
2321	16222	A	2338	97	354	AKAPSLSLVLFSFSTFFLGIQGLALLPM LECRGAITAYCSLNLPDSSGPPTSAPSP TPY/RIAGATGTHHNALLLFKFFSRDGL PL
2322	16223	A	2339	391	45	LMFFHLSHKHRSGEAPSIHWSIYLSIHP SIHPSLYHSSIHLSIHSTIYPSTCLSIH /CISIHPSIYPSICPSVHLLAHSFIHST ICPSMHLPIHVSIQHFLSAQILPVSVFG EVSDI
2323	16224	A	2340	506	0	RDHEQLGIVRADKKKKKKKKKKIKKKKK KKKSSSSSSSPGTFFRG/VPLKDPVG
2324	16225	A	2341	203	1	VELRVRATEPGFNFLKGIYCTSMVDWIK KMWYIYTMEYHAAIKG/DRIMSFVATWM ELEAIFLSKLMQ
2325	16226	A	2342	402	40	PYPPKKKASPTDA\FSSSSSSPPPFFFF SPPPKKGFFSKPFFFFSPRFFSFPPFLK

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						PPPQFFFFGPLKKNFFFPPPALKFFFFK SPPPLFFFFFFFFFVEAGVLLCYSG
2326	16227	A	2343	181	1	QLKDQASDLLGKNGDEVKETIPSFLPSS LPPF\LPLFLHQFLPSFLPSFFPPSLLP FLS
2327	16228	A	2344	2	407	FVASQLGCSGV\RVRDPLEEAVCPFSDL QLRAGRTTALFKAVRQGHLSLQRLLLSF \VFLCPAPRGGAYRGRQAFLSCGGLHPV GASRLLCLPKQAWAMAGAPPPASLPPCS LISDCCASNQRDSVGARPSEPGAGH
2328	16229	A	2345	405	178	IIKFIYEKATA/LLNG/EKLKAFPLKLG TRQGCLHSLLVCNTVLEVLTGTLRQEKE IKGIIIEKKEVELSLFADRIL
2329	16230	A	2346	2	412	FKASKASLSPLLGANTAGDFKLKPGLIY HSLH\LKNYADSILLVLCQWNNKAWMIA HLFTAWFTEYFSPPLRPAQKKISFKMLL FIDSAPSQPGVLMEMYKEINVVFMPANT TSILQPMDQGVILTLKSYWLRDTFH
2330	16231	A	2347	2	397	ESLEPGRRRLQGARIMPLHSSLDNRVRL CLKKERKKEIGVLIRCWQECKIVQPLWE IVWYFLKKLN\ESPYEPAVPLLNIYPRE MKIHVYTNTCTQIFIVALFTIAKSGKWW GTVACACKPSSSE/WLRWVDYL
2331	16232	A	2348	3	423	EGCSELGSHHCTPAWAT/AESVSQKKKK PKKK
2332	16233	A	2349	49	262	QMCKGSNRRRGKRVGSRQISKKKTNAPI KKWAKDMNREF/DIQMANKHMEKCSTSL IIREMQIKSTMRYHLY
2333	16234	A	2350	356	2	FVTAPLHSSLGNRARSYCKEKKKVQVAA KAVLRGKFIIAYTVFKKRKISNINLSIS LKTLEKEEHTETKADGAQYVTKI\RAKI NKIETANETKSRSLEKTSKTVEGKCLRD ILLSAQI
2334	16235	A	2351	360	19	LDAQFLEVGLGELLFRSTVPTLQPPGCG ASFPVLNTLPF\SLSPSQSSSSPASLVR PWVAPPFLCPHGEPDGGPDSTTSLPFPG PAATGPAARLIQHPASRQPRPASHTHCG V
2335	16236	A	2352	360	0	NTFLAAFRLVFCQMTSYSLALLSHKLAL MPLNLSDLLTRWTHCMGELFFLDILAIQ NPFHTVFFLGHPEWGMESRFVVQAVVQW PDLRQLQPS\PPGSMRFSCLSLPNSWNS PSYGRL
2336	16237	A	2353	34	474	EGWRPCKELAARQVGCPHSCFSPHWQLL QKQEKTAGAVSVCVCTSTLCVCVCVCVC VCAQAMCVCAGA/CFCVCVCAGA/CLCV CVGA/CLCVCAEAVSVCVQ/VAVSMCVC RS/VSLCVCMQGQSLCVCAGA/CLCVCV CGIPPPVLCLN
2337	16238	A	2354	297	16	KFFFLKSFFFFSFFFLTPPRFFFFFPKK KKIFFFPPRKIFFFFLIPPPPXFFFFFF FFFFFFFFFFFFFFFFFFFFFFXRHGG WFEEITILTV
2338	16239	A	2355	3	315	PVTPATRETEAGETL\HDLGEPGGRGCG ELRSCHCTPAWVTEQDSVSKKKKKKRGA RFKESNFTTPGLQRNIFFLGALKLISGA GVLKRRDGKTLGFPQFNRPWG
2339	16240	A	2356	399	154	PGQRGEIPSLPKIQ/ELAGCG/GHLNPG

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						GRIFGEPRSRHCTPAWATEQDSICKSHS RSGLWCYKSSSVYLSTRGVWVRGIASV
2340	16241	A	2357	416	2	FFFFFSETESRSVAQAGLRT\QWRNLGS LQAPPPGFTPF
2341	16242	A	2358	209	2	KKNLVPWPRGGYFKSLQPPPPGV/SCPN PPKKLEYRVLFPQPSNPFFFFCIFSRDG VSPCCPGWSRTPD
2342	16243	A	2359	279	380	RGYNP/WPGAVAHTCNPSTLGGRGRQIT RSGDQDH
2343	16244	A	2360	415	224	FFFVFFFFLLITFILMLNLLPCHKFLFL QFLLGYLFLLYL\CAFFLLVALNIFITS FQQLDYYTF
2344	16245	A	2361	278	2	ISDPFRFWNIYRIHTGLISLIQISENCV SCQKFQILEHFRFQIRDAQSVLRK\RKA WTGAVAHACNPSPLGGRGGWISRSGDLV HPGQHSETP
2345	16246	A	2362	139	282	KKKKGGRGGGGGRGGGGXXWGGTKKKKK GGEKKNLWGGGKGGGKGGGS
2346	16247	A	2363	19	409	PKPPSVLGGGGPARYPSPLGGPNRPVPL GPGVGAPPGPPGKTPFFLKIKKIYPARG GPPVIPASPGGEGKKSPLPPRPRVPLTQ IFPP/PPPPGGPNQG
2347	16248	A	2364	159	383	HSHFKNLSSIIKKLHRNNTFTEHFSLSS SLNQCFLNLTVFYSHLGNFKNSN/SWPG AVAHTCNPNTLGGRGGQITR
2348	16249	A	2365	400	221	GRLRQENCLNSGGRECSEPRS/HLHCAP AWAT\EQDSVSKNKKQNKQKQTHIYTVL LCARH
2349	16250	A	2366	383	14	GGRGCNAPRSCHCTPAWVTERASPQKTK KQKNTHTKKRISSCCYKMEDPLRQA\TF LQCPRAEGPSQKAARMELMEKQEKNQGP ARHRRQEQPLTSRPCPDHLCVVLSQVSS TPAQGLSLLICK
2350	16251	A	2367	274	1	PRKILKARGKEHLASRGTMIRMTSDFYL QTMQARREWSKIL/NVLEEKIHQHRIL/ PVKSSFKSEEEIKTFSDKQKLRGLVTSR SDLGKDVK
2351	16252	A	2368	161	2	PFFFFSETESCC\VTQARVQWRHLGSLP GSSDSPASASQVAWITGTRHYAWLIF
2352	16253	A	2369	361	198	NGRLIFVFLVEMGF\TMLARLASCDPPA SASQSTGIRGMSHNSQLKCFTEFDSFC
2353	16254	A	2370	116	300	HLNGDAVEERDFMKCTVSGIIVAHCNLE FLG/SSDPSASAPRVAGTTGMCHHIWLI FVILVEM
2354	16255	A	2371	2	192	MKLDPHLSPYTKVNSRWIKDLNLRPKTI KILEPNIR/ITLLGIGLGKDSMTRNPKA IAIKTKLAR
2355	16256	A	2372	1	133	AGELLEPG\GRGCSKPRSCHCTTAWATE QDSSPEKKKKKKKGGF
2356	16257	A	2373	43	403	LHDSPALASQGAGTTGVSHHARPAAGIN SRIGQAEDRISELEDWLSEIR\RQSGRN MDKRMKMNKQNLQEIRDYVETKSM/NTR LIGVPERVGENGSNLENIFQDLIHENYK GKPIRLMVDL
2357	16258	A	2374	404	215	GQGGRITRAQKFETSLGNVVRPGSEAQE LLE\PDDRGCSEPRSCHSTPAWTTEQDS VSKKRRKC
2358	16259	A	2375	3	397	SKQLEFTQLYTKLNQLNKTKISDLKKEK

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						YPIRLFSKENTQMASRYRTKYSTWLIIR EMQIKTTFRHKLAALASSRCLLGLG\AT SAHCCTVGAPLW
2359	16260	A	2376	413	1	PKKGLFPKPIIWVTPGFFPPPRFKKPPP KKIFGAPKKKKKSPPPPAKKFFFFKGAP PPFFFFFFFFFFFFFFSGDSQERVREAM PVAGGP\PRPHSLSAPHAPGGTAWTPMH PVQTHKAQSPKLPASECPPPTTPLS
2360	16261	A	2377	398	247	RRFHHAGQAGLELLTSSDLPALASQ\SA GITGMSHHAQPSATHFQKHLVS
2361	16262	A	2378	2	143	QENRLNPGGGGCSELRSCHCTS\AWVTT AKLCLKKKKKKFFGKGGG
2362	16263	A	2379	417	90	FFFFFFFPGGGRLQVCPPPGILLFCFLY KGGSPPGGSTIFPPPPPGEVGPPGPPPP GGFFFFFLE/QGGVSPDGPGFFVLPTPK KPPPPAPQKGGEPKFKPQVWGPPWPTF
2363	16264	A	2380	36	427	VHPLNHHDQKGQASSTQKKKKKKKKKKK KKKKKKKKG/WKGGGAF
2364	16265	A	2381	402	2	NFFLKGRGWGPLPPFLPRGPPPRGGPQK /RGGLGGPPPFFFGSKTPPAGGSRTPMG QKKKGPPLPEGPLFGGAGQAPFLPPPVP RGGVPSPKKKKG/APPPFFPPPFFPPPP PPFFFFFFLRYNLALLPRLGCSGT
2365	16266	A	2382	166	5	THGHVIYVDQEMQMMIENM/WPGTVAHA CNRSTLGSRGGWITRSGDLMVKPRLY
2366	16267	A	2383	2	457	TSQPSLLSSWDYRSTSPRLANF\ILFYF IYFFFAFSVETGFHRVSQDGLNLLTS/S /IPSIPRIPKHWDYRHDP\RTWP
2367	16268	A	2384	2	417	GRVGFSQSNGNPSSLSFTLLKVDFEVTI PGEGKDRIFKVSIKWLAIVSWRMLHEAL VSGQIPVPLESV/QALDVAMRHLASMRY
2368	16269	A	2385	318	32	TMEIMLDKKQIQVIF/FEFKMGREAVET THNINYTSGPETVQWWFKKCCKGDESLE DEECSGRPEVGNDQLRAIIAHASADAWV DRDSGRCCCACP
2369	16270	A	2386	409	3	ISQAPSTPPRKRGFR/PPQKTSFLGPPF YAAFYQEKKFLFFSSDPPRETGDKGKQK GFPPPKVAPKKKGFFKKGPPPGKKKDPP SFFKHKSQPTRPPRAPALEGPRSR/SAA LQPGDRRR/PPSQKKPTRPPTRPPTRP
2370	16271	A	2387	415	10	KKGFFPFGPFIFLFPPPGFLPPPPPPIF WFSGFCPPPPPLFYFFFRGGPK/HILVF PLFFLPPPFFFFFPIFAKESPPKKGPGP LNFFFFGPKKN/SPPPFFFFFFCEMEFH SCRPGWSAKWHDLGSLQPPPPVFK
2371	16272	A	2388	410	95	KATMDKSDHIKLKSFYPAKETPTKVKTQ PPEWEKVFANYPSDKGLIPIIYKELKQP YG\KKSNNSIKKWAKDLNRYFSKDIQMA NRCMKRCSRPGAVAHTYNPST
2372	16273	A	2389	362	92	RFLFFFSPPPKKGFFPKPFFFFSPRVFP PPFFLNPPPKLIF\GPPKKKIFFPAPGG KKIFFLKGPPPFFFFFFFFFFFFFFFF PVENTFY
2373	16274	A	2390	131	487	ATEHEKTEKSSLSFFSISKRKKKMEKLH DIGFSSNFLG\RPKAQATKGKTDWTSAK LKICSSRDTISRMKRQPKEWAKTFANKS CNNKKPEKIDKNKKKKKKKFLGGALLKK TNLKPRG

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2374	16275	A	2391	408	145	RWSLALSPRLECSGVSSAPCKVPPPGVT PFSCLSLPSNWEDRCESPPPAQ/IVFIG EGFYILHGFF/RRGPKIRCFISGCPPPV LSFPT
2375	16276	A	2392	1	203	LPFFAFSVETGFLHVGQAGLEPPTSGDP PVSA/FPMCWDYRHD
2376	16277	A	2393	386	16	TPSAGGRHIELSLSTCPSCAQHQGKEHL EGGEGGGAQSLTTAPSSATSSQDPISAH AVEDKLSIRLETDILKTKS/WPGAVGHT CNPSTLGRRRQANHLRPGVRDQPGLVIC RPRPPKVMGLQA
2377	16278	A	2394	3	396	QLLERLKQEDRLSTGSQGCSELRSHHCT PAWATEP\DSVSK
2378	16279	A	2395	273	416	FFYSFLIKIRWKKQPGMVAQACNPSTLG GQGGRI/TLRTGVRDQPGQHG
2379	16280	A	2396	329	76	FIPIESACSQECLKPNLRQEW/YIFGTL KLIFFETESHPVTQ/DWSAGELL\DPRG RGCSELRSCHCTPAWATRAKLCLKHTHK IKK
2380	16281	A	2397	210	7	GGKKMYCRKPGGGGFFAAVWSPKGLFS/ RIWKEAPILSPQKKKKKTNNPIKKWAND ANRHFSKEGTQQ
2381	16282	A	2398	48	393	SILKTRKPPLKKGRGRRKKEKESVRTHV FFSYQSNAFPSKPLNNSMTLGRLLSFSF FLVHFFFYTDGILLCCPGWSRTPGLKGS SHLSFPKCWDYIHEPPHPAYHS/LFCR
2382	16283	A	2399	128	383	EEAPKHFPKPNLH/QKKVLVTAWWAAAG LIHCSFLNPWETITPEKYAQQTNEMHQK LQCLQLALVNRKGPILLHHNVRLHITTH AS
2383	16284	A	2400	54	384	LFTFILNSVFHTYMCLYFWTLFFSVNPF VSMPIPQCLDDSSFIISLDSEINPNIYS QLIFDKKTQRGKNSLPDRWCWENCIFTY KRMKWDPYL/SPYTKIISNWMKDLNIK
2384	16285	A	2401	393	1	HRGENTHQQGGGLSRWRRHSRQRGTSRW IRHTRQWGPSRWITPSRQRGSSRWRKRS RAGDIEVEKTQQSEGALEVRIRSRQRGT SRWRSFSRQRVSFRWRICSRQRCSS/KV RRRSRQRGTSRWRRHSRQR
2385	16286	A	2402	1	330	RPPPPPHCWDYR/HEPPR\QPTLWVIFK LSVETRLCYVAQIGLELLGSSKESSRLD LPKCWDYRHELLCWMVIFQEKLV\SGFL FKIPRFFKAGMEIFKQIEGFWSSHPLAT
2386	16287	A	2403	3	407	ADAWGLRGTHGPWEQAGISGISPSNSFL FVCFRQSVALVSQAGEQWRRLGSLQPPP PGCGRESC\PSFQGGITPSCFFVFLEKM GLHRVGQAGLQLLMSGEPPALCSQRRGI TGVSHHARPPSKGFIWHTGAPAM
2387	16288	A	2404	239	573	VCFGVFSLSHFFESEFSSITQAGVQWLN LGSLQPPSRGFKQFLCLSLPSS\YWFTG TPPLVGGGSAGLRGG
2388	16289	A	2405	1	122	PTRPGRGCGELRSCHSTLAW/VNSETTS QKKQRKEKKLPLL
2389	16290	A	2406	417	130	QALRVKHVQLVPSSDFLAKTRAQSVNNL LRHSSSSSSSSSS/SSSSSSSSSSSS SSSSSSSSSSSSSSS\SSSSSSSSS SSSSSSSSSSSSSSSSSFLFLFFFFG LRGAFLGRFCPIRR

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2390	16291	A	2407	327	3	RQSQSLRYMAHQPVCCFTCSILIRAELN EI/ETKNKKIEKINET/RKSWFFEKINK MGAITPDATERQNIIQGYYEQLYMQNLE NLEYMDKFLGRFKPPSLNQEELDTLNR
2391	16292	A	2408	178	404	AAYRINSLQEVQHPTKRHSQPRKQSKLR EGNAQRNNIRRGPGMVAHACNPSTLGGQ GGQV/TLRSGVRDQPGQHG
2392	16293	A	2409	94	386	TSFALVALGGRSCSEPRSCHCFPAWVS\ SETLSQWKRKTPTLNNAKYWGGRFLRFF FLTRGGGGRFFFFGGTKTKSLGAGFKKG GGGKPGGPPNKGLG
2393	16294	A	2410	1	384	PTRQVRIKLFPRIYVHTRKRLKNIYGNT ETFITQPFKNHSVWQLIRNNRNAKKQEN VAHNEEKNKKQSIETN\QKYTHNKNLDT TKKKKKKKKKKGGGPLKKTIFKARGGEN NFFFLGPQKLNSGAGF
2394	16295	A	2411	423	2	FFFFPPPQKKSLFPPFFFCGPKIFSSPP VFLTPPQKIFFCPPKKKKYFPPPRGKIF FFLK\PPPPFFFFFFFFFFFFFFFFF FIFFFFFFLGFLLSSLLIGVPFLLLNAN IMILLQKKILKDEVQIISSFPSTKNRNV L
2395	16296	A	2412	218	112	LKKENNTKCYYGWGTTGTLIHC\WW\KL IQVLWKTD
2396	16297	A	2413	64	403	LKNFFFFFFFKKKGPPGAPGGSKPRGLG EPPPPPPQRGGNTGGGPGARPKKNGGGF FFFWRGEPP/PPPPAKGGGQDLGPGPFG REETNNFPAPAPPGPKNKNLGPRAQKIL CF
2397	16298	A	2414	217	409	VKYLSYSVLLTIICTVQACYQELRPGAM AHTCNPSTLGGHGGRI/TLRSGVRDQPD QHG
2398	16299	A	2415	416	0	ERPPPSSFFPPLAPGQVGQFFYGKGPWP EKSKKKNRFWGTKPFPPEGGGPPPPPNS PPGGGEKSPLFFFGGKGNPTWSPGPKFL KKRVIKGPLHPGGKGYKKTREFGLKPGP PPPKFFLGGG/PGFQNWEKPPQP
2399	16300	A	2416	277	0	PFVLLSSSSSSSSSSSSSSSSSSSSCS LLVRYLCKVKHKSSLCAHPGTVPFLELI HDTDSFAH/VFPADLL
2400	16301	A	2417	205	486	RHGYGFGFWKNTCMQHRHSYRRVYIHRH IHLTFLAYVHRESPEAMSALLTQILLFF KLLSFLRRCLA/SVTQAVVQWCSLGSLR PRPPGFKRFWC
2401	16302	A	2418	364	1	KESLGDPVKDTVILFATRNPMQMGSNYQ FFIYLCLTHLLSRSYCWFGCKMLQ/PLW KTVWQFLKKLNAEFPYDPAIPL\DICIP VFTASLFIIAQRWEQPKCASTDEWINQM WHMHTIEHYPR
2402	16303	A	2419	281	492	LFPPSLPASHPKLSTQQPERSHSVTHCG /VDRRGSDLGLLQPRPPRLKPSSRLSLW SSWDYRPAPPRPANSC
2403	16304	A	2420	63	465	RLQRFLLSF\VCLCPAPIGGAYRGRQAS LSCGGLRPVRASLLLCLPKQAWAMAGAP PPASLPPCSLISDCCASNQRDSVGVGPS NPGAGYYLVARRFLSPLEKRSIQVGVTL FSRCRLSPLSLTRKGNSLTPCAS
2404	16305	A	2421	61	482	QRARITGVSHHAQ/LRFCLFDMRSHSVA

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						QAGVQWCDNSSLQPPPSGLKML/STSAF QSL/WDYRCEPQHPIHY
2405	16306	A	2422	90	444	YCFSSECSEKCRCPGHDLQLSPGLCHHG VSGLAKPLLCFWPWIWKPQPLCSPTTSL PFLPLPPFSQCPQGPAWLELEGRPSLWK QGGLQSLAIKR/REGSRAQWLTPVIPAL WEAEAGG
2406	16307	A	2423	1	444	PGPGPGCGPVATLGSPSRPARTDSPSLP PHSQLREAEARNRDIEAHVRQLQERMEL LQAEGATGESLMCPLPRRT/WEEVGRLL
2407	16308	A	2424	189	418	SRRAEPGSFRGCLRVGVPSCTCV\SLWV CVCVCWG/VCVCVCVCVCARA/CLCLCA NFSL/CSHVSLCLSLSLSL
2408	16309	A	2425	30	895	LDEQCTSEIHRRGEATARPRAPEHPAPP ATAVRGRDAASQNLKRRPGSGTDGLRLQ GAEPSRLLRTYAGGAVIPRGTPERAQPP PPQDPLGRRRWLSRNTWGPWPGTTQPPS PQLLRNDWGSCGFMVPEAARGKVFQDSQ EGAHIRRETVSKSVCAEPWRHQRARDPA PTNFPLKCQKQRGASTSSGQHGDRVNLV FFIDDDYSPPSKR/PKTNEPPQPPVPEP ANAGERKMREFNSGPHNPVEETKLICLC PSGHASCQVHLWTGAMLLGFQSWRKLPG SGLKARILQ
2409	16310	A	2426	494	154	SSRVRCQCA\LLGGASQLGCSGVRDPLE EAVCPFSDLQPRAGRTTALFKAQMEMQK SPVFCVAHAGSCRLELFLFGHLGSSLHG LWN
2410	16311	A	2427	416	1	PQRGPLLALEPGRQGAAPVEDLQPQGPD KPPPPPLPQPFRARTVVTAAVPRHPPPV ACHPPQPLAASKPWP/SVAGGDLLPLPG PERPVHAFFIGFIFVHLGLGGVSGRGAV APARSGPVPPRPPSSSTSRFSLFFLHE
2411	16312	A	2428	84	409	DYKHAPTMPRIQNFVYHSPQQPRCENRI NFTPKKKKKKKKKKNKKKKKKKKK\KIF WGG
2412	16313	A	2429	1	389	LRDLSSDRSNPGRFLSTSNSSLY/EKDK RNKAYFTK/RPSPVNDIIST
2413	16314	A	2430	456	0	PGWPGRGAP\PSQTGWPGRGAPHIPDDG QPGRGAP\PSQTGWPGRGAP\PSQTGWP GRGAPHLPDNGWPGRGAPYIPDDGQPGR GTP\PSQTGRPGRGAPHIPDDGRPGRD/ GSSLPRRGGSRAEALLTSQTGWPGRGAP P
2414	16315	A	2431	3	344	CRERRSCHCTPAWAT\SETPSQKKKKKI FFGNGPPGGPQAGLKLRAWGFFQKRGTM GPGTKNHPGQRGEPPLLQKKQKITRPGG GGPGAPPPQGGGAGKSFNPGGGMFQGGE IP
2415	16316	A	2432	1	109	RPLRRLRQENRLNRGSRGCSEPKLC/HL CTPAWAT
2416	16317	A	2433	1	239	QSFAVLPRLVSNSWAKVICL/PSVSQNA EIT
2417	16318	A	2434	3	464	DWLQLEMQGEIVALVHSHHGGLPWLSES ARRLQVQSDLPWWLVCRGTIHKFRCVPH LTGRRFEHGVTDCYTLFRDAYHLAGIEM PDFHRENDWWRNGQNLYLDILQAPGLYP VPLSAAQPGDVIMCCFGSSVPNHAAI/Y

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						CGDGELLPHIPK
2418	16319	A	2435	3	427	EGARTSSERHPCNKYLLLHSLAHLFINA LNLVLKGLSPSPFPALPISFPPIFFFSPH FLGTPTLEGGRADLPFLQPPGAPG/QPA PLNYGPGPYRNPCP/RLPQLKPAGPGHG LLKSPPPNPGRNWPLLGSLFDFFKKRTS IPLP
2419	16320	A	2436	238	400	QFRWKRGKAIFFFFFLRQSPSVTHAGMQ WSNLSSVQPPPPGFKQFLC\PSVPSS
2420	16321	A	2437	11	442	LGTRPRATDWGVRLELSRACPVLGHPAK HPRPQRWCKVNFSYSPEQADELKLQAGE IVEMIKEA/CGNPDMPSVSPGPQRPPKT TEDKGWWEGECQGRRGVFPDNFVLPPPP IKDAQPLLLFGIDQEAGPTESGISGIRF RRLSC
2421	16322	A	2438	411	80	PQAEEGAPTPGSENFNPPPPRGGGAPPP PQKNFFPPRGVNPGGGGGQKRPPPKKGG /SPKKNPGGDKNPPPKKKKNIGEGGGFI GAPRGTPKKTPPPRDGYFQVFFFIVSLK
2422	16323	A	2439	290	1	QLNKIKKTPLLFLPWANEKVPKIPPNYP PGPKKKGYPPSIFFFFFLRQGL/NSVTR AGVQWRDLSSLQPPPPGFKRFSCQKPNS AFPHASADAWVDP
2423	16324	A	2440	440	213	PFSRPLFFFSPPPKKRASPPPFFFCFPR VFFPPPPFF/SKPPPKFFFFPPPKKKKIS PPPPKKIFFFFSPPP
2424	16325	A	2441	131	408	GCVPPEPAFLCFVLEIVSSVAQAGVQWR NLSSLQPSPPGLKRFYRPRLPSS/QDYR RAPPLA
2425	16326	A	2442	102	351	QASSSVLKLCVCVRARLCV/CACVCACV CVC/VCVCECVCVC
2426	16327	A	2443	190	3	PQGAREKSHRPGPIGRRLKL/DPPFLSP HVKINPRWIKDLNVKPTTIKTLEGNLGN TLLDTCPG
2427	16328	A	2444	410	30	VCVAPPLCVCIGTLCVRTHTQFCVCVHT HSLCVCR/CQFLCVCVQ/VAVSVCVCRA SLCVCR\ALCVCVCR\TVCVCVHGTVCV CVCRDSFCMCVCAGAVCVCVCVCVCV\C LCVCVASAQLLGRGFCSSVNIKGAGP
2428	16329	A	2445	243	1	KVMVQNKGPFSNLFFFGPTINFFTPQFK QGGGQNPNPFLFFFFFMRQGL/DSVTQA GMQWCHAGSLQHLPPGLKQFSCLLP
2429	16330	A	2446	276	408	MLKNCAFWPGTVAHACNPSTLGGQGGRI /TLRSGVRDQPDQHG
2430	16331	A	2447	24	405	LGDVCAFFFFFYLKNQLNPGGKLILPVG PAGENQRWEQFDKLQKGGIKMNPLRGGI SVPLTKKKNQ/WARGE
2431	16332	A	2448	239	3	SPLCGNNVYKPSTVEKTNQVEKMPPSKQ IWELCVELLWQ/SNRGIAGSGAHACNPG TLGGQGWRIMRSGDRDHPGQHGETP
2432	16333	A	2449	406	144	GCSEPRSRPCTPAWVTSETLS/RKKRKR RKKKSCLLRAILSTSPELTHFTLTTPLF SRYNDYPHFRDEKTEARRVYATCSGSHS WKRLG
2433	16334	A	2450	349	1	GGAIFLTPRPKVPLTPITPLAFNPGHQE EIPLPKKKKKIVRAIYDKPTANIILHGQ KVEVFPLKTSTRQGCPLSSLLYQHKTRM PSL\PLLFNIVLDVLARAIKQEKEIKGI

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						QIR
2434	16335	A	2451	382	19	DLGRMTAGSGDQRCAVGVKLLSFSLGAA GKGPKHSEAEASLPRNPGSYNRQAQWPQ SSLHLKGTIPDTTSLNTPWKMLSSLKVP SWQGAVAHDCNHSTLGG\RGGWITRSRV RDQPGQHG
2435	16336	A	2452	3	396	FKLKLMLIYHSENPRALKNYTKSTLSML YKWNNKAWMMAHVFTTWFTEYFKPIAET YFWGKKKITLKILPLVDNAPGHPRALME MYKEINV/VQICILQPMDQGVISTLRSY R\KNTFCKDIAAIDGDSSDRT
2436	16337	A	2453	115	411	KGCNFPPPPGGGGEKKIW/PNGGPPPRGK RKPPPPPPGGGGKGGHHPPPGPIFFFEK KKKGLFGG/PGGAPNSHPKRNPPPWFPE GGELTNPPTFFFEGGAF
2437	16338	A	2454	3	114	HHV/GQAGLELLTSDDPPASVFQSAGIT GVSHRIRSVS
2438	16339	A	2455	397	1	WSWQK\NRRIDQRSNIESPEMNPRMYGQ VIFDKIAKNTEWEKDSLFNKWCWKNWI/ LKRMKLDHPHLTP\KQKSKWMKDLIRPE TEKLPEETGGNPHDIGLSNDF\LDLTPK AQGAKVNTDKWDNIKLKNFPTRP
2439	16340	A	2456	424	3	PKKKKIFFPPPGFKIFFFLRAPPFFFFL CLSHFLLNRSRSLSCTTSCCVSTIPTSL CNKSSGV\CGLHCSLLAI/CSLIHLTLC PFCVLLVCMCDTVCVCVCVCVCDTVCVC PCPYGTLDIAFKHFFSRWSLTLVAQAGV QR
2440	16341	A	2457	266	379	HWPGAMAHTCNPSTLRGQSGRI/TLRSG VRDQPDQHG
2441	16342	A	2458	10	409	SRTGPNPRAQTDRPVVCVAFACFELPLW RSVDSATREAEAGGLL\DPGGRGCSELQ LCHCTPAWV/TSETL
2442	16343	A	2459	184	387	IVHFQMHKMINVAYIIPQFYSFILEIQS HSVTQAAVQWHSHSSLLPLPPGLKQSSH /LSLPSSWDY
2443	16344	A	2460	110	1	KNRVSFFF/CSFETESRSVTQAGVQWCN LGSLQPPTP
2444	16345	A	2461	380	2	FFFFFSETESRSVAQAGLRT\QWCNLSS LQAPLPG
2445	16346	A	2462	382	29	NGPGHGGPPVIPGTWGGQGGGFPRF\GS KPGFTWGNPPFLKNHKNYPGGGPPPVIP NFLGGKPGNFFYPGGGGFQ/SGPGAVFP PPPGQRRSIFLPKKKKERKLILFFSLEQ RLQNCDA
2446	16347	A	2463	228	1	KKGTLFKPPPPGGRFFFFFFFETQSRSA VTQATVQ/WMPSRLTANPTFRTQGILLP PGLKGSSCLSLPSSWDYRHV
2447	16348	A	2464	395	1	RLRRENHLNPGGGGCSEPRS/HPAWQQS ETTSQKTKTKTKQKALASDTVLSPRQSS EERFHLSLFHSSFVTPFGIFSFLTTSPH PILPVWLAPQLPAIYCYGDSVIKSNFQL WLSKELQESLSRLLWTQAFS
2448	16349	A	2465	29	299	ETPNEASPKTSWDYRHVLPCLANFFIFF VKTGL/HRAGLELLTSSDLLCFPKCWDY RH\DRSTWPLSSVFGSIFLVYYWPLYLI ETNMLTTL
2449	16350	A	2466	1266	1473	YFVPQSTQNHAAVFRVGSLLQEGCGKIS

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						KLYGDLKHLKT\FDRGMVWNTDLVETLE LQNLMLCALQTVNG
2450	16351	A	2467	49	356	VQVILLPQLLRRLRQENCLNPGGGGCSE PRWSHCCP/PAWVTEQDSISKTKK
2451	16352	A	2468	115	3	LSHTKWSAWPGAVA/STLGGRGRQITRS GVQDQPDQHGE
2452	16353	A	2469	3	404	FVAPGGGQGTFPGSLQPWPPRGPGASGS PSRAPLIFGFFGGKGVSPVGPGGFLLPG SRD/SGPPGPPKGWGSG/GLGPAPGP
2453	16354	A	2470	404	218	FAQVVIKWGALSSPKPPFPGFKLFSRPS PPSYWDYR/RRPRPPRLFFFFFLRQGLA LLPRLE
2454	16355	A	2471	386	258	AGGLLSPGVQGYNKLLSCPCKPAWTT\S ETLSQKKKKKKLPFY
2455	16356	A	2472	2	364	HHTQIIFVFLVETGFHHVGQAGVELLTS GDPPASWDYGR\GHRTWPYSHIFNNL
2456	16357	A	2473	1	292	DRGCSEPTSCHCTPVWAT\SETVSQKKK KKKKKTPLLRGPEKKNGNPPFRGFFRKN PGFKRKKGGAPPPGLFKIGRKKSPVGGH RHTFILGGPLPRF
2457	16358	A	2474	1	307	SLSCSSIVRRACFPFTFYHDCKFPEA/S PVMLPVKPVEL
2458	16359	A	2475	2	596	MKNAEDILTMEVLKSTMKQELEAA\QKK HSLWELLRIPNICKRICFLSFVSSSSSS SSSSSSSSSSSSSSSSSSTKITAW/LP PLEASFYRSTCLMPARALLFASTIPFWG LTLHLQHLGNNVFLLQTLFGAVTLLANC VAPWALNHMSRRLSQMLLMFLLATCLLA IIFVPQGEKSSQVEERKCLSLFSQGLPW SHLS
2459	16360	A	2476	367	44	YQEDITIMN/TYALNIGVPTYLANI/DL NREIESNIIIVEYFNTSLSKMDRYRSSR QNIDKETVDLKYSI/HINQMDLTDRYRT FHPTATERDSISKKRIKIKIKINKSLT
2460	16361	A	2477	12	362	HHEPG\GGGCSELRLCHCTPAWVTELDS VSKKKKKKKSQKKK
2461	16362	A	2478	401	1	FFFFFSETRSHPVA\RLECSGAISAHCN QCI
2462	16363	A	2479	3	353	YMCVCVCACVCICVLPWMCLCVC/CYCV CVCWYLCVCLCVSLCGHQHLAVSGKRSQ PPSHESFKTSLLLWVFKNLPPLLCAWVP QVSQNMPLDGTRTLNNVSLPDEKVHDLL LPLTAA
2463	16364	A	2480	57	361	MNESLLSCKRWSLLAFSHI/CVFCLICS TDISALCVTVCACMHVCGCRCVCMCLCV CLCLCVCRCMYGRVCAPMCLCVCVHCVL ARMCACGCGCVYKAECPI
2464	16365	A	2481	3	381	YMCACGYICMHA/CVPVCMCVCTCLCAH VCL/CCMCVCTFVPVCMCVCICVCLCVC TPIITLPFLSQERISFCTDLRSFRATAK RSHEEVKNCVYLQTIWNQYLIIFYLQNP NFGWAQWLMLVIPAVWE
2465	16366	A	2482	2	380	IHVLGNCLYFSEPQFPHWQQRITRSFLE GYGENLMRLHMSYIHMCLHICAYICI/C /LCVYICVLLCAYICVCVYLCVCICMCI FVYLCTHICVFVCVLVCIYLCV/C/VCV CICVCI
2466	16367	A	2483	296	1	NGTTIRRMLPIFSRYRPGMPGLVQCTIQ

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						SCTANSVPYSHGFIYFFIYLLRDRVWLC YSGWSAVAPSWLTITSN\YRLKPSSCLD LLGSWNYRQMPPCI
2467	16368	A	2484	1	319	NTVGLCVCV/CLFVCVLSLCV/CLSLCV /CLCVCVVSLCVC/VSLCM/CVSHCVCL CVYLWLCVSVCVSLCVSLCVCVYECVIS STKRSLGAPSRAEAAKLPRNWAPAKQSH
2468	16369	A	2485	3	334	NHFIISIDI/DKHFRKIHQPFVPKAITK LGIKGNFLNLLRGTSVKSTGNINM\NGE KPNNLPLRLVIQGDVLFHLLLEVLASAV KKKKKKKKKKKKKKKKKKKKKKKKKKK KK
2469	16370	A	2486	17	409	CLDNKKPRKEYCQKTHLIKKNPLLSRIC KELLKLYDKRMINPIKKWAEALYRCLSK GDV/HEMASKHMKRCSIS/L/SIRKMQM KMTL
2470	16371	A	2487	410	165	LECNVTIMAHCNLRNLGSSDPPTSAS\Q TAGIHHSLQHFFFLFFVETGFCYTQAGL ELGSSDLPTLASQSVGVTGTGHGTWP
2471	16372	A	2488	142	417	VEQLLEGYRTKSLYLRSFFLFVCMFLRW SL/DSVSPGLTNCHHLGSLYPPPPGFKQ FSCIS\LWAWRRTP
2472	16373	A	2489	1	404	KAGAQMGIKHPQHSSRLRLRRPSPRLPS SQKPLNTHYFPSFSFCAHRHTHTHTHTH THTHTHTGV/HLHPHT
2473	16374	A	2490	373	146	YGLERKISFKIL/LFVGKSPSYPRALME MCKINVVFMHANTTPTLQPIDQEVILGP GTVAHACNPGNLRGQSGRNA
2474	16375	A	2491	427	85	KTPPPP\RGPFFFYFFFFFKKAKNFFPP PPTPPLGKKKNP\PPPEKKISPPPGFPP PPFKKGPPKTLFKTPLKKKKGPGAPQKK PFFFKTPPPFFFFFF
2475	16376	A	2492	443	240	FLFFFFFXXFXXFFFFFFXFFXFFFFXFF FFFFXXXXXXXXXXXXXXXXFFFFFFFF FFXGCLFIYLFI
2476	16377	A	2493	3	135	ISAHCNR\LLLPGSSNSTASASPVAEIT GACNNNRQDFSFIILQI
2477	16378	A	2494	37	420	AHVCVCTCVCVCICLSRRVVVCAHSHVC AGIFLHLINQTFTTHL/CVCKVMALRVT PSPCLQGA\QTQLAGQCMCAKVCMNFMY IFIEGHICPQTCSCLGEPIRGGLSPLVC IC/MCAGFFVSFC
2478	16379	A	2495	402	178	RQNKTPFGVKKQITGGGGRGRVSYFLRG VSQENPLNPGGGGCSEP\RPPGWGTKNP LFQKKKKSSKQQEGRGED
2479	16380	A	2496	138	439	RTFILGDHHHHPSAVHFHLPRRKLCTHE TGAAPPPPALGATVPPSVSVCLTGGGPQ ITPPPPALGARDLPSVSVRLTMGGPQIT PPHPDQQPL/SPPSVSVC
2480	16381	A	2497	118	382	VKSFCASMRACVCECVYMCVSMCVCVCV CVSACLICVCLCQ/CDLINKCV
2481	16382	A	2498	164	439	VKSFCASMRACVCECVYMCVSMCVCVCV CVSACLICVCLCQ/CDLINKCV
2482	16383	A	2499	1	411	ISTSFYTDTINRTALHFAVGRNHLSAVD FLLKHKARVDVADKDGMNALHFATQSNH VRIVEYLIQDLHLKDLNQPDEPKESPLH LVVINNHITVVNSLLSAQHDIDIL\IRS SKPPLHVAADRGNVKLVE/LLLKAGCD

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2483	16384	A	2500	80	404	RTAAAVSTVSFPQDFEGQSPKCTQGVRE ALRQIK/RLVPTGSLRH/WPAGSLA/LC QPLSDEKDLTQLFMFARNAFTALAMMDY PYPTDFLGPLPANPVKGRRRLPRRRERP
2484	16385	A	2501	215	1	AAIQQGSLACSHSVPPATTPRAYTPVPP QLLVRNF\YPKTLELRSQLRCARRFPRE TGADCRHAGAGRQTK
2485	16386	A	2502	423	214	WQAQVGGLLEP\GGRGCCELRSCHCTPA WVT\GEILSQNNPKRQQNKTKQKMGPGV PGSWGSPRAGGLTV
2486	16387	A	2503	294	1	LHWNQRQRCPPPPPPPLPPPPPLPPPPL PLR\HRIAGAGQTGAKIRVVGRVVRVGA GLGVAAA/DSRESCPDGAAAGGGEGGGD SAATAGPGGGGGGGTK
2487	16388	A	2504	331	411	PFLKTGNKGAPPPTKIFFLFFKKKGG/W PGAVAHACNPSTLGGRGGRITRSGDRER
2488	16389	A	2505	407	195	GGRGCSELRSCPCTPAWVT\GEVLSQKK RKSSNKKSRCLEDQAEVGGERQLVQVSV PSTCQRRVGAWFIYL
2489	16390	A	2506	1	468	RQGSMNKLETERQIKKAPARNPERERER ERESKKGEDRHTDICRP/RERERQNYRD RQ
2490	16391	A	2507	27	380	FVCLCPAPRGGAYRGRQASLSCGGLHPV RASWLLCLPNQAWAMAGAPPPASLLPCS LISDCCASNQRDSVGVGPSEPGVGYNLM VRRFLSRSEKRNIRVGVTRFSRCVCHPF L*LGKG
2491	16392	A	2508	396	234	RQENCLNPGGGASSEPRSRLCTPAWATE RDSISN/QNKQTNKSHILRAAFSRPSCY
2492	16393	A	2509	1	421	AKKIKPPFPLKKKKKPGRGGPPPPPPP/ AKFGRETPLNPGGKGSIKPKLGPPPPPP GGPPNLPPKKKKKKAIPK/PLVPSHVKS TGFPPSCS/RSALLRAFTQ
2493	16394	A	2510	197	3	TGPPDFNFFFFLEMKSHSVAQAGVQWRD LGSLQPPSPQFKQFYYWGLQGA/LPPCL NKICIFSRGGV
2494	16395	A	2511	114	454	QGPLEKKGAPFKNKFFKTGVLFFGSQNI PPWWFKKGFSRTPFEIKKKNPPGILGGS PKKFFFFFFFEMVLLHHPGWSALAQSLL TTASDF/LRLKQSSHLSLSS
2495	16396	A	2512	3	495	FFLSRGLFIHLESAPAIFQCLLFVVFLV FVATGSHYVPQAGLKLLASNEPPASNSP KCWVYRHEYPALKCLCFGLCLF/AFLP
2496	16397	A	2513	25	437	PLLFSPPAGHAMEEDILPPAPSFLFYFF FYWLVWVKIIYLYVLAQAATTNYHRLSG LNNKHLFLTILEPRMP/SIKVPA
2497	16398	A	2514	2	256	QAPSAEGEMTSYVLLAYLTAQPAPTSED LTSATNIAKWITKHS\NAQGGFYYNQDN LPYSLCSGRNESTAFGTNGQDIIHPVHS S
2498	16399	A	2515	2	284	KCQCDELCSYYQSCCTDYTAECKPQVTR GDVFTMPEDEYTDYDDGEENNNAIRHEQ A\GFTSVISDLQAQIIWISEQKHAMSFV EEMTVLEVIL
2499	16400	A	2516	2	432	RDCERESSRAAEYTASLKASCWMGDLAE SPSLDPQVAMGTPPAGPCGWSVGTRSQP FPRGPSRGPCCVSPPSWTPEPGTGQ/CG EGGGRWSPQVPP

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2500	16401	A	2517	401	2	GGEAAIRGQTKPQLEGKAPECSECEKKI VRS\PRLIRRQRTPTGEKPYECEECGKS FSRRYRLAQHQR\TRAGEKTYECNECGR GFSERSDLINHYRVHTGERPYKCDECGK NFSQNSDLVRHHRAHTGEKPC
2501	16402	A	2518	398	1	ETFGK\SGGRSIVPGQFLAVGPKGRAVM ISAIEKQKLVYILNRDAAARLTISSPVE AHKASALVYHVVGVDVGFENPMFACLEM DYEEADNGSTGEAAGNTQQTLTLYELDL GLNHVVRKYKEPLEEHGNCI
2502	16403	A	2519	384	3	GGGID/SDASLVIAGVRLEDEGRYRCEL INGIEDESVALTLSLEGEALPLPPHSCV AAGPPRLGLPGLLPSISSAPLGTPAPSP RPRRPSSPSAPIRWPSPGSPPPPRCGVS VPTQPGPVPVQLLRGVY
2503	16404	A	2520	1	426	GDRQMITALLRKLKQQSRESVEENRPRL LKALKELGDFYLELHWDFQSWVPLLSRI LPSDACKIYKQGINIRLDTTLIDFTDMK CQRGDLSFIFNGDAAPSESVVVLDNEPK VYQRLRHEES/QEKNRTQVDCLTP
2504	16405	A	2521	2	425	ALPIGRMPIMVRSSR\CVLTGKTPAEFA KLNECPLDPGGYFIVKGVEKVILIQEQL SKNRIIVEADRKGAVGASVTSSTHEKKS RTNMAVKQGRFYLRHNTLSEDIPIVIIS KPMGVESAQEKIQTVSPQEPEWR
2505	16406	A	2522	2	376	IQSFSVVYGYHLCSQGILSERVSASKFP LLFFFFFKKGGPPFMP/QGGKTKGPLKP GDPQSPGIKGFPCLAPPNKGKKGGPPPP RGNFLGFKKKKRFPQVGGGGSKPPREGK PPPLAPQGGGNRGG
2506	16407	A	2523	403	3	GAPRSLSEKERQLMGMINQLSSFREQLL HAHYEQKKLAASQIEKQRQHMKLGKQ\Q QEQIARQQQRLIQQQHKINLLQQQIQVQ GHLPPLMIPVFPRDQRQLDALAQQGFLL PPGFSYKAGCSDPYPVQVIPLY
2507	16408	A	2524	2	369	NARCLILRAAEYMAACVYVCISVFACMC FCVRVCVPVCVSGCLCVCVSMNVHLSLC /VEQCACLWMCVSLHVCLYICACLCVSV CEAVCLHLESHCRGGSRPFPVVGPAFSL SSCLILAPPSVT
2508	16409	A	2525	59	380	RNRNFNKNSSFFFFFKKGPWGGGPGGTK GPKQRQGEP\NHWGQKNFPGQTRKPRKP TPGPPPPKKIFFFKPLEKKGPGQGPQGG QKPGGQKKPPGGAPQKRGKTGGET
2509	16410	A	2526	1	371	VMPLSRKHPKGFFSNHTLVLHVARSEMD KERVFQATRKSSP/CFVPLLPWPT
2510	16411	A	2527	445	3	RWLGLALIALKRELKKGDL\PEMRWWDS SIIPNG\FDLTEETPKREDYFGIANLVE HPAQLNPPVDNDTPVTLGVYLTKKEQKK LRRQTRREAQKELQEKVRLGLMPPPEPK VRISNLMRVLGTEAVQDPTKVEAHVRAQ MAKRQKAHV
2511	16412	A	2528	1	478	RPTRPKRKLKSHRLQSRQESKKVRVL/T NAEDNEMEEETDDGPLLVPRVKVAEDGS IILDEESLTVEVLRTKGPCVVEENDPIF ERGSTTTYSSFRKNYYSKPWSNKETDMF FLAISMVGTDFSMIGQLFPHRARIEIKN KFKREVYASAIEDQATSVHT

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2512	16413	A	2529	385	1	QKKCEDLK\DQDNPIVRPPPTPGSCGHG GVVNISKPYVVQLNWRGFYYLYGAWGRD YSPQHPNKGLYWVAPLNTDGRLLEYYRL CNTLDDFLLYINAREIRITYVQGSGIAV NYNNKYVSMYNTVNV
2513	16414	A	2530	1	1228	FRATLRPETMFGQTNCWVRPDMKYIGFE TVNGDIFICTQKAARNMSYQGFTKDNGV VPVVKELMGEEILGASLSAPLTSYKVIY VLPMLTIKEDKGTGVVTSVPSDSPDDIA ALRDLKKKQALRAKYGIRDDMVLPFEPV PVIEIPGFGNLSAVTICDELKIQSQNDR EKLAEAKEKIYLKGFYEGIMLVDGFKGQ KVQDVKKTIQKKMIDAGDALIYM\EPEK QVMSRSSDECVVALCDQWYLDYGEENWK KQTSQCLKNLETFCEETRRNFEATLGWL QEHACSRTYGLGTHLPWDEQWLIESLSD STIYMAFYTVAHLLQGGNLHGQAESPLG IRPQQMTKEVWG\YVFFKEAPFPKTQIA KEKLDQLKQEFEFWYPVDLRVSGKDLVP NHLSYYLYNHVAMWPEQR
2514	16415	A	2531	335	2	KKKALFFIHPPPFVNGRPHKNPKIKSLG SPTPFSLIFLKKKFCFVNQDGVRWLYFG SLQSLPSRFPPFFCLNLLSSWEYRGLPP RPGKYFFPFIFFYFLVEM\GFTVLARMY
2515	16416	A	2532	3	380	AINSYIRGDDPSSYPEVVQSASRSSK\W SPLPRALHLTDAK
2516	16417	A	2533	3	2083	SSEGYLRGNMSENEEEEISQQEGSGDYE VEEIPFGLEPQSPGFEPQSPEFEPQSPR FEPESPGFESRSPGLVPPSPEFAPRSPE SDSQSPEFESQSPRYEPQSPGYEPRSPG YEPRSPGYESESSRYESQNTELKTQSPE FEAQSSKFQEGAEMLLNPEEKSPLNISV GVHPLDSFTQGFGEQPTGDLPIGPPFEM PTGALLSTPQFEMLQNPLGLTGALRGPG RRGGRARGGQGPRPNICGICGKSFGRGS TLIQHQRIHTGEKPYKCEVCSKAFSQSS DLIKHQRTHTGERPYKCPRCGKAFADSS YLLRHQRTHSGQKPYKCPHCGKAFGDSS YLLRHQRTHSHERPYSCTECGKCYSQNS SLRSHQRVHTGQRPFSCGICGKSFSQRS ALIPHARSHAREKPFKCPECGKRFGQSS VLAIHARTHLPGRTYSCPDCGKTFNRSS TLIQHQRSHTGERPYRCAVCGKGFCRSS TLLQHHRVH\SGERPYKCDDCGKAFS\R ASDLIRHQRTH
2517	16418	A	2534	434	3	APLHSGKRSPTKCN\ECG\GAWNRSSLL DRHKIIHSEENPNKCEECGKAFKQASRL TIHKIIHAGEKPYKYEECGKVFSQSSHL TTQKILHSGENLYKCKECGKACNLFSNL TNHKRIHAGEKPYKCKECGRAFNISSNL NKQECI
2518	16419	A	2535	46	454	PSTFSSKVMDKQTLCSSQATSNTSRYAA ALYRQGSIYPKEMKTCVHTKPYTVVHSS IFMIAKKWKQPRCPSA\DSWRNRMWSIH AMGCYLTMEKNEAVMLPRR/WSLENIVL SERSH
2519	16420	A	2536	13	476	ALKTYKYSHKKAFNPKKVYGKCSQKDPF PINHCLPTEKLHLCDKIGEGVFGKVFQT

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						IADHTPVAIKIIAIEGPDLVNGSHQKTF EEILPEIIISKELSLLSGEVCNRTEGFI GLNSVHCVQGSYPPLLLKAWDHYNSTKG SANDRP/DFFKDDQLY
2520	16421	A	2537	162	296	YVCQRYKL\NPFLPSYTKINCKWVTDIN VKPTSVKLLQEKRRKSL
2521	16422	A	2538	495	348	FGW\HAFIVKEPRVEKLCKASARAKPQP PAIIAKTFKAGGITGQYAQAAL
2522	16423	A	2539	480	63	ARSEAWISIADAYMASPGDRIAQLLLLP YIKVGNSEIKRTGGFGSTDPTGKAAYWA SRVSENRPACKAIIQGKQFEGLVDTGAD VSIIALNQW/PKNWPKLKAVTGLVSVGT ASEVYQSTVILHCLGPDNRDSTSHYSKT R
2523	16424	A	2540	2	509	NVDADDVRLAIQCRADQSFTSPPPRDFL LDIARQKNQTPLPLIKPYAGPRLPPDRY CLTAPNYRLKSLIKKGPNQGRLVPRLSV GAVSSKPTTPTIATPQTVSVPNKVATPM SVTSQRFTVQIPPSQSTPVKPVPATTAV QNVLINPSMIGHKNILI/TTNMVSSQNT A
2524	16425	A	2541	501	1	QWQVVEDPGPGPRPREEASSYKCELREQ \LPQYVRDFFRKKAE\SGMDSSRNLEKL AERFLAKTCSTKDQQFKKDQNVLSPVNC CHLLLTQVKRESRAHTTLSDIYLNNIIP RFVQVSEDSGSLFKKVQRYFFTEVRGWS NDTIFKILLDIMLITWVTQLSVHQTPV
2525	16426	A	2542	473	287	EKDFNLPPKDLRL/KTSDV/TSTKENEF EDYCLKRELLMGICEMGWEKPSPIQVC
2526	16427	A	2543	268	482	KKKKAWGLQRGGKNFPAKAELPTHGIQI NSCSVRL/VDIKKEKPFSILKVEGQAQA RTHLNRAFDIIVLTRGG
2527	16428	A	2544	407	1	CKKICYLIHYWWEYKMIQPLWKTVWQFL \KKLNILYDPAVILYDIYPEELY
2528	16429	A	2545	28	399	FRHSSFQRSGRGSQLMVHFLSL/SVMPK IGSVAGINYGLVAPPATTGETLDVQM/K GEADTENH
2529	16430	A	2546	2	365	FVVNVDEVGGEALGRLLVVYPWTQRFYE SFGDLSTPDAVMGNHKVKAHGKKVLGAF SDGLALLDNLKGSFATLSELHCDKLHVD PENFRLLGNVLVCVLAHH/FDKEFAPP
2530	16431	A	2547	375	1	GFACRRMQKRVREVSHAEAESAASKKVR ANGSGKQNEGMNVTWTATLALSQAVISS ATYTQMQPHSLIQQQQQIHLQQKQVVIQ QQIAIHHQQQFQHRQSQLLHTATHLQGA \QKQKQQQHEWR
2531	16432	A	2548	3	376	ELGSDVA\GAEALVDRRQERKGEIDAHE DSFKSADESGQALLAAGQYASDEVREKL AVLSEERAALLELWELRRQQYEQCMDLQ LFFRDTEQVDNWMSKQEAFLLNEDLGDA VDS/IKEILKKHE
2532	16433	A	2549	360	1	RGEMLWTV\NNRFLKNFVPGKIEPFKSH SLYPPCYVHDVSFWIDQKKGFDELEFHT VGRAVSQDTIISIQFLSRFQHPKTQQVS LCYRLTCQTCDKALTQQQVASMRSQIRK EIQQHQY
2533	16434	A	2550	2	403	VVAEEDTELRDLLVQTLENSGVLNRIKA ELRAGVFLALEEQEKVENKTPLVNESLK

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						KFLNTKD\LQGLEGRENLARDLGIIEAE GTVGGPLLLEVIRRCQQKEKGPTTGEGA LDLSDVHSPPKSPEGKTSAQTT
2534	16435	A	2551	1	409	VPRNPTPLGGPGGPILRSREGGPPGLPR EPPSVLKKREPPTRGGGRPPGFPLPRRV RPEKWVNPGGQTFPEPKLRPRG/HHPGG QTKNPFPKKK
2535	16436	A	2552	256	1	HEMDGTLLGPFPPPGSSKGPSLTGPPIL FQSPGP/APHTPSSSPANLKT/CTPVCP SHLPW/CCPLCLPMRLPWSPVPPVSKSS PPALY
2536	16437	A	2553	398	3	ARQQQQLLQQQHKI/NWLQQQIQVQGQL PPLMIPVFPPDQRPLAAAAQQGFLLPPG FSYKAGCSDPYPVQMIPTTMAGAAAATP GLGPLQLQQLYAAQLAAMQVSPGGKLPG IPQGNLGAAVSPTSIHTDKRCI
2537	16438	A	2554	20	517	DRPPSTKRRDTPQLRGAPDLSPRGPAPV PECPEH/SPRKKTSACRPPLPLRPSHSS PLP/SPQPSHSTPQASCPLPEALSPPAP FRSPQSYLRAPSWPVVPPEEHSSFAPDS SAFPPATPRTEFPEAWGTDTPPATHRSS WPMPRPSPD
2538	16439	A	2555	361	3	KSSQEALEEALRQRLEELKKLCLREGEL PGKLPVEYRLDPGEDPPIVRRRIGP\AF KLDEQKILPKGEEAELERLEREFAIQSQ ITEADRRLASDPNVSKKLKKQRKTKYIN AVKKLQVY
2539	16440	A	2556	470	2	LKAAVTAGLEVPSDVSDRAFE\WLSAFP L\DSPYSIHHPRRIQVSSEKEAAPDAGA ERITADSDLAYSSKVLLLSSPGLEELYR CCMLFVDDTAEPRETPEHPVKQIKFLLG RKEEEPVLVGGEWSPSLDGLGPQADPQV KVSNAIRCAQAQTGTV
2540	16441	A	2557	2	315	VVAEEDTELRDLLVQTLENSGVLNRIKA ELRAAVFLALEEQEKVENKTPLVNESLK KFLNTKDGKMFSLFLFIYL\EFLNLDTI WEKSGISGLFFVFNCYRSSF
2541	16442	A	2558	372	3	CNISSHFANKKCQDVIVAARNVMTSQIH HAV\KIIPGFNINVPGLPPPDEDTELEV QKVSNPQYHEVMNLELENTLDQHSYSLP TCRISEYVKKLMELAYHSLLEAASSSDQ CADQLFYSVRCI
2542	16443	A	2559	64	435	WGDASCTGRAQLGIAHKSVLPTLTDKFN TIPAKTPMSFFKEPDKLTPKFT/WKNRT PRTVK
2543	16444	A	2560	113	375	VPGPARDSTQRRAVKNDKKELMSIPGIP GPVQVPGGGLST\GMRGFPGSSLGFLTI PGGALIPFSPAFFSRVGGDLSPRNTGPG QKPG
2544	16445	A	2561	431	51	RKIYRVYERENFRVEIMFRFSHTSKKVC KGNV/DVAKFIKLHRDGWHVLNVQCACH QKGGIYWFRSIHVELIGYPPPRSSSHIK IGDKVRVKASVTTPKYKWGSVTHQSVGV VKGNIIWVIKFLMLTFH
2545	16446	A	2562	1	455	PEGIALEVVTESTGKEREHTFQPGDNVE VCEGELINLQGKILSVDGNKITIMHKHE DLKDMLEFPAQELRKYFKMGDHVKVIAG RFEGDTGLIVRVEENFVILFSGLAMHGL

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						KVLPPPLQLCSETAS/SIN/VGGQHEW
2546	16447	A	2563	407	1	KWDHPLSKCEVPCGGSIISSNGPVSYPG FPSPY\TSSQDCVWMITVPSGHGVRLNL SLLQTEPSGDFIAIWDGPQQTAPRLGVF LRSMVKKSVQSSSIQVLLKFHRDAATGG IFAIALSAYPNTKCPPPTIHPCI
2547	16448	A	2564	382	1	TQEVEVAVSLDRAPAFQSGCQSETLSQN SNSSNKTWILDHFGLSDFLDQRFSACTV FTPREQVSSHTRMFIAALFTIAKTWSQP /KYPPVIGWIKK\MWHIYTMEYYAAIKK DEFMSFAGTWMKLEAMY
2548	16449	A	2565	429	0	PLQSSCQTSCHQNCSRKTSLHFPGDVLA TPEQVGGSPAQVPIPYLDDDIPLLEVEQ EPVSLELGDVSLVSVSREGLQPASITGS RGHLIVQLQELLHHWVLWSAVKSRWVIV GLFVSILILSLVFAIRLR\SASRAPVLL RP
2549	16450	A	2566	464	1	VIHGVI\NPFVHGDQYKKKFPLK\FYQE IYESPFVTETGEYYKQEASNLLQESNCS QYMEKVLGRLKDEEIRCQKYLHPSSYTK VIHECHQRMVADHLQFLHAECHNIIRQE KKNDMANMPVLLRAVSKGLLHMIQEHVL RALGRIPTSYVRMQS
2550	16451	A	2567	3	178	YNPGGGVCSDLISSHCTPVWVT\SETLS QKKKKKKKKKKNFLPETRERALPGKKKG GGG
2551	16452	A	2568	215	411	IHLIFIHLVFIDYLSVRHSSKILGYISE QIRKRNS/WLYVVAHTCNPSTLGGGGGQ ITRSGVQDQPG
2552	16453	A	2569	170	430	TSSQLAPQCLAV/VSGPLAACPELTSAT SPWLQVRTNAMASPLLKFSAEDLLFKAA LSQFCVIMLNAKLSVQKYEK\LISAFSD SR
2553	16454	A	2570	3	463	CRFFGYSTAAAPMTPSSGGSTLSGITAP AVPNIPSPIGVNGFTGLPPQANGQPAAE AVFANGMHPYPAQSPTVADPLQQAYAGV QQYAGPAAYPAAYGQISQAFPQPPAMIP QQQREWPEGCNLSIYHLPQEFGDS\ELM QMVLPFGNVISSKV
2554	16455	A	2571	3	424	LKTMKGGTGNGLEIMLDIQQDEYLPVWG ETGTSPTSGAPLHGSRPQP/PARGFLGF TVRPG
2555	16456	A	2572	1667	2046	YIFFFTAFLWAALTFQVTTTLAPLALLV RSAKMMRASHDKPTANITLN\GKTGRAS KQRREERNRQEVKLSLFTDDMFLYLESP IVLAPKLLLLINFSKVLAYKINVQKLLA VLYIKSSRESNEEHN
2556	16457	A	2573	1	399	FAISQDHPALPSRPPSLHHPKPGTLTFH PDLPHQATCSRPIRHQRTWPEDAPLAKA DTVSPAEHPPAAATKAP/TR/PAPDKPG GTSDPQTGPAP\PASPPCSGP\APQPVP RKPSRAAPSKVSVTVPRRVPRTFPP
2557	16458	A	2574	2	452	AKVNEMKSPMRKGHTLLKNKEEKLNQLE SSLWEEASDEGSLGGSPTKKAVTFDLSD MDSLSSESSESFSPPHLDSTPSLTSRKI HGLSHSLRQISSQMSSVLSILDSLNPQS PTPLLASMPAQLPP\RDPKSTPTP/SYC GRCRGFSLTS

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2558	16459	A	2575	2	369	TLVYPAITFILLSICICYWIVTAVFLTT SGVPVYKVIAPGGHCIHENQTCDPEIFN TPEIAKACPGALCNFAFYGEKSLYHQYI PTFHVYNLFVFLWLINFVIALGQCALA\ GAFATYYWA
2559	16460	A	2576	406	1	RQEGTGPSYLLLVGITPRSFWGFSPPLG PSGKNPIKTFGGPLQGFFFRVQMGVLLP LPGPSGN/CSIKVSALNSSFSPSGVNPG EASLPWF/CFFEMESRSVAQAGVQWQPP PPGFKRFSCLSLLGSWGYRRPPLV
2560	16461	A	2577	3	410	YISPFYITHMRAHTNLPGPF/KLNQRAD ALVSAAFADAQTFHSLTHLNAAGLRKRY GLSWKQVKEIVKHFSAGEVLHLPHQGAG VNPRGLSPNSIWQMDITHIPTFGKLSFV HVSVDIYSHFIWATYQTGEATAHVK
2561	16462	A	2578	386	1	TERIRQRQYQRETEKDKRYTERQRKTER IRESDRDRERQNQIERDRRAT\RERDRE KQRESDRETYRERENQIETERDRKRQSD RDRETQRETGRIRYRERERQHQTESDRD RERESDRETQRHRECI
2562	16463	A	2579	2	432	LLYFAKRYGAAFGECCQAADKAACLLPK LDELRDEGKASSAKQRLKCASLQKFGER AFKAWAAARLSQRFPKA*FAEVSKLVTD LT*VHTECCHGDLLECADDRSDLAMYIC ENQDSNFSKLNECCEKPLLEKFHCIAEV END
2563	16464	A	2580	3	426	NLLNDALAIREKTLGKDHPAGAATLNNL AVLYGKRGKYKEAKPMSKRALEIRKKVL GKDHPDVDKQLNNLALLCQNQGKTEQGE YYYPRALHIYHTKLGPDDPNAANTKNDL VACYLKHGTVKQA*SLNKENLTSAHEWD V
2564	16465	A	2581	10	389	KLAG*GLWGHTLITNPLTEPLTYPFLGL YL*SIIITSSICLLQTDL*ALIAYSSII HIALVITAILIQTP*SFTGAVILIIAHG LTSSLLFCLTNSNYERTHSRIIILFQGL QTLRPLIAL**LLA
2565	16466	A	2582	1	192	LIPTLAIITR*GGQPERLNAGTYFLFYT LVGSLPLLIALIYTHNTLGSLNILLLTL TAQELSNS*ANNLI*LAYTIAFIVKIPL YGLHL*LPKAHVEAPIAGSIVLAAVLLK LGGYGIIRLTLILNPLTKHIAYPFLGLS L*GGQPERLNAGTYFLFYTLVGSLPLLI ALIYTHNTLGSLNILLLTLTAQELSNS
2566	16467	A	2583	2	438	QAHGPLAGCRLRPRSPSPVLWRRRRRWW RQRRKWKTKTATAAAGMYASWTKACRGL EELINLTRLNVSYNHIDDLSGLIPLHGI KHKLRYIDLHSNRIDSIHHLL*CMVGLH FLTNLILEKDGDDNPVCRLPGYRASIFQ TFAQL
2567	16468	A	2584	3	415	GRAILLLEEAIQYLSGIEIDLIDTDRGE WDSLTPQARR*KEAGLQMFVQLARFHNI VCKEAFGTLAFLTSEIKSLFGHPFLAER IISMLNYFLQHLIGPKMGALEVKDFSEF DF*PQQHVSDSGAIYLDLGDEENFC
2568	16469	A	2585	2	453	DAKMYLSYKYATVIRNLREGTCPEAPSD ECKPEKRCALSHHQRLKCDEWSDISVGK IKCVSAETTEYCIA*IMNG*ADAMSLDG

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						GFVYISGKCGLMPVLAENYNKSDNCEDT PEAGYFAVAVVKKSASDLTWDNLKGKKS CHTAVGRNAC
2569	16470	A	2586	3	413	MAVESRVTQEEIGKEP*KPIDR*KTCPL MLRVFTTNNGRHHRMDEYSR*NVPSSEL QIYTWMDATLKELTSLVREVYP*ARKKG THFNFAIDFTDVKRPGYRVKEIGSTMSG RKGTDDSMTLQSQKFQIGDYLDIAI
2570	16471	A	2587	1	798	LEVMLMLVKAGADQRAKNQDGMNALHFA TQSNHVRIVEYLIQDLHLKDLNQPDEKG RKPFLLAAERGHVEMIEKLTFLNLHTSE KDKGGNTALHLAAKHGHSPAVQVLLAQW QDINEMNELNISSLQIATRNGHASLVNF LLSENVDLHQKAEPKESPLHLVDINNHI TVVNSLLSAQHDIDILNQKQQTPLHVAA DRGNVELVETLLKAGCDLKAVDKQG*TA LAVASRSNHSLVVDMLIKAERYYAWREE HHESIRDPSTGFTL
2571	16472	A	2588	2	285	AWSIAPSHPHSKVPPGPRRGKAEGRPGA AAQAAEQAEVHPPSSGPSPLPARQPPVW QIPPTPSLKTTTRRGAQPQHSRKRLA*S RSVSVLFRKM
2572	16473	A	2589	11	438	AYYGLNWHLGATLSQKKKKKKKKKKNFP RGGGPPRNPHFWGIGGRPGTGPPRGEKN GLKNQKKEKFLAPR*KKSTGKPLKPPQG KGWGGGPKFPKKKRPPRAGGGSLKPKGK NREPFLALKSLPGVFLGGFGGNPGMGLK NQ
2573	16474	A	2590	313	391	VHLVRVKLGL*SRIYKELLQLNNTT*DN PI*KWATDLDRHFSTKYTQMVDRLMEKC STS
2574	16475	A	2591	62	616	EVHQGTEVRDSEVRRRPQARGPLMPAER AGRQRWLVPALQPRRGGLRR*RGAVRQH GAHPHGLLLQDQKIPALPGRKQAGSLHA PGTEGEPDHGGDPVLDAGIQHHRQQRHP TADHLNPGEHRRGEAHVRAAV*PAAGAE GAAKERRAHQANTALQVHRR*LGSFAEL RLLRKPGRTSVWPSPM
2575	16476	A	2592	345	438	HKRWLPVPILYQHLF*VFGHPEVYILIL PGF
2576	16477	A	2593	479	313	QDGLDLLTS*STRFSLPKCWDYRREPPL KLINLQSSGVGLHVQLFPPSFCFDQLL
2577	16478	A	2594	3	419	LTLHSNTLPPPEMSGLT*PPATNAYWTF LPSAIRLFPEIFFIAVLLSVSLFDETET LSDAHSWRLTFKYERDANYHLLMSAQER LERLFGLHGGTIPIVPTADFHDSISGAS DTDIAHSGLAYTMERSARQIMRTAMKY
2578	16479	A	2595	1	419	HKCEGRYRGKTYGGYWSLCATVNKALDE RIPITSASYYATVTLDHVRNILGSDTDV SMPLL*ERHRILNETGKFLVDKFGGSFI NCVR*RDNIAHKLMHLVVESFPSYRDVT LFEGN*VAFYTRAQILVTDTGTVLEGK
2579	16480	A	2596	199	397	SPTALNTDDVNPFMGSSSRGHHRQFQTG IVSDHPAEAGPIS*DEQELPYAVLHFHK VQPLEPKVTD
2580	16481	A	2597	154	3	MLSLRGFFCLFVCFETGS*YAAQAGLKL LGSGSPPISSFQSARITGVSHL
2581	16482	A	2598	425	223	QITGHGGKCL*SQLLGKFGQENFLNLGS

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						RSFN*PKLLPGTSGWVTMLNSLGKKKKV TAYLNKWMPTP
2582	16483	A	2599	3	441	QGPSRDLVSELYQINAFDTPESLLMIGK DHSDPIHHTFDHMWRTKEHNEAGWLLLR SVDKVMKENDELGDSISQLQKQILSLKY AKIALTERLISCPV*TEIVLNYT*SLIM LLTDLL*KVHAQSHHAHSGQASNCNVMT LIGLQH
2583	16484	A	2600	131	423	GPAPMVILPHLTGFLLAFLPLSHLLTSY LVPWILSGTDGHTFRSACLPRWLEAEWI FGGVKYQYGGNQEGK*CFFTG*SYVYNG SSGKVPWETFSRT
2584	16485	A	2601	222	447	SGIPSFGL*VVEQNRPGRLNAQILKDLG VSPGSDYGKLKNGISSGLDNGVTTSDHD VLKMAIVGRKIWILGDWSG
2585	16486	A	2602	2	457	FICDPLIKAIGTEGDTDVLSEIMNSFAK SIEVMGDGCLNDEHLEELGGILKAKLEG HFKNQELRQVKRQEDNYDQQVEMSLQDE DECDVYILTKVSDILHSLFSTYKEQILP WFEQLLPLIVNLICSSRPWPY*QWGLCI FDDIVKHCSPSL
2586	16487	A	2603	1	297	DHRQKLYAHTECGKALLWKSVICVHQKI LEEEKPCEGTKYDNIFSNRGCPPVPRMV HAVEIPCK*TECEKATGVHGPRGASEFL PERPTGMNMAKCESR
2587	16488	A	2604	1	405	RFDVSDGLELRPKYNGIAHRLTTIWYLD GLRGLYKGVTPIIWSAGLSWGLYFVFYN AIKSYITEGSSERLKASEYLASTAEPGP MTLCITNPLWVTKTGLMLQYDAVVNSPH *QYKGMSDTLVKIYKHGGVQGLY
2588	16489	A	2605	165	3	PEELLLVFFPVLKNTGIRPGAVAHTCNP STLGGRITRTGD*DHPGQHGETLSL
2589	16490	A	2606	3	455	KRYGCFSKRMNKRSATNVFFCARKGEVL GLLGHNGAGKSSSIKVITGDT*PTAGQV LLKGSGGWDALEFLGYCPHENALWPNLT VRQHL*VYAAVKGLRKGDAEVAITRLVD ALKLHDQLNSPVKTLSQGLKIKLGFCLS ILGKPSCGILA
2590	16491	A	2607	1	429	VDYTVRKFCIQQEGDMTNRKPQRLITQF HFTSWPDLGVPITPIGMLKILQKEKACN PQYAGAIVDHCKA*VGRTGTFGDIEAML DMMHT*RKVDVNGFESRNRAQSCQKVQT DMQYVFIYQALLEHYLYGDTELEVTCLE TPW
2591	16492	A	2608	166	435	KFLSNNYVHFKQNFKKVLKFIKHLVLNY FKNIVLGQV*RATPGIPALWEAETGESL EPRSSRPTWAMWRNSISTKNAQIKNIVL RILDPG
2592	16493	A	2609	228	431	IFSKICIFNGFNYFPIVGHIGRIYLFIE TGSHCVTQAGVQWCDYGSLQP*TPGLK* SSHLRLPSSWDH
2593	16494	A	2610	439	175	RNGGLHLWSQLLRRLRWDYHFSPGSQGC SKS*SYHCTPAWVTQGDSSLKKQKRKIS TYTSILSVLNETVYIIVYYTKKLDTSFK RKKL
2594	16495	A	2611	1	439	LLGSILSSMQKPRGLVDQETLRKAR*QA ARLNKLQEHEKQQKVEFRIRMEKEVSHV V*DSGHITT*VQSMNSIERSILHEVVEV

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						DGLTSFYFGEDDDCRYGMIFTKDAAPSD EELDSYRRAEEWDPHMADDKRKLTELAQ RPDDDA
2595	16496	A	2612	1	439	VIRKVTGTEGSSSTVLDYTIPSSTGGMP VRKSEDQTDTKRTVIKTMEDYNNDNTAP AEDVIIMIQVPQSIWDQDDFESEDQDDK STQPISSVGKPATVIKNVRTKPSAIVKY PEKESEPFAKILKFTMDVSHEVIPHEVK SS*YSA
2596	16497	A	2613	2	453	EKPEKEECNLWTEMWQENVPGSFGGIRL YLQELMTITQKALHSQPWKMKAQGAIAM ASMALQTNSLVPPYLGMILTALVEGLAG RTWALKEELLKAIACVETARSAEL*KSV PNQPSTHEIIQADLKECSKENGPYKI*P VICAADILHA
2597	16498	A	2614	2	441	LEPALPGRWGGRSAESPPSGSVRKTRQN KQKTPGNGDGGSTS*APQPPRKKRARAD PTVESEEAFKNIMEVKVKIPEELKPWLD EDWDLVTRQKQLFQLPAKKNVDAIL*EY ANCKKSHGNVDNTEYAVNEDVAGIKEYF NEMLGT
2598	16499	A	2615	1	430	RGDRDLHCTESQSEASTEEGHDSLSVGI FEEDSQLEFILDPPKSKPPAWLNGIMTC *DFELLNPRRVRFLLEVKDLALTRRQIL LHKGLSDYEKSTTLQELVLKKSSRSGPP LSIEDLGLNFQL*PSSRVYGFTAEELKP SGE
2599	16500	A	2616	373	552	ICKIKYKLFNSALLFFRQGLALLPRMEC SGAIKVHCSLDPLGSSNPL*RKIKESTL NLEKSLCTRGIFLCKYEEVPKQFLKICF QIFLETGSRSVSQAEVQWHDQNSLQPRT PGLKSFSCLNLPKCWDYRCEPPRRALCS
2600	16501	A	2617	498	157	QLIGSSTHQAALRSRSLPPPAGPGTFHF HYQGKAWVVKGGTSPDSLPSLLGRGVSV QLHPRGKEQRGASDT*HKCPVKLWTIGG KYRVSETSRIFSLPPTTLQRAGLDSGSG SL
2601	16502	A	2618	255	389	LSEFYTYEGPSIRPPIGS*GTNLPLPLS YIPRSPSAVDDENLLDE
2602	16503	A	2619	3	207	QHSSLIIIRAIAIKLGIAPFHF*VP*VA QGTPLTSGLLLLT*HKLAPISIIYQISP SLNVSLLLSGT
2603	16504	A	2620	3	207	QYSSLIIIMGVGIKLGIAPFHF*VPEVA QGTPLTSGLLLYT*QTLTPISMIYQISA SLNVSLLLSGT
2604	16505	A	2621	45	447	WRRIDCRLNLCVTTASLKHFFSIAHKFH LHNGSHLQSQHSCEAQLRRTARFIICCL PYGESGQSWPTLTLERANLNWLTVYFNN WKDWEYDSDQYMSNFDRSSEMMNIIVW* RSIDNLPHIICSTLINTKNSFL
2605	16506	A	2622	3	142	GNQATPKTAPATMSTPTILVATAVHAYR **VAEKEHPLKFGGRACS
2606	16507	A	2623	2	453	HGPGGLLDYIDKERIRDFLNGECMCEVP DGGLVPKSLYRTA*DLENEDLKLWTDTI YQSASVFKGAPHEILIQIVDASTVITWD YHVCKGDIVFNIYHSKRSPLPPNKDYLI AHSITFPDGNNVHLNNKVWMLGPDYIMW ITTLITNNEN

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2607	16508	A	2624	1	315	EEKQAPGFTTGRGKLTPLFCAHAVRFII STSLIYKGAYP*ALKGKEKY*LAVFWVY NKKGLNNNNLFLDGVHLCFVPEVRKYLA GKGLPFSIGLYHLIILLFFFF
2608	16509	A	2625	232	478	LDCGNYFTV*MYIKTSHCIP*IYIILNF HLYNFRYNLGDYNGEIVSEVMAQRQPMK PTYAIPIIPITNSSQFKHQEAMDVKE
2609	16510	A	2626	3	430	TSTPNVHMGSTSLPGDSTTIEDAIQSHS ESASPSALSSHPNNLSPTGWSQPKTPVP AQRERAPVSGTPDRDKLRPCGQRD*GYY WEIEASEVMLATRIVSGSFGTVYQGKWH GDVALAILQVVDSTPEQFQGFRNDVAGL RI
2610	16511	A	2627	2	341	ALQKHEDTDCPCVVVSCPHKCSVQTLLR SE*SAHLSERVIAPSTCSFKRYGCVFKG TYQQIKAHEASFVVQHVNLLKEWSNSLK KKGSSFDKECVDKNKSIHCWHIQICSSV I
2611	16512	A	2628	2	179	RHTGLWVTSLPAVFPGQVRRTLFITGLP RDARKETVESHFR*AHWLVGDFSPCCIS RTGEADPVHHRTPQRCQEGDCGEPLPVS RWVGSFLIHYIQEHCL
2612	16513	A	2629	1	418	GFSFCHPVPVKWRHRDSPQP*TPGLK*S CLGLPKCWDYRHEPLRPANISY
2613	16514	A	2630	3	442	FTCGTIIIAIPNGVKEFT*LATLHGSNM K*SAAVL*ALGYIFLFTVGGLTGIVLSN SSLDIVLHDTYYMVAHFHYALSIRAVFA IIEGFIH*FPLFSGYTLHQAYA*IHFTI IFIGVNLTLFPQHFVGLFGMPRQYSDYP DAYTTR
2614	16515	A	2631	2	454	AAPMELICWSGGWGLPSVDLDSLAVLTY ARFTGAPLKVHKIINPW*SPSGTLPALR TSHGEVISVPHKIITHLLKEKYNADYDL SARQGADTLAFMSLLEEKLLPGLVHTFW IDTKNYLEVTRKWYAEAMPFSLNFFLPG RMQRQYM*RLP
2615	16516	A	2632	131	410	WMWSSKAPHCFRLPSIGDADTVHQCAMS FQKGHSALEGVLHLVFKPDLVYQTLLQM PPRKCCLWPGAVTHACNSMTLGGRSR*F TRSGVQDQP
2616	16517	A	2633	2	230	FFSETSSLLEIQGIARHGGTWRLRQENN LNPGGGGCSELRSCSCAPAWVTVRLDLR KKRNRNP*KILKNYLKIFVI
2617	16518	A	2634	2	370	GTSSSDPAQPGDDKEFIDASRLVYDGIR DIRKAVLMIRTPEELDDSDFETEDFDVR SRTSVQTEDDQLIAGQSARAIMAQLPQE QKAKIAEQVASFQEE*SKLDAEVSKWDD SGNDIIVLAKQ
2618	16519	A	2635	2	376	MTDTDALY*RELFDPADKDKMDHSRRGI ALVFNHERFFWHLSLPERRCTCSDRDNL TRRFSDLGFEGKCFNDLKAEELLLKIHE VSTVIHSDADCFVCVFLSHGERNHIYAY DAKIEIQTLTALF
2619	16520	A	2636	1	461	DMAFLILTERKILGYGQGRIGPNVACPY GLLQPFGDAI*LFTKEPLKPVTSTITLY ITAPTLALTIALLL*TPLPIPNPLGNLN LGLLFILATSSLAVYSIL*SR*ASNSNY ALIGALRAVAQTISYEVTLTIILLSTLL

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						IKGSFNLRSLITT
2620	16521	A	2637	2	384	ENFKALAMIAFGQYRQKRPFEDHVKLAN D*LNFAKTCVADESAENCDKSLHTLFGD KLFPIATLRETYLELADCCAKQ*PDIHE CFLQLKYDNPYLPRLVKPNVDVMCTAFH DTEETFLK*YLYEIA
2621	16522	A	2638	1	373	TFIYLLFLFSSAYSRGVFGRDAHKSEVA HRFKDLGDENFKALVLIAFAQYLQQCPF EDHVKLANEVTEFAKTCVADESPEN*DK SLYTLFGDKLCTVATLRETYGEMADCCA KQEPDRNECFLQ
2622	16523	A	2639	2	375	KGPCYRLVSTGTQRRHPGAVYLNKHLC* CNVGKA*GPHCEKCTLPCTFNEEPLKAL TFFREHGP*VSDPEVATAPTEKEIPSLD QETTKLEPGQPQLSPGISTIHLHPQFPV VIEKTSPPVPVEI
2623	16524	A	2640	215	478	KYFLASHTSLFIICYTAHLTCTIAEPKQ IESHFGKRLDADLVF*KSDDSTVVDVIP SKPV*TSGLFSGKCL*HIVEGIIRAVDP RKLY
2624	16525	A	2641	208	376	ILRNLIKNHFWPGVVAHACDPNTLEAM* GQITRSRDWDHPDRHGEAPSVLRIHRLA
2625	16526	A	2642	424	2	KGEPLPPLGGWKT*GPRAFPQAQIPHAG FKTRGCPFPLPQGRNKAQVPNPFCPRER FLPGKGSGRVAPLKNGAQLGGPPFYPHP FGGPSPRVPLGFGVQTHLGNKPKPPFFP KKKKGGTGCSVGNWGPKSSQTLPSPQAS
2626	16527	A	2643	190	3	ELSTRGFQGPHRRIAGLKQCLVMFPELE RSGGLSEH*HLHLPGSSDSRASAS*IAG ITSVCH
2627	16528	A	2644	2	339	CCEKPLLEKSHCIAEVENDEMPADLPSL AADFVESKDVRRNYAEAKDVFLGMFLYE YARRHPDYSVVLLLRLAKTY*TTLEKCC AAADPHECYAKEFHEFKPLVEEPQNLIK
2628	16529	A	2645	81	369	VEVTGQPQNASFVKRNRWWLLPLIAALA SGSFWVFRTPDG*TSVVR*IHNHMTQLI NNHLRA*YSVYRDIYFLWIAI**SS*PA SVLLFTADYCPE
2629	16530	A	2646	1	348	DMDMNPLRPQNYRFG*ELKADIDYHFKE DNDEDDHQLSLRTVSLWAGAKDD*HIVE SEAMNYEGCPIKVTLATLKMSVQATVTL GGFEITPPGDLRMKCGSGPVHIMGLHLV AGEE
2630	16531	A	2647	1	178	GYTDTILDVRSQRVRSLLGLSNSEPNGS VETKNL*QILNGGESPKQKGQEIKRYDL YLT
2631	16532	A	2648	181	244	TIKRYKNVMIFYYFNFF*R*GLNSLAQA AAQWCNHGSLQNQPPGLKGSSCLSLPCS *GYTIFYLSIHQLIDIWIVSTFSKLFLH VSAYSSIKMS
2632	16533	A	2649	2	369	KWITFISLLFLFRSVYGKFEFLLDAPKN DVAHRFIDFGEQHFKALAEIAFDHYFLH CPFEDLVTLVNE*TEFA*TCLADESA*N CDKSLHTLFGDKLCTVATLR*TYGEMAD CCAKLEPERI
2633	16534	A	2650	1	349	VTFISLLFLFSSGYSRGVFRLDAHKSEV AHRFKDLGEENFKALVLIAFAHYLQQCP FEDHVKLVNEVTEFA*TCVADESAENCD

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						RSLHTLFGDTLCTVATLRETYGETADCC AKQD
2634	16535	A	2651	21	403	CVCCVCVRESRTESLPGDNEDFNVKNAS VKDVRCVHFDCDSQNDPPMEATGFTAQV TIYSLINLLHRLKYFETLDLH*IAIFFS KVSILNHPGQIIADYAPALDCHTCHIAC KYAELKEMIDRRSVK
2635	16536	A	2652	1	355	ARMSITDTYGQHLIAGGLMTQEDVSEIK SSYYAKSNDHLNNMAHYRPTALNLQAHW HGLAQAEAQITTWSSGVPFDLLLMVGMM TVQVP*ELQMHSHLLKTHDQSRMENMMY GIKLDW
2636	16537	A	2653	2	360	LFEHLG*YKFQNALLLRYTMKVPQVLTP TLVKVSRNL*KVGIKCCKHPEAKRMPCA QDYLSVVLNQLCVLHEKTPVSDRVAKCC TESLVNRRPCFSALEVDETYVPKEFNAE TFTFHAD
2637	16538	A	2654	360	314	YTCAIVPCKLFWWCCRDRVSLCCLYWSQ TPELK*SSCLSFPKC*NYGHEHTWPARI IFLNLYNKSG*TATRKCPPTKVTPSSHQ Q*HCTWPYFYFK
2638	16539	A	2655	1	353	NWTL*TLKKIFSLKDAIKRIKIQSVRWK KIFAKHTSDKGVESKYI*RTLINQ*ENN SIKNWSKNLNRRFTKDIQKANKHMLSAT SLVH*ESKLK*Q*YHYTSIRVAKMKKTD YVTSW
2639	16540	A	2656	340	10	GREDKSEKCYLKPGRSQPDRGAPKSSPG VP*PPAPPALPGPGRSSPFPQGSLAGKD LRPRQPSQPGGPGELIFPVKTKKKKIKE RKTLLAWTRSNERPEIAQREGGCLRQ
2640	16541	A	2657	509	261	IPYFKIHCLHSALGVAETEKETAEHLDL AGASSRPKDSQRNSPFQIPPPSPDSKKK SRGIMKLFGK*VKQ*TSGMGPVLHVA
2641	16542	A	2658	345	3	SAHLSHPKCWDYRREPLHLARISFLFKA SSPLYGRATFYLSTPPLMDGRWVASIFW LL*IVLP*AWVYKYLSETPLSIF*KTGS LSVAQAAVQWHNHGSLQPQTPGLKRSSH L
2642	16543	A	2659	271	56	VILYIVMPIPRPCPHPHPYIHTHTHTHT HTHTHTRLGKREF*LYSW*LPGYSTNGN KIFLEIYLLPILLKM
2643	16544	A	2660	366	68	PGQQSKIMPQTERKKGRKEEREEREEKE EREGRKEGRKNEGTETVIEGGSSKTQEQ TRIKAS*LNSLYTTVKPQRRLKGGKKHP KDSNFKD*RNISPHR
2644	16545	A	2661	351	199	LLRRLRQENLLNPEGRGFSEPRSHYYSP DWATE*DFWSNKIK*QKVQYSKY
2645	16546	A	2662	1	160	ERAWLHLSPGDGVCSEPRSHHCTPTWVT E*DSVANQPGWDRVRLCLKPTWVTE
2646	16547	A	2663	233	3	GRDNWLKTVAKPESLSGKRGPSLLRKVF NPFPVYILFLPQAPKGKWLSPFPPFFFF FFFLRGSLAM*PGCSAVAQS
2647	16548	A	2664	96	349	QMPSSVLTRVANAYYSGFFFWFLKQKFC FVTQAEVQGRSIS*PGPLVPGFKRFLGL TLLSTWNCRRAPPGLVIACGFKMSLLTL
2648	16549	A	2665	322	74	DTYTLPRLNQVESLNRPITGSEIEAIIN RPPTKKSPGPDRFKAKFYQRYKEELVSF LLKLFQ*IEKGGIGWARWLMPVIPVL

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2649	16550	A	2666	2	228	NLALSPRLECKSQGFTMLIRLVSVS*PC DLPASASQSAGIMGVSHHAQPFLHSYLR PLILIKGDQFKYAFNLFSC
2650	16551	A	2667	129	301	VRPLAGLGSPLIFFFFFEKSLAFVAQAG GQRHNLG*LLPLPPGLKGFSCLNLPSTW D
2651	16552	A	2668	318	21	FSLLVKDFQNDLAVNSSSIFPSTFLFLV RS*LDFVNLNFFNFYLFRDEFSLCCPGW TRIPRLKQSSRLRLLSSWGYKCVPLHPA INRFL*CDFSISGY
2652	16553	A	2669	2	322	QDGLDLLTS*STRLGLPKCWDYRREPPR PAPINKCLLSIYHGPGPSLGTEGEKGQD YIPAIEQLTDQWRRLTWTGCYCAAVAED SMGVVWPLLPGYEAEKEAGRFH
2653	16554	A	2670	29	261	EFNTLSKCVWIY*LFSLSLSLSLCVCVC VCVCVCVCLCVSVCLFYGSPICLHFMHP DTLSEESFHFLQIISKELLKC
2654	16555	A	2671	5	224	GSAWWLTPVIPALWECKAGRSPEVGSLR PA*PRDPPALASESAGITGVKKNLIAEL WEVKSCILLIFISLDKV
2655	16556	A	2672	126	321	WGRRGARARRDSHRALRVSPELALLELR PSTMAHICNPSALGGRGGWIT*DQEFET NLANLEKPC
2656	16557	A	2673	360	74	SRLLRKLRQEVGLNLGGRGCSGPRLHHC TLAWATERDPDSKNKTNQKNKQRR**TL PETNSLLAWEPDCVCKTNKLATRLEIMA QKSCSQRPQYH
2657	16558	A	2674	192	357	RIRKWLYYYYYYLLRWSLALSPRLECRG TILAQCNFHL*SSSRSPASASPVAGIT
2658	16559	A	2675	236	375	EEVLYSRKDRHVASYSRK*W*RSGAEAH ACNPSTLGGRGGWITRSG
2659	16560	A	2676	236	2	ATKVSINSIGTLGVKVGGLLEGRRLRPG PKQSSCLGLQSSWDHR*VQPHPGNNFTL FVETRSMLARLVSNSWPQAIFQ
2660	16561	A	2677	164	389	LTVQHGLRGLRKLTVMVESEGQASHLLH KAAGRRSECQQGNCQMLIKSSYQPCAEA HACNPSTVGG*GERITRSG
2661	16562	A	2678	208	1	CSVYEGSCFCILRVRRVCVCVCVCVCVC VCARSCIYVRSENH*KQLPSSSILT*RF *IQSTFRSNKRLR
2662	16563	A	2679	159	382	RWLIKNHPTQARIQVRGLLDRDCQTQTW LWESGVQPLATTPRRHSEMGGWPGAVAH ACNPSTLGGRGG*ITPPRPESKLEDCLT GTARHRLGCGSQGCSLWLPPPGGIQKWG VGRAQWLTPVIPALWVAEAGRSLEVR
2663	16564	A	2680	29	367	DCQSEQLRKLRWEHHWSQGV*GCSQP*S HHWTPAWVTEQDPVQNKQTKNYNTHQRA GEVWREINCLSTEQLTELYSEITQILAL SVRN*KLL*YVKSSVISAETQISGGKIF
2664	16565	A	2681	256	1	ENIVPVRFLCIHRLFAILIMVQ*LERKR DHIVIHLNLTLETVYLKKWQTRPNAVAH ACNPSTLGGQGRRITRSRARDYPGQHGE T
2665	16566	A	2682	1	395	LLIEHILIAMALLILTERKILGCIQLRK GPNVVGPYGLLRPFTDAIKLFAREPLQP VTSTITLYMTAPTLAVTMAVLL*TPLRI PNPLVNHDLGLLCILATSSLADY*IL*S R*ASHSNYALIGALRACPH

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2666	16567	A	2683	3	349	VRIDNAAVCLLY*AWAEFIWALANLIIR PDLDHPGNLLGNDHIYNVIVTAHAFVII FFIGIPIIYGGFGN*LVPLIIGAPDMAF ARITNIRF*LLPPSLLLLLASAIVEAGA AGT
2667	16568	A	2684	99	2	LTVAHACNPSTLGGQSG*ITRSGVREQP GQHG
2668	16569	A	2685	325	4	SSFPMSFIINSFIIIFLYTTIFLIFYDV VYSPEFKP*VCFCLTECWDYRREFQCSF LPCKRV*VLAPFIKNFFFFFFFLRWNFI FVAQAGVQWRHLGSLQPPPPNFK
2669	16570	A	2686	382	269	MGFHHVAQADLELLGTNDPPALASQSAG ITGVSHHAQPKLTF*TFSY*ACVGGSSP QFILVVQHGLAGNSFCCF
2670	16571	A	2687	3	381	GHLYALTFFFNSQICLFPRIYKTCKKSF WLPFLNLVSLCAIEGYKTKKVPSNV*KG IFIHHQTGFILRMQGWLNI*TSINGIYH ISRIEDKNHKTMFIDAEKWFHNI*HPFI IENIRPGVVAHICN
2671	16572	A	2688	289	91	IKYKELGVACSKTSRNVSYYCYHHHHHH RCHHYHHHS*RLAALCEESGWRKALGST SMGRVAFHRH
2672	16573	A	2689	3	211	LHHVGQDGLDLLTL*SAPLGLPKCWDYR TEPPFPAPNEFLLLHSLLSKHYALGRPH TPRERKKASGILR
2673	16574	A	2690	2	197	DLLTS*SAHFGLPECWDYRREPPRPASY AFIKYFCPALSCFWCIETGPYLIFAYLR EESFVRSRT
2674	16575	A	2691	253	356	AVPVKMAIVKKTRNNRCW*GCGEIGTFL HCWWEC
2675	16576	A	2692	211	339	PGHPLSIILQWIWGEDTRRGPMHEALH* PCCSELRSCHCTPAWPTE*NSIF*KKKK KWLGELKEKQKNMACANDP*PGHPLSII LQWIWGEDTRRGPMHEALHGKSGDGVYA VRLLTAY
2676	16577	A	2693	1	175	RHEGLNLGGRGCGEPSSCHCTPAWVTE* DSVSKKKRKGKKKSALILIFSNGVLFCH LG
2677	16578	A	2694	234	13	KTSREPWSEFLSIKGEQQCSFGLLYVFC FQMESHYAAQAGV*WCNLG*LQPPPTGF KQFSCLSPLSPSSPASAS
2678	16579	A	2695	149	2	SQGEDFTKTRALQWRSRRSVVAHACNPS TLGGRGWWIT*GQEFKTSLAN
2679	16580	A	2696	2	194	CIGLGVVAGACSSRLRQENDMNLGGGAC SETRSHHCTPAWVTE*DSISKKKRKRNR WGGTRFSN
2680	16581	A	2697	338	357	YLIRRKKISNSKS*FSWPGVVAYACNPS TLGGRGRRTTRSAVRNQPGQHGDPKFFL VSS
2681	16582	A	2698	53	293	TISIKSKKWKNKQGEYNKWCMENWLAIC RRLKLCPYVLVHSCIAIKNYLRLGNL*R KEV*LAHSSTGCTGNMAEKPHGRR
2682	16583	A	2699	2	335	LYAAKVPLQKACIRTFSYISFFIFFFFF FFGKQSSFGPPGLKARGGTPLIGTPPLG VKRNFLPQFSGKPGITGCPPLPQKFWFF KKKRGLIF*PGGVPNSDPKGIGPPNPP
2683	16584	A	2700	166	3	DYRRVPPRLVKR*GFTVV*AGV*WRNHG SLQTQTIGLKQSSHLSLATCWDYRYE

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2684	16585	A	2701	209	340	YRMTVFPARHGGSHTCNPSTLGGRGGWM T*CHEIETTLGNMVKP
2685	16586	A	2702	78	341	EVACNCLLPAIGCFASVTYV*SSVLL*F EL*VLNENSSF*NFIH*FF*NRVLICCP DWSVMA*S*FTEALTSQTIRSSHVSLPS SWDY
2686	16587	A	2703	258	185	TMIAPVHSSLGDRARPYLFKQKR*GLAL SPRLEWTGAIIVHRNLEFLCSSNPPTSA SGVTGITEMEVERHGWIQETFWK
2687	16588	A	2704	361	41	NFGPVYKTNPGPSRPGWGPLGKPPGPQK FFPFGVPPSPPFPKKGSVFSPPGGQKGP FKGVFWGFP*PRGKKTPTQQPGPSPKVP NWDFPKGGFPKKKKKKRKILRN
2688	16589	A	2705	12	329	SCTLQLTTPRLK*SSRPSLPNN*DYRHV PPHPASFP*FSEMF*DSTQIFLNSLKFS S*YYLVIFFFKMEPCSITQDGVQWCDLS SLQPLPPRFKRFSCLSLPSTRP
2689	16590	A	2706	232	1	KRKRKSFKTYYKKFFLNSSFKNQCPYAI GHIFRSIIFFFFLRQSFGLVA*AGVQWQ DLGSPQPPPPGFKPFSHLRLR
2690	16591	A	2707	135	1	CFFLIFFFFSSDTQAGV*WPQPPGIKRS SQLSSPRSWDYRRISPR
2691	16592	A	2708	1	157	LDLLTS*SARLHHPKCWDYRREPPRPAD YKYFLKEVASLIVKLYLFCKLNFE
2692	16593	A	2709	88	344	MQEHYYFIKRGNKMIIRKYVQLHANKLD SLDKIDKFQVKNHQN*L*KK*KSWPGAV AHACNPSTLGGRGGWITKS*DRDHPWLT C
2693	16594	A	2710	1	383	LHKVTTVLRFLSKFHILVLYFYYTCVHV SVSDMWCWFLY*IFTDMYNAVFQ*LDFF KLSIKFLRCIC*CVY*IFIPVFIYCFFL YLICLFLSYFLFNIYVMLLFYILCIIYF YVIFSSSSIF
2694	16595	A	2711	227	1	IFFFSNSFLKISLGFFLNFAFF*KPKFF PFLSFKINQNFFFGFPFNFLKIFFKFFP NKFFKF*IYLTFFKKTKPK
2695	16596	A	2712	1	136	KNTKISQGWWPTPVIPATQEPEAGGSLE RGRQRLQ*RNLGSLQPLPPTFKRSSCLR LLSSWDYRRRPPPLANFCIF
2696	16597	A	2713	3	349	LIPRGQGSTVVLPYNPATSIFGNDLNEI KMYGHAKTCIWMFMTSSFIIDRTRKRQ* CSSVREWINKQ*CIQTMELVFGRNFFFF FFFFFFFFFFFFFFGGPPPPKIQIFKEI NPQ
2697	16598	A	2714	181	342	TSQLLNLPLPIIKA*AIRQEKEIKGIQL GKEEVKLFLFAHDTIVYP
2698	16599	A	2715	3	205	FRHVAQAGLELLSASSLPTLASRSAGIT GVSHCVQP*TVSSLRLGFYDTSFKIADI QSCFSWVLYYCLQSAEL
2699	16600	A	2716	388	23	ASNQSKNSFEKGEKNQQSVMVKTSQQAL NKRAFFDMIRSVYQKTYK*RNA**ERQS FSLKVENKKEYPSSLLLFNIVLKVLVNT GHKEK*KAHRFDRNIIQFANDMIVYVEN PKDSTKRLS
2700	16601	A	2717	4	194	FSCLSLLSSWDYRSMPPHPANFLYF**R RGFTMLARLVLNSWPHSAGITGVSHHAQ PFNYFFI
2701	16602	A	2718	1	212	LCCPGWWETARLKRSSRLSLPKCWDYRH

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						ESLHLAFGFFLL*YFGPYLMVYVFSFNL YDFSLVYSLYGTSI
2702	16603	A	2719	53	299	KAVHVNIFFITKVHLTMETQIVSLSLFP FPSFLHPSLSLSSFL*RDRVLLCYPG*S AVVQS*FTWPQIPGLR*ASCISLVSS
2703	16604	A	2720	139	320	QPTMRHSFSF*KQEISIFLKVSSSLHHT LRFLFFFFLLDRVSLCHPGWSTVALS*L TVAW
2704	16605	A	2721	1	99	IILAYSSITHIG*IIAVLPYNPNITILN LTIYM
2705	16606	A	2722	215	361	LTFFFFFFERESNFVTQAEMQGGNLV*L KPRPPGLKHFYYLSLQSTGNY
2706	16607	A	2723	335	24	AIPLRPEF*THPGQNGKTRFPLKPQNLT GVGGNARYSQFPKRLRLKIPLNPEVGPS INPNFHPGIPFWAQKENFFPKKKKKKEI IMLNFSLICYNLFFLYICY
2707	16608	A	2724	27	314	WKQLKYPPSDEWINKMWCIHAMEYLAIK RNKVQLCVT*RWRWLMDTKKK
2708	16609	A	2726	1	112	GFHHVSQDGLNLLTL*STHLSLPKCWDY RHEPLCQAR
2709	16610	A	2727	271	3	RSPMLKNQAIKSVIMVYIGTIWRSAGPF AIFFIAEYTNIIIIITLTTTIFLGTTYD ALSHELYTTYFVTKAVLLTSLFL*IRTA YPRFR
2710	16611	A	2728	121	1	ENKYRPGAVAQAYIPNTLGG*GGWIT*G REFETSLTNVEK
2711	16612	A	2729	2	290	NRHFTKENIQMPTRHKKRDPQSSLVIRE MQTKTKVRYYFILTRMAKVKKIDNTTC* *GYEKLNSPKLQTTKCPIFEWVNKLWHS QIVEYFSGIQHA
2712	16613	A	2730	98	264	LVSSE***IYQILFFFPEMECHSVSQVV VRGSNLC*LHPLPPDFKRFSCFSYWEG
2713	16614	A	2731	2	286	PFYKATVIRTVWYW*KN*QIDQWNRKES PEIDLHK*SLLIFAKGAKAIQWRKDSLF NKWC*NRWISTCKNESMLGVVAHTCNPS TSGGQGGRIA
2714	16615	A	2732	323	181	RDFVLLVEITMLARLVSNS*PCDLPASA AQSAGITGVSHRARPFLDL
2715	16616	A	2733	272	131	GRVDRLNPGGGGCS*LGSCQCTPAWVKE TPSQKKKNKIICFYAFLFI
2716	16617	A	2734	227	87	AASTLTLTSLIPPILTTLVNPNKKNSYP HYVKSIVASTFIISLFPTTIFMCLDQEV IISN*H*ATMDFT
2717	16618	A	2736	25	415	FSKYLLDHQLSAGLLVEQHRGSLCPLSL LHSDSSLSFAVSGKVSLAASIRNKLELP ET*RALMM*NHGHPLEFGGM**PWT*EP GS*RC*ELGQPGQARRLACNPSTLGGRG GWIMRSGVRDQPGQDVET
2718	16619	A	2737	390	1	KGFFLETKRKFFFTNGFFPLLGGKGVPF PGKRLGPPILGFYPPQRVFPFPKPPFFP PGPFKRGQKPPGGGKNF*RGPPGPPKKG GAPTGKKKKKEEERKEKEKKTPRNISKP LSHPFPNFPFCATVRGFS
2719	16620	A	2738	96	331	QFTYTHGLFPFNFNRLCVFFFS*KLVGG V*LCCPGWL*TPGLKQSSCLSLLSTWDY KGVPPCLAEHFFFFEKKSPLSL
2720	16621	A	2739	379	14	LREVFPFFSPPKIKCFSKNSPQKYFPPP VVFKTPPTPPFFFPPLFGKNFFFPSLFN

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						FCPPRGFF*RPPLFFFFFFFFFFFFFFF FFFFFFFKVFYSLLLLYFLFILK*MLTF KTSISTQCY
2721	16622	A	2740	198	38	ANPLFFFFFFLRDGVLVYRPGWSAVVQS *LTADSTPWAQVILQPQRNPIEHDF
2722	16623	A	2741	290	39	MSKVGPLLGVLGTSFRVLLKGPEIKGDP LLANPLFFLFFFLRDGVLVYRPGWSAVV QS*LTADSTPWAQVILQPQRNPIEHDF
2723	16624	A	2742	1	399	ILIRKHSDIGTLYLLFDA*TGTIGTDLS VLNRTELEPDQATLLGNDPVHEVIDTAH ALGIIFFIVIPIIIGGFGN*LVPLIIGA PDMAFARINNISF*LLPTSLLLLLASAI EEAVPGTG*TVYPSLA*NYCR
2724	16625	A	2743	398	2	SPPPLIFFLWGFSYIFPPPKKFFFLINP PPKFSPPPFFFKPPPPFFFFFPP*EEKK NFCSPPPFSPPPPFFLLPPPLFFFFFFS LKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKRARSRSRTSPTRP
2725	16626	A	2744	295	185	FFFFFFFFFFFFFFFFFFFFFFFFFLF FFLFXFFXF
2726	16627	A	2745	374	4	LKKHKSTRVP*NVKSGK*NFSPPFKIRP WAQKRAKKKGAREKKAD*EKGEFGKLKK KKSFRPGKKV*G*PKGFQRNFEKKPVKS QGPVNMGVIPAFEKKPRIPPVAKIPI*G AQKKKGRPLAI
2727	16628	A	2746	2	382	QDATAPIIDELISFHDHALIIICLICFL ILDALFLTLTAKLTNTNISDAQEIETV* TILPAIILDLIALPSLRILYITDEVNDA SLTIKSIGHQWY*TYEYTDYGGLVFNSY ILPPLFLEPRDLGLL
2728	16629	A	2747	2	374	DWPPTVKRKTNPRAQSTAADRFILLFTV RGLTGIGLANSSLDIVLHDTYYVVAHFH YVLSLGAVFAIIGGFIH*FPLFSGYTLD QTYAKIHFTIIFIGVHLTFFPQHFLGLS GMPRRYSDYPDA
2729	16630	A	2748	55	230	QIPAK*INKYLQN*KKKKKKKKKKKKKK KKKGACLKKPHGGAKEKSWGRQKLFSFK GG
2730	16631	A	2749	161	3	NGNYTLVKKCFNTKEKIKWVKN*IFFFF MRWSFTLVAQAGVQWCKLGSLQPL
2731	16632	A	2750	362	1	PEKKSFAIKGVKKAGKQCKFCDAPKKGN PPKKKNPTGTPKRVLKK*PPREEKKNSP QRKKKNTAKNKEKEAPQEEI*KGPPRYI FFFISFFFFFFFYFFFFFFSIVINLFGT FIATTLEA
2732	16633	A	2751	311	110	ITLPRHGGPHVQSQLFKRLRWKDHMSLG DRGCSELSSCHCTPVWRQSKTFSKIKYG RNGTDKAATCNPGRFRSWGRKVA*GQES ETSLSNSRTRL*KNKIWSKRDRQGGYL
2733	16634	A	2752	223	16	KKTPQKKKNTEGKGPVKKSPPQKFLKST PP*IFFYVFCFFFFFLYFIYLLFRIFSF FFILFVYYLFILP
2734	16635	A	2753	367	10	PAPRGGVYRGRQASLSCSGLHPLRASWP LCSPTQA*AMAGAPPPASLPPCGLISDC CASNERGSVGVALS*SGAGDNLLVCRLL SGKCRNHPSSASLTLAAVDWSCSYSAIL APPLKNS
2735	16636	A	2754	14	341	PGPNF*FGGQNSPGKNQNLSLPT*KGNG

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						PGNPKNGGPTVPGTPPETRGSLLRTLQG PLRPSGTPPTRRAPGTPVGNPGF*PRDF FAQKGPNVREGLKQGPNPKGLNPPP
2736	16637	A	2755	15	172	HSWWECKLVQPL*KTVRRFLKKLKIDPP YYPAIPLLGIYSEERKSVKQSRRG
2737	16638	A	2756	263	2	QKPLPPRNDPVFPKGPERTPRPTWGFIP GGVPLGKFFTLLVSPFFFFSPSPNLFF F*NRVSLCRPGWSAVV*SWLTAASTSQA QAI
2738	16639	A	2757	311	106	FVCFLRQRLALLPLECSCVILAHCNLRL LCSSDSPG*QSETVSKKKKKKRKKEKET GNL*RSLDMKGR
2739	16640	A	2758	23	328	NITYYT*LFVLYFYVPGHTVVFFFXFXF FFFFFFFFFFFFFFFFFXFFFFFFXFFF FFFXFFFFFFFFFFFFFFXXFFFFFFFF FFFFXFFFFFFFFFFFF
2740	16641	A	2759	1	338	DR*LFSTNHGYIGTLYLLFGA*AGALGT ALSLLMRAELGQPGNLLGLDHTYNGIDT AHAFAIILFMSLAIIIRSFGN*LVTLII GAPVLAAPRITDISW*L*PHSVLLLLA
2741	16642	A	2760	120	2	INKYAWLGTVAHACNPSTLGGRWTA*GQ EFKTSLANMVK
2742	16643	A	2761	251	3	CRGQIGTPTLHYSSSSSSKWIKDLNVRV KTIKLSENTGVNLRELELGDCFLDDTKS KNSTRKIRK*SLKLETFFLGGTR
2743	16644	A	2762	11	303	ALVLKRSSCLDLLKCWDYRHEPLHLALS EILMYRFCL*IFDIFFYWYSREIDLIFV Y*FFFFFLETGFWFLLPRGDLG*WEPPP PGYKGSSCLGLPR
2744	16645	A	2763	236	356	DWLIFVFSVERGFCHVAQVGL*LLGSGD PPASASQGAGIT
2745	16646	A	2764	2	332	LTQTPGLK*SACLCLPECWNYRCEPPHP AGFLF*RHFDKGVS*LLIYPGTGWS
2746	16647	A	2765	297	19	KKKSWFFFKKKKCWGGATKFKN*RGFFL KFVFYFFFIG*GVFFFFFFLISIIIFFF FFFFFFFFFFFVFFYFFFFYFFFFFFLF FAMKINVFY
2747	16648	A	2766	1	147	QILRRLRWENCVNLGGGGCSEPRLHHCT PAWVTV*NSVSKKKKNPLLFF
2748	16649	A	2767	357	183	NWDYRPLSPRPGKFLDF*VNRGFPLLTK LVSNF*PCNLPPSTSPKAGISGFNPRAQ P
2749	16650	A	2768	2	193	RWESCLNPGGGGYSEPRSCHCTPSWVTE *DSVSTTTTKEKERKQNRTWSESNSLQK YKDTNHF
2750	16651	A	2769	333	173	VSQDGLDLLTS*STHLGLPKCWNYRREP PRPAQKLLMVIWLGFMSSPKSPLEL
2751	16652	A	2770	3	331	CMENCMVIPPKKVKHKNYHMIQKFYFWK AVQQLSTELNIL*PYDPAITLLGIYPKE LKTSFRTKTCT*MLTASLFVIAKTWKQP RCPSVGE*LSNL*YVQTMECYSVLK
2752	16653	A	2771	209	55	RPGRPQVLRRVRPQNRLNPGGGGFSEPK *GPCPPAWGAQRDFISKKKKTIT
2753	16654	A	2772	213	57	RPGRPQLLRRLRLQNRLNPGGGGCSEPR *GPCPPAWVTQRDFISKKKKTIT
2754	16655	A	2773	148	1	KATGRKTWVKSRCWVGTVAHTCNPSTLG GRGR*TARAQEFKNSLRTLAK
2755	16656	A	2774	2	364	WSAVRRDWITALQPERQRETPSQKKKKK

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						KKKKKKKKKKKGGVRHGVKSRKP*TSGR PGRKNHWRQIQGQPKTPRERAEALKNRV GLKKLFKTPGHVNGAGNPKFRNGKSGKP PEVHLNGAW
2756	16657	A	2775	121	2	HLRSGVSDQPGRHGKAPSLLKIEKLAGS GGTCL*SQLLG
2757	16658	A	2776	195	3	GRVDINTLLALLLIIITF*LPQLIGYIE KSTPYECGFDPISPARVPFSIKFFLAAI PFLLFDL
2758	16659	A	2777	3	285	FLNIRNKVSLCCPS*A*TPGLKQSCCLG LPKC*DYR
2759	16660	A	2778	135	379	HWSATVKLYAILLGLLKWESGTLLCSKD VLFFL*G*SSAYSIESVIMQIKAT*VKG KARVQLGAKKLKAYWQRKSPGIPAG
2760	16661	A	2779	364	1	GSFTGAVILIIAHGLTSSLLFCLANSNY ERTHSRIIILSQGLPTLLPLIAF**LLA SLANLPLPPTINLLGELSVLVTTFS*SN ITLLLTGLNILVTALYSLYIFTTTQWGS LTHHINNIK
2761	16662	A	2780	356	1	GCLRAHIWPQKGNHEGQVHLFIDKVCRQ PMTEDCINEITTQVAQIFLVHFLLRQSL TLSEKRKKRKKKRKKRNRIESPEINTHI YCQLIFNKGAKKIK*G*NSLFNKTYLDP WISTCK
2762	16663	A	2781	1	204	AQVGLQDASSPRIEELITFHDHALIIIF LICFLVLYALFLTLTT*LTNTNISDAQD SETDCYSQSYIL
2763	16664	A	2782	1	522	YKCNECGKVFNQQAHLAQHQRVHTGEKP YKCNECGKTFSQMSNLVYHHRLHSGEKP *KCNECGKTFSQMSKLVYHHRLHSGEKP *KCNECGNTFHHNSTLVSHKAIHTGEKL YKCNECGKVFNQKTTLARHHRIHTAEKL YK*EECDKVFGCKSNLETHKKMQFSKTD SAFSLQ
2764	16665	A	2783	1	327	ENRLNSGGGGCSEPRSHHCTPAWATERD SVSEKEKEQKQNFHLNAQSNCQKLKSP* KYLKHPEKTDILSKASQYNNQLTADQSI LKFKTKTFDQKKGRPKGHGMTYSNS
2765	16666	A	2784	335	128	FSLIFCRAGILPCCPGWS*TPVLKQSSC SSLPKCSDYKQEPPYLACATLKCYQIPN FYCWPHIFKRMFY
2766	16667	A	2785	208	3	RPICPLSLWGVSFLFFFFFLRDRVLICH TGYSAVAQYCNTAHCYSPRLK*SSCLSL PSSWNHNLIPPR
2767	16668	A	2786	49	332	VEMGNSPINRKYVYPKSYNRCLKCNTEE GVLNDLGIAEFNTCSKSLLLLIFFKGRI LLCCPGWIEVVQSQLTASSTLGLK*TFH LSLFGSWDHR
2768	16669	A	2787	331	187	GCSEPRSPPCNAAWATKGDSVSKEKKKN KKREEKKH*HNTSGEKINLI
2769	16670	A	2788	325	34	RSQLRGLPSMSIS*I*NSRLR*LRPRRL FIFCRDRVSLCCSGWSQTPGFKQSTHRS LPKCWDYRREPSPLAQIRYLGLFFSQGL SSAFCYVAMVSGF
2770	16671	A	2789	3	150	AASTRQLIFHFTSKHHFGFEAAA*YWHF VDVV*LFLYVSIYWLG
2771	16672	A	2790	86	311	NIHPLNDIFTRLKNGFKKKEISLVKNEP NKGT*SLISIKVLFHT*K*FIRPGVAAH

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						T*NPSTLGGQGGWIT*SQE
2772	16673	A	2791	2	123	GGGACSEPRSHLCTPAWETE*DSISEKK EEKK*LQIYTNI
2773	16674	A	2792	302	162	PLLRRLRPENCFNLLGGGFN*PRSRNCP PAWATKRDSLLKKNLKNF
2774	16675	A	2793	1	258	GGCSGLRLCHCTPAWETD*DPVSKKKKK KNFTRAKLLIFGTLVLGKVKRGGPFKPR ILKLPWETWQNLVFTKKKKIFFLKNRGG GE
2775	16676	A	2794	199	3	VGPIFRHDKPPHSKQLCTYSPAFTQLFS SGKILKNIHLWPGTVAHACNPSTLGG*A RWITRSGDR
2776	16677	A	2795	1	302	GGCSEPRSCHCIPAWATEPDSI*KINK* INK*K**KINRNKKGKNHFLSSST**PQ VASSFLTGQHRYTKL*SSQKVLLDSATL QSKSNAEVKRVNRTTD
2777	16678	A	2796	228	326	NDNGQSGVVAHACNPSILGGQGGWII*G REFKT
2778	16679	A	2797	270	1	KFGISAPFAPSPKV*KRGFF*NFLGNGP PVKIPPF*TPL*NFSKPGKNFPPFF*KT RFSKIFPNGFFFFFFFFEGVLLCCPGWS ALTRSW
2779	16680	A	2798	307	36	FKNFCCG*EVSLCCPGWSQAPGVK*PSC LGFPKCWDYRCELPCLASCSL*CDRNQT RISAVVLWIEFHLSPILPVLPLFLKKPQ AGLLCF
2780	16681	A	2799	132	5	IFEVTV*CTK*HKRNMQPGVVGHACNPS TLGGQGGWIMRSGV
2781	16682	A	2800	32	314	KQHPGNGPNPSGKGPGRASRFLKKKNFF F*KTPPKKPHTPCKPSPKGKGPERLPWH FFNQKFGPLPMGPNPDQRAGFCLRDP*G GGKNRSPPTL
2782	16683	A	2801	139	3	AASTFYIFFETTLIPTLAIITR*GNQPE RLNAGTYFLFYTLVGEG
2783	16684	A	2802	238	3	AASTSHVISSMYNIYIIIQFKTFPVFFF RDKVSLCHTGWSAVAQS*LTAASAALTS CVQGILPTQPPEYHTRPLRLFL
2784	16685	A	2803	110	291	KKLGVFGFGFGFKTKSNFIMQAKGQLPN LG*LKPLPRGFPQFSGLSLSGTWDYKHT PATR
2785	16686	A	2804	97	2	SYNNQDSVVLEKEKTNRSVKQN*APIPE KKKKKNKVGGLTLPNCKTYYKATIIKTV WYWRKKRQIGQ*NRIESPEIDPHKY
2786	16687	A	2805	268	1	ATFLLFYYVFRPQIPYYL*IFILSLF*Y RHSGPPYVGPPQQYPVQPPGPGPFYPGP GPGDFPCRLPIRKWWLVWLMPQLNPTVW PTIIT
2787	16688	A	2806	153	3	IPLPKGLLVPLFGVFLKVFFFFFFFF*D RVSPCRPDWSAVAQSRLTASS
2788	16689	A	2807	3	216	NAARDHIVKPSP*PLTGALSALVMTSGL AM*CHSHSISLLILSLLTSTLTIYQ*RR NVTR*TSYQGHHTPTDQKGLRYGIILFI TSEAFFLS*FF*AFYHSSLSPTPQLRGH WPPTGLSPLNPLEVPLLNTSELLAS*VM PLSLHIASNTKPTNQHTNHIPMKAQCNT INLIPRPPHTN
2789	16690	A	2808	168	354	FLERESGFVAQAEGQGQNLS*WKPFFPI LKHFSCLSLLRSWNYGPTSPVPAKVGGF

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						WRNKIY
2790	16691	A	2809	61	360	YVSNSKCSNHRK*SLFFFFFFERESSFV PQVELHGRDLG*LQLWLPGFGKFPGLTP LRNGDDGPRPQPPANLGLLVKTGFSPVA HLGVNLGTLGDCPALP
2791	16692	A	2810	236	3	KMFFQMRYTMLKK*QATFGFILALKNVL KTFLAPIFFFLRRNSALVAQAGVQWRDL GPLPPLPSGLKRFSCLSLPSC
2792	16693	A	2811	140	210	NAKITKC*KGYGKRGTLMHCCWQFKMGQ LLWKTGYQFLKKLKLELLSNVPIPYL*I WKKGNPYALLLAI
2793	16694	A	2812	230	1	VKLCPVSLKTGVRPLLTSSEVIFILNCK FNIGV*LLPGSLLLLLASAIVEAGAGSG *TVYPPLAGNYSHAEPYALV
2794	16695	A	2813	3	345	HEVRIDVHTRTCFTFGTIIIAIPTGVKV FS*LATLHGSNMK*SAAVL*ALRFIFLF TVGGLTGIVLSNSSLDIVLHDTYYVVAH FHYVLSIGTVFAIIGGFIH*FPLFSGYT LD
2795	16696	A	2814	2	184	ARVGFHHIDQAGLKLLTL*SAYFGFPKC WDYRHEPPRLALKFNNIKKKKKKKKTP GEKI
2796	16697	A	2815	276	3	ARVHRIDHGLM*HQPLGLK*SLCLSLPS SWD**SMQPCPDDYGTRSDQKKPTFKSP YVSQTGLEHLGSSDLPASASQRAKITGM SHHALV
2797	16698	A	2816	3	94	HENQYSSLIIIMAIAIKLGIAPFHF*VP EV
2798	16699	A	2817	93	1	GGGGCSEPRLHHCTPVWVTE*NPVSKKK TRA
2799	16700	A	2818	1	197	GTRAQSLLLGRLRQKNQLNLGGRGCSEP KSGHLTPAWAT*PDLVSTKSCTLIYLVT QALHITLLP
2800	16701	A	2819	109	2	GVF*GVFLAQGLTLVAQAEVQWHDLGSL QPCPPRLKRLV
2801	16702	A	2820	2	347	ARAPGFAENEVFVFSSCFVWMVPGGKGE NAELMQPSSY*ESQHFFPAPPRCSSCV* LCSLGPSLLGTLIFCQFTLSELPRFRKG *FSSSLKKVFCFGDRVLLCHPGWSAVVQ TQL
2802	16703	A	2821	1	353	CTRRDVTRESTYGGHHRPPVQKGLPYGI ILFITSQVFFFT*FF*TFYHSTLTPTPQ L*GHWPPTGITPLNPLKVPLLNTSVLLP SRVSIT*AHHILI*NNRNQIISSLLITI LLGLY
2803	16704	A	2822	261	400	VEHSNSNKENFLGQGTGCHACNLNTLGG RGGRITWRSGV*DQLDQH
2804	16705	A	2823	273	97	LNTPRMQRLTQLATVILRFHKDQGFAML PRQVSNS*AQAICHLGLPKC*DYRREPP GQK
2805	16706	A	2824	159	355	KKFFSIFFFFFFFF*DRISLCHLGWSAV VQSWLTAAST
2806	16707	A	2825	67	338	LSPEL*LY*IF*KPFS*QLSLTSHSPSL FSALLLLSISPPTWLHSQSDKNLHLFSF LFRDSVLLCCLGYSAVT*SWFTVASNSW AQVVLS
2807	16708	A	2826	3	359	HEQKYSFLHDSQTLFCF*DSIPTPSNMD ETQQKSRLELVRISLLLIEPWLEPERLL

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						RSMVANNLVYDTSDSDDYHLLKDLQEGI QTLMGRLEYGSRRTGQMLKQTYSKFDTN SHNHDAL
2808	16709	A	2827	3	338	LERNLDTTFLDPAGGGDPILYQHLF*FF GHPEAYILILPRFGIVSHIVSYYFGRLE PSGYLRMG*PIISVGLLGFIV*SHHIFS VGVDIHARAYSYFGSLVMAIPCTLEVFT
2809	16710	A	2828	1	406	RHEGEKLRRPTFGPRHRGAGTAKMSASL VRATVRAVSKRKLQPTRAALTLTPSAVN KIKQLLKDKPEHVGVKVGVRTRGCNGLS YTLEYTKTKGDSDEEVIQDGVRVFIEKK AQLTLLGTEMDYVED*LSSEFVF
2810	16711	A	2829	332	3	GIIVMQATIATALIGYVLPLGQISL*GA TVIAYILAAIPFIGTDLVQ*I*VGCSVD SPTVTGFLAFPFVLAFIIAAVAALLLRF LQGTGSPNPLGGASQSDKIAFQFSC
2811	16712	A	2830	186	349	YSEREVAFFFFGNGFCF*TQAEWNGGNL G*LNLLPPR*KEFSCKIFPRTWNYSP
2812	16713	A	2831	303	590	NILTTLLNKQSKSNQLQNKIIHTVYIKI KIFFFFLRQSLSVTQADVQWHCLCSLQP PPPGFK*FSCLCLLSSWDYKHAPLHPAN FCIFSRDGISPS
2813	16714	A	2832	1	370	EELITFRDHAVIISFLICFLVLYALFLT LTTKLTNTNILDAQDIQTV*TILPAIIL VLIGLPFLRILYITDEVDDPSLTIK*NG HQWD*TY*YTDYGGLIFNSYILRPLLLE PGELRLRDVDN
2814	16715	A	2833	207	1	QFFIFLRHSFTLFAQAGMQWRDLGSLQP SPPGFK*FSYLSTLRGLARKITLAQEFQ TSLGNMGGPHPRA
2815	16716	A	2834	223	1	DNLAHKGKTRVYLKSRNKLGKGGGAGNL VSLDSIGSRRDHRRAPPCPANFVFLV*M GFPHVGQDGPELLTSCSC
2816	16717	A	2835	1	321	GTRKPSP*PVTGALSALLMTSGLTM*LH FHSITLLILGLLTNTLTIYQ*WRDVARE STYQGHHTPPVQKGLRYGIILFITSEGG LFAGFF*AFYHSSLDRTPQLGGQ
2817	16718	A	2836	57	370	IWMGRVLWKDRLYGVFCRAFNRAVTSRV WAEDPWRVPKTLSVDPRKLPPFS*ISVR GQIYFT*FFFFFETESHTVAQAGVQWWG DLG*LQPSPPGFKRFCLSLP
2818	16719	A	2837	2	345	ARAHRQLDEP*L*RRPGERHPSW*SEET VERQRTKT*SESSQTGTSITSSRNARRR ESEKSLHLETLNKEEDCHSPTFKPSTPD HPLKVMPAPSPKENAWVKRSSNPPARSQ SS
2819	16720	A	2838	15	376	AKIEPLYSSLGNKSETPSQKGKKKKKKK KGKGGGEKKKKKKTEGGTRGLTQETQFF GNPKGPKHLGARN*KHRAKQAKRGNQPR EYRFTEEKKGEKLFNPGGGRSQKPKTGQ WNSAGGKK
2820	16721	A	2839	3	336	HELLASILLIY**CRDVTRERIIPLAHH TPPVQKGLRYGIILFITS*VCFLAGLF* YLYHSSLPSTAQLRGHWPPTGITPLNPL EVPLLITSVLLASLCSFI*AHHSLIEH
2821	16722	A	2840	338	3	KIIFYLFFLRSIAFLAQIEGHWAVFSSF KLWPPGFKHFSASTFLVNRVFKGGPRAR VNFGFFIKSGFFPIF*VGF*LFFFFFFE

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						TESRSVAQAGVQWHDLCSLQAPPPSSC
2822	16723	A	2841	2	149	ARGCSEPTLHPCTPAWVTE*DSISKKKK KKVECSNGNVCRTMCILCCFW
2823	16724	A	2842	348	175	SACKVVSITGMHCHA*VIVSVLLV*TGS LHVGQVGLELRTSDDMHTLASVSGGITG MS
2824	16725	A	2843	338	118	DPGGGACSEPRLRHCTPAWVTKRDFVSK KKKK*NIKC*HAKSGTVLYSFLYLFYS* YFLMRVVSVHIPGPSTK
2825	16726	A	2844	189	47	KCVALLLSLFLSCSVM*RNACFRFAFCH DCKFLEASPAMLPIQSVEL
2826	16727	A	2845	335	139	EVSPSWPG*SQTPDLKRSACLSLSKCWD YRPGVSHRARLNGSFLTQLYEMLTYFPI IWVTLQVFR
2827	16728	A	2846	3	352	HEQRLTPEWKKAATALGDVVKVGAVDAD KHHSLGGQYGVQGFPTIKIFGSNKNRP* DYQGGITGEAIVDAALSALRQLVKDRLG GRSGGYRSGLQGTSYRSSKKDVIELTND SFDN
2828	16729	A	2847	2	269	ARGLFSTNHKDIGTLYGLFGA*AGVLGT ALSLLIRAELGQPGHLLGRDDISRIHVK RIIPGCGTLDGISVGRECACLWTPACSR KCARG
2829	16730	A	2848	317	28	SFLPN*KLAGHGGRPL*FQVLRRVRLEG CFSLEG*GCSEPWSCPCPLTWATETDPF SREKKKRRRREEKAEKRRENRRVPSLSV FLEEYVELTLIL
2830	16731	A	2849	326	107	FHHVGQDGLDLLPS*SAHLGFPKCWD*R CKPPCPASRNFKTLKLYHIFSNNLIE*N *KSITRGTLETVQLPGN
2831	16732	A	2850	224	3	SILQAWLKVPSPPGNPLGLLQSQVDFFF *RQGLALSPGLDCSGMIMAHCSLKLLGS TDPPTLAS*VAGTPSSC
2832	16733	A	2851	27	329	VRTAAINRPGFLLPCFIGQNFFFY*RFE TYRLGV*MILTPH*YLLSSLSGLDCVIF FSFILFFYWFIVYCHVFMVYLFFFLFVI LFVLCVFVVCFYFLLFV
2833	16734	A	2852	351	60	NLLSSLQGGRLPRPPGLSPHPQIFTPHG GVPL*LPGPWKSRPEASLNPRS*PPPGQ PRGNPFPPPKKNFFFFETVLLCRPGWSAV AQFQKKKNLLIC
2834	16735	A	2853	186	365	LTQLLNLI*YQNQIEYPQPYAQCGPRSG NAQQIGHSFPNG*QVPASGMHGLPWTHQ GLKK
2835	16736	A	2854	17	239	HFTTLQISMSLLTETLARHDSTHLWSQL L*RLRRNDLLKSGAGGCSELGLHHCTPT WTTEQDPVSRPGAVASEH
2836	16737	A	2855	325	140	GFHYVSQDGLDLLTS*SACLAFPKCWDY RHKPPCLAAYIFIQSRVFLAVISISTHS SFQLL
2837	16738	A	2856	1	157	GTRGFHHVGQAGLEVLTSDNLPVSASQS AGITGESH*AHERSDGYANTNSPG
2838	16739	A	2857	157	361	LLLRIVSLFWRKSSPLGVQAEMYRPDLP VTKPPPPD*DKDSCLSLLITWDYRLAPP LPANLEF*I*TG
2839	16740	A	2858	3	346	HEGNHKFKIINVHLR*LNQNL*SGLEGD KVIWRNI*TSVTFLFC*MNGKMNPDLFR QFTYEVGRIFFFSLKD*VWLCCLGSSTV

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						DLGSLQPPPLGFKQFSCLSLPSSWEPPC PA
2840	16741	A	2859	18	233	KNPTILCCKGGGAQA*KPRLLGRLRQEK GLTPGGEGCRDLKSPLGIPPWATRPKLL LKKKKKKGGKKKTLF
2841	16742	A	2860	356	3	RVNFKIFGKKGFCPGGPGGFEVLTPGDL GPLFFQKGGDSPSKPLKPFFFCFALKST TLNYFQFAFCVLRPTPN*SVTQAGMQ*H DHSSLQPQPPSLK*SSQLGFPSSWVYRH APPSC
2842	16743	A	2861	115	374	IVCGKILNV*YTQ*HNKLQNKNKVD*PT IKLMLISQSLGILIFIQKRDFEVNYGMI LKKRGWPGPVAYVCNSKTLGGQGGQIT
2843	16744	A	2862	163	360	LKRIWLLILHSHPHTSPHDRGVTQLEAI GPRWY*TYEYTDYGGLIFNSYILPPLFL EPGDLRLLDA
2844	16745	A	2863	1	236	GTSPFFSFFFLSFFPSFLPFLSFFNPTT LLLSLHSNIS*KKVLFSFEMESHSVNRL ECSGTISAHCSPAWATGTDSIS
2845	16746	A	2864	67	364	VCVCVCVCVSVSVCVCVCVYICTYICMY VCA*YRIRRYIMLPTLVYNSCPEIHDSK SCALHTGAITRATR*PCLCIHIPVCLTV CLTVWLHICLSVCMD
2846	16747	A	2865	2	155	ARGLTQENRLNLGGGGCSELRSHHCIPA WATE*DALSQKRKKKKGTYRGII
2847	16748	A	2866	344	81	IQPNSFIFLKIFISRDGALLCCPGWSPN SWAQQSSRLNLPKCWDYRHEPPHLVVQF L*KHYMYKWHKVHCVFSHYNKIFTGQTK TEN
2848	16749	A	2867	217	340	RVFSDFYMNLKWSLRKRRTWPGLVAHAC NPSTLAG*RGQIT
2849	16750	A	2868	3	349	HEATSPIIQELITFHDHALIIIILICYL LLYALYLTLTTKLTITIMSDAHEIHTA* TILPAIILDLIDLPCLRILYVTDEVNDP YLTITSIGHQWY*TYEDTDYGGLIFNSY ILT
2850	16751	A	2869	1	352	GTRIDVYTRAYFTSATIGIAIPTGVKVF S*LATLHGSNMK*SAAAL*ALGFIFLFT VSGLTGIVLANSSLDIVLHDTYYVVAHF HYVLSIGAVFAIIRGFIH*FPLFSGYTL DQTYA
2851	16752	A	2870	2	342	ARARFRTSLLLAFALL*LPWLQEAGAAQ TVPLTTLFDHTMLQDHRAHQLAIDTYQE FEETYIPKDQKDSFLHDSQTSFCYSDSI PTPSNMEETQQKSNLELLRIFLLLIESR L
2852	16753	A	2871	254	2	YPGYQAISQSDMQSYAYRHL*LQPPGVK *SSIVSLLSS*DHRPVPPCLANEKNFFF *RQGLAMLQSRLVLNSWLLLYSHAEPRA
2853	16754	A	2872	282	3	HTHILHYIYIHHGHIST*HLSPPTNIYS LCNIKILIYTPYDH*IIRIPLHQEHAVH RRRLIHIHIHTSVCVCVCVSVCVACVCV CVCVWVLV
2854	16755	A	2873	278	3	LWPLKNSGPQPWPQMDLGKPQVKTPVVY YKKGP*KKFFRKF*KWPGFFFFFFLRQS HSIAEAGVQWRDLGSLQPLPPGFKRFSC LNQISSC
2855	16756	A	2874	2	348	ARA*SLILVSLIIPNATSNLLGLLPYSF

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						TPTTQLSINLAMDIPL*AGTMVIGYSSK IRHALAHFLPRGTPTHLIPILAMIESMS LLIQPIAMAVRVTDNITAGHLTMPLTGS PTV
2856	16757	A	2875	1	260	GTRENHLDPAGRGCSKSRSHHCIPAWVT D*DSLKKKKKKKPQIILGNGGTEGNQK* RGNPFRGPWGPSRQKIKELGPGGKHGKS KF
2857	16758	A	2876	176	1	EHLFCKKLLGEEKGSLSKEFGKCWVNPR *KWNSRPGVVAHTCNPSTLGGRGGQITR SG
2858	16759	A	2877	168	1	GVRVFGFSSVPEFSFDTCAGAQWRNLGS LQPLPPGFK*FSCLSLLSSWDYKRTPRA
2859	16760	A	2878	67	333	WQGLGRAVARVPRSYEITWAGNLKGAA* FQQLFFFFFFHLLFFFFFFFFFFFFFF FFFFFFFFFFLFSFFFLFFFFFFFFFFF FFFFL
2860	16761	A	2879	335	1	GRKEGRREKEKERKKKKERKKERKKTIF KKHIPSPLAFPRKAWKLKEIQIKLVAH* KINRQAIRGCPPNKRPHPFQNMIKPGRE EGEGGLETSRDGERNLWIFGPSVGPLR
2861	16762	A	2880	3	345	HERHETASIILLIAILFNNILSGQ*TIT NTTNQYSSLIIIMAIAIKLGIAPFHF*V PEVAQGTPLTSGLLLLT*QKLAPISIIY QISPSLNVSLLLTLSILSIIAGS*GGLN QT
2862	16763	A	2881	347	156	WLIFVLLVEMGFFHSGQAVLKLLASSDP ASMTSQSSGITGLRHCAQPR*AFLIALC LPPSAKI
2863	16764	A	2882	338	2	IKKAL*HE*LREKKKSPIRTSQSSKAP* NLPRSKKKKESSNNYQLL*AHKLQKVKE MGKLLETPNLPLLSQKVAEPLNQPITSS KIETLIKKPYHPEKSYGHDEVTAKFSRA
2864	16765	A	2883	206	1	IRTRPFTPMFIFYMFVYLATRSCPFTLA GVQWHNHGSLQL*PPGLKESSCLSLLSS WDYYACLHAELV
2865	16766	A	2884	341	140	DGGCREPRSRHCSPAWVTE*DSKQNKTK QKQKRYTNISSPQTSPLCYSFSAYTPLH NMPGNIMFSSL
2866	16767	A	2885	360	247	FHRVSQDGLDLLTS*SAHLSLPKCWDYR REPPRRPKAL
2867	16768	A	2886	229	351	KLNNRPGVVAHAFNPSTL*KLNNRPGVV AHAFNPSTLGG*GGWIMRSGVRDQPNQH GETP
2868	16769	A	2887	359	2	FYSSSSSSSELVPCRQDVQVPHYLEGLF LRSCFMEIKYDT*KRKIKYTHVHTHTHT HTHTHTQREKERDFPRFTAKWKANLEAG SGYATASSIRAVLWTTITLV
2869	16770	A	2888	4	305	ADSHMWKYKAPGITKILLKKSKI*GYHQ DWISSRYQDLFHKDMIFKIMSYWYKKRQ VDHWDRIESPETSSQMYEHLIYNKDNIA EW*EKDSFLSKWCWDN
2870	16771	A	2889	1	436	IAILT*YDYTLL*RVGPRGQEFGTRATV ITNLLSAIPYIGADVVK*G*GGYSLDSP TLTRFFTFHFILPFIIASLATLHLLFLH *TLSNIPLRITSHSHQITFHPYYTDQYS LRLLPFLLSFTTLLLILPNFLFYPP*TT LTFPF

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2871	16772	A	2890	1	218	RKISPLIKLINHSFIDLPTPSNISA**N FGSLLGACLILQITTGLFLAMHYSPDAS TAFSSIAHITRDVNYG*IIRYLHANGAS IFFICLFLHIGRGLYYGSFLYSET*NIG IILLLATIATAFIGYVLP*GSLLGACLI LQITTGLFLAMHYSPDASTAFSSIAHIT RDVNYG
2872	16773	A	2891	3	368	LSNS*ANNLI*LAYTIAFIVKIPLYGLH L*LPKAHVEAPIAGSIVLAAVLLKLGGY GIIRLTLILNPLTKHIAYPFLVLSL*GI IITSSICLRQTDLKSLIAYSSISHIALV VTAILIQTP
2873	16774	A	2892	3	342	HENLI*LAYTIAFIVKIPLYGLHL*LPK AHVEAPIAGSIVLAAVLLRLRGYGIIRL TLILNPLTKHIAYPFLELSL*GIIITSS ICLRQTDLKSLIAYSSISHIALVVTAIL I
2874	16775	A	2893	2	361	ARVCLRQTDLKSLIAYSSISHIALVVTA ILIQTP*SFTGAVILIIAHGLTSSLLFC LANSNYERTHSRIIILSQGLQTLLPLIA F**LLASLANLALPPTINLLGELSVLVT TFS*SNIT
2875	16776	A	2894	229	3	YTFVQSFIFSVVLFICKVCLL*PAHSMV CACECMCVCVCLCVCLSSLKIIPLLECL IYLQLILVLSSAIYNSRFE
2876	16777	A	2895	3	391	GFLITNNISPASPFQTTIPLYLKLTALA DTFLGLLTALDLNYLTNKLKIKSPLCTF YFSNILGFYPSITHRTIPYLGLLTSQNL PLLLLDLT*LEKLLPKTISQHQISTSII TSTQKGIIKLYFLSFFF
2877	16778	A	2896	381	2	GRCRVSGSIIDHRMAPQKWRYTKGGPHQ WHNFCFF*KKGVFPYGPKVFLFRAPVFS PPGPPKRWEIKV*TPPPALFFFFFFFFV EMGSHCVAQAGLKLLGSSTPPTSASQGA EIAGVSHRAQPHAS
2878	16779	A	2897	324	1	LYTNNTKHINPQQNNTK*YQRNTKNRRK KEQQTKNNIKRHITESARKNS**HRNIQ KANKSQQSNKHYRARSRHNNNNNNNNNN KKKKIENSHAASD*ITSSGGRSRA
2879	16780	A	2898	120	345	PPAPSS*YTTSLIQDRLFLMMAVLSSAS LMRGNVGSNIMNALSHFLPQGTATLFIP VLDIMEAISLLIQPIALAV
2880	16781	A	2899	381	219	CVSQDGLDLLTS*STRLSLPKSWDYRCE PPRPAGSGHLYSSFKKQTGDTHHNF
2881	16782	A	2900	1	224	LSWCLTLYFAYLLALFYFYFLKILDLAI LPRLVPYSWP*ASSPASASQSSGITGMS HYTWPLPQTLNPFLFFVP
2882	16783	A	2901	1	228	KYLINNRLITTQQ*LIKLTSKQMITIHN T*GY*YNRSGSSFNGVYDYHLLRSESEH PWMIVDNTEYDEIYTRGGIE
2883	16784	A	2902	2	332	LPPSFSLLLAPSPSSSLPPSPSSSLPPS PSSSLPPSPSSSLHTSHSSTLTPSASCT LTITESFTQRLAQSYITILP*ASRTTMQ LLKYRTLQTTRNNTHSMTRPKALTKI
2884	16785	A	2903	3	243	DIGFGTDFSDMTPKAQTKQVDQLDFIKI *NFWPGTVAHTCNPSTLGGRGM*ITKLG V*DQPGQRGETTQKLAGHGGVDAV
2885	16786	A	2904	179	2	CGYFNAYICYSLLCFLYLSLCNQPFWKK

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						IFLPLFGLVFFFFFF*NRV*FCCPGWSA VSQ
2886	16787	A	2905	108	2	GRVDIKLTSKQMITIHNTKGRT*SLILV SLIIFIA
2887	16788	A	2906	318	2	YKESNSKNNEKKKITRQRKRQKKNRPSM MVHTCNPSPMAGRDGQIPSILFNQPHSP RIIRLTLILNPLTKHIAYPFLVLSL*GI IITSSIGLRQTDLQSLIAYSS
2888	16789	A	2907	17	308	KLAGYGGMCLWSKLLERPTRMNHLSPRS EGLMEP*SHNCIPDWTP*QNPVSVQITG FCFLTPNLAMPPRLNLSGPICCQLSLRL LGPRLFAASVSGV
2889	16790	A	2908	378	1	RSLHSTETAAKTHGHQTHPGLSTFSK*T PTPIASIPIPNPHNCLPAFNSTTSASYF SECVLTSSFKEIIADFR*KYSSTN*HPY HLFLLKFVFFCSRDGSLTMLPIRPGLNS RSQAILPPWPPKVL
2890	16791	A	2909	1	129	HLFGTNHRDIGTLCLLFGA*AGVLGTAL SLLIRAELGQPSTRP
2891	16792	A	2910	1	323	CVCWGYRIPRCNIGHHLKFFFFSLFFFF FGNKVWFCSEG*RAGDQLLIMEPLASGF KGIFFLNLPQNWE*RVSPKLPGKFWIF* LKTGFPLVAQVVFELRTSGDQMA
2892	16793	A	2911	367	136	ETPGNHLSPGV*GCSEL*SCLCTPAWAT EQDPISKQKRTKKSKTLLKNTKADLTRW KHIHKSACVCICLCMYMCLRE
2893	16794	A	2912	258	140	FLIFFCLDCFLNIKVLGVPGFFFSLKKK QT*RQGLALSPRLECSGLIIAHCTLEPL GSRNPLTLAPQIAGATGMSH*VQGYNEL
2894	16795	A	2913	48	242	YSMIFCVLILPVSFTSSDGIFLLINLFL FY*STYPLAFFKTESHSVTQAGVRWHHL GSLQPPPPR
2895	16796	A	2914	309	76	GFIICVCVCVCVCVCVCVVFIFTEYSFH *SLFC*IRCCVFYFLALSLLIGFYLFWNR* YLEVYNISFEVWASLFNRFLLL
2896	16797	A	2915	1	122	FSVETGFHHVGQPGL*PPTSGDPPSLAS QSAGITGMSHHA
2897	16798	A	2916	167	1	GNMCSKESVSGTNINRKPD**YNPRLGT VAHAYNPSTLGGQGRWITGGQEFKTSL
2898	16799	A	2917	2	356	ARGILLLRIMLTTLTRYP**RDVTREST YQGHHTPPVQKGLRYGIILFITSEAFFL PRFLPPFLSSSFPPTPSLLKPFPPSSFP SLPSFFPPFLPSSLFL
2899	16800	A	2918	2	351	AREYTSLQLILQMTFIMAFTCTDRTLYE LAFEC*LMRTLDIITR*GNQP*RPNAGS YWLFYTLLGTLPLLIALIYTHNTLGSLN ILLLTLTAQELSNS*ANNLI*LAYTIAF IVKI
2900	16801	A	2919	32	321	ALMGITFFFFLGKGVLAPRGGGRGGNPG LWGGPPPGLGPFSG*SLQGGGA*GPPPQ AGANFGFLILRKTRGSPGCPGGFWIPGP GDRPAGAPQGGG
2901	16802	A	2920	1	361	GTSTRLGVLLLSLHHAGSINPLGITLHS *DKVTLHPYYTIKDALGLLLFLLSLMTLT* LFSPDLLGDPDNYTLANPLNTPPHIKPE *YFLFAYTILRSVPNKLGGVLALLLSIL ILAIIPIL
2902	16803	A	2921	3	152	HERLYSVPLRILRRLPDPLSIPQGWRHV

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						IRESAYKSHLTLPARRGLQDGIILFITS EVVFFAGFF*AFYHSSLCPTPQL*GHWP PTGITPLNPPESPLLNTSVLLASGVVIT *AHTKAISHYLREEAFKTG
2903	16804	A	2922	410	1	RAGYRQKWGSLATVIGQLGLPVERGWYG PSGEGGTPQRHCSELVLDDLHVITQNRA NHRPRCGGSLLSELKFAPLALQPGRQSK TLSQKKNKQTTTKKNTKKQPGSVAHACN PSTLGG*GRQITLPSGVRDQPGQH
2904	16805	A	2923	2	145	ARAARGDVI*SFHVFAQRDLNLLSSRDL PALASQSTGITGMSHQCPG
2905	16806	A	2924	29	340	EMNEVERRGRK*LFHDSIQSR*EYRCAP QCPANSCVLM*RWGFAMLPKLVSSDLPA LASQSAGITGVSHCAWLVFLPLLSTSFI SQRHLYLPRA
2906	16807	A	2925	2	337	ARVLILPGFGIISHIVTYYSGKKEPFGY IGMD*AMISIGFLGFIV*AHHIFTVGID VDTRAYFTCATIIIAIPTGVKVFN*LAR LHGCNMI*SAAVL*SLGFIFVFIVSGQA
2907	16808	A	2926	76	388	RYCTPAWATETPSQKKEKKKKCQTFEPE SSFPVCLENGGGGNFISLFFLFLIILSL FFYFY*FFFIIFVYSYYYFYFCLFSYFF FYFFINLIIFLLLNYFFFFI
2908	16809	A	2927	48	374	KDQEPTDMGSAHFQVFKGWRQVGGANED RINSHGGPVMFSGQYYGQLVRFLVY*II IFFMLLFFSLFYSYFLFISIFFVLVFYC LFIFLFYFSFFFIFVFFFYYFIVIF
2909	16810	A	2928	3	294	HEGFHYISQDGLDLLTS*SARLGLPKCW DYRREPPRPARFPTLRIWLYILKALYTV LGCYREYEAYRPWCWTHRMDGGQEVEGR REGTGGGHILGF
2910	16811	A	2929	7	420	IRRRDVLLLTLTSLSPTAARICYNGGRR GNRLNSLAYLSKELLAAWSLRKPSHGLL TPIRCVLYIRGHHF*LLPPSHLLLLASA IMGAAGGTG*TV*PTLARNYSQPGVCVN LAMVSLHLSGVSSILGAITFITAIMNME APAITQYQTPLFV*YGLITADLLVLSLP DLTAGITILLTDRKLSTTFFDPAGGGDP ILY
2911	16812	A	2930	11	253	GLLHKAPSP*KFFFSPKPFNFFWKFSPI FSPPKKKFLSKNPHIVFKFPPFKGKIFT FPPPLKFGPPRVFFKAPPPFFFFFFFFF FFFFF
2912	16813	A	2931	70	341	DSSFFS*LATLHGSNMK*SAAVL*ALGF IFLFTVCGLTDIALPNSSLDIALLDTYY VVAHFHYVLSLGAVFAIIRGLIH*FPLF SGYTLDQS*AKIHCAIIFIGVYITFFPH HSLGL
2913	16814	A	2932	3	340	NYSHPGASVNLIIFTVHLAGVSCILRAI NFITTIINIKPPAITQYQTPLFV*SVLI TGVLLVLSIPVLSAGITILLTDRNLNTT FFDPAGGGDHILYQLLF*LFGHPEAYIL
2914	16815	A	2933	2	364	RVQKGLRYWIILSITSEVLLFAGYF*AL YHSSLAPTPQLGGHWPPSGITPLNPLEV PLLYTYVLLASRVSFT*AHHRLIQNNRN HIIQALLITILLGLYCTLLQAS*NFEPP FTISDGIYG
2915	16816	A	2934	2	367	PRVRPRVRYLLFGA*AGVLGTALSLLIR

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						AELGQPGNLLGNDHIYNVIGTAHAFVII FFIVIPIIIGGFGN*LGPLIIGAPDMAF PRINNISF*LLPPSLLLLLASAIVEAGA RTG*TVYPPL
2916	16817	A	2935	3	365	YHIV*PNP*PLTWALSALLMTSGLTM*F HFHSITLVILGLLTNTLTIYQ*WRDVSR *STYQGHHTPPVQKGLRYGIMLFIT*DR FFFAGVF*ALYHSSLAPTPHLGGHWPPT GITPLNPLE
2917	16818	A	2936	3	144	DSHGRHVING*TCVTICFIRQLIGHFTS KHHFGFEAAA*YWHKKKKK
2918	16819	A	2937	3	422	QRLLATNHHDIGTLYLSFGA*PGALGTD LSLLIRAELGQPRDLLGNDHIYNEI*TG HALGILFFIGLPIIIEGFGN*LHALIIG APDMALPRINNISF*LLPPYLLLLLASA IVEAGAGTG*TVYPPLAGNYSHPGASVE
2919	16820	A	2938	3	382	RTRGLFSTNHIDILTLYLLFGA*AGVLG AALSLLIRAELGQPCNLLCNDHIYNVIV TAHAFVIIFFIVIPIII*CFGN*LLPLI IGAPDMAFPRINNISL*LLPTSLLLLLA SAILEA*SGTG*TV
2920	16821	A	2939	225	3	NISWRMKQIVPKGEPYNGVPVFVSLWFH KMFIFETGSHSVYQAGVQ*RHLGSLHPH PPGIKQFYLSLPSSWDY
2921	16822	A	2940	1	247	PTRPPVIYSTIFAGTLITALSSH*FFT* VGLEINMLAFIPVLTKKINPRSTEAAIK YFLTQATASIILLIAILFNNIKKKKK
2922	16823	A	2941	3	369	TRDSTYLGHHTPPVHTGLRYWRILFITS DAFFFAGFF*AFYHSSLAPTPRLGGHWP PTGITPLNPLEVPLLYTSVLLASGVSVT *AHHSLVEDDRYQIIQALLITILLGLYF TLLQASEDFE
2923	16824	A	2942	3	401	LTVCCVIVLRLKTLFFFFNKPFLTQKGY FNTPEEGFFKKPNRRVGPPSPMTDPTML TNLIKGKVPKAPPRILMGGGINMTF*GF VTPRAPFPLTLRLNPMLQQGIDLLTLKA SGGSPASGNFLKELGLRSINF
2924	16825	A	2943	189	348	RNARGWVTDKEKRLRLGMVAHACNSSTL GGDGR*IA*GQEFETSLANMVKPCL
2925	16826	A	2944	2	349	ANSNYERTHSRIIILSQGLQTLLPLIAF **LVASLANLALPPTINLLGELSVLVTT FS*SNITLLLTGLIILVTALYSLYIFTT SQWGSLTHHINNIKPSFTRENTLMFILL SPIL
2926	16827	A	2945	621	929	GCSSGTGCCPILCDLPRPWSCRGVGGSP SSTAHLCPRGWRSGRCFLPPLSAS*VDS AMSLIQAAKNLMNAVVQTVKASYVASTK YQKSQGMASLNLPAVSWKM
2927	16828	A	2946	379	395	SQHFGRLRREDHEVRSS*PRDPPALTSQ SAGITGMSHCARPLVATSIHKIDNRYID DRS*NINIGTIFINLLIFYLSIYLSIYL SIYLSIMYSFTVAQAGVQWRDYGSLQPE SPGPK*SSCISLSSSRNHSHTPPHGWVD PKIP
2928	16829	A	2947	2	357	HTYDIRKPRR*TLACALSALLTTSGLAM TDCFHYITLLILCLLTNTLTIYQ*WRDE TRESTYQGHHTPPVQKGLRYGIILFITS EAYFFAGFF*AFYHSSLAPTPQLGGHWP

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						PTGITP
2929	16830	A	2948	2	357	PRVRYSTDHSDIGTLYLLFGA*AGVLGT AISLLIRAELGHPGNLLGNDHIYNVIGT AHAFVIIFFIVIPIIIGGCGN*LGPLII GAPDMAFPRINNISF*LLPASVLLLLAS AIVEAG
2930	16831	A	2949	2	217	KNLKIVQYGDMCLWSQLLRELRWEDRLS SGG*GCSELCSCHCTPAWTTQQDCLKKK KNFWPVGEVKGRHML
2931	16832	A	2950	2	354	AIPMTTARLTIHEAYLIILERTTTTTKD VKNPRRIAAAITASCLGGGLEDAISCQY GIATKDRPTGLGTPEVLLGALPGAGGTQ RLPKMVVVPAALDMRLTGRSIRAHRALK M*LVD
2932	16833	A	2951	3	150	LFSCSPTFSSDPLTTPLLILTT*LLPLT IMASQRHLSSEPLSRKKKKKK
2933	16834	A	2952	283	344	EKKKKKKKKKKKKKKKKKK*KLRKKKK KKKKKKKKKKKKKEK
2934	16835	A	2953	3	378	DAWADAWNQTPLFN*SVLITAVLLLLSL RVLAAGITILLTDRNLNTTLFDPAGGGH PILYQHLF*CFGHPEVYILILPGLGIIY RIVTDYYGTKEPFGYIGMV*AMRSIGFL RFIVRAHHIVTVG
2935	16836	A	2954	3	387	ILYQHLY*FFGHLEGYILILPGFGIISH MVTYYSGKEEPFGYIGMG*AMISIGFLG FIGRAHHIFTVGIDVDTRAYFTYATIII AIPTGVKVFS*LATLHGSNMK*SAAVL* ALGFIFLFTVCGLTGI
2936	16837	A	2955	2	432	PRVRPRVRKHIAYPFLVLSL*GIIITSS ICLRQTDLKSLIAYSSISHIALVVTAIL IQTP*SFTGAVILIIAHGLTSSLLFCLA NSNYERTHSRIIILSQGLQTLLPLKKKK KKKKKKKKKKKKGGGLLKESLGGPNLTG EGK
2937	16838	A	2956	12	391	SYFISSSKPHLSPPWLSSPDEATSKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKK KGGGFK*KRIGGSFKKGGGEKKIFFFKG GKKKKTGGFFEKKFFLGGEKY*DNLPKK NKTVGEKKNFLGGG
2938	16839	A	2957	1	352	PTRPYFPVDAGEAQHHPRTCRRPLRALW SSHHERWKVTLCTHCSLGVFFLYCCTYY IFVLFIP*SSCGLTLIFITCIILFGSIS FFLFFTIVFSIIIVTTFKFRLLYSIIFL SYLLC
2939	16840	A	2958	1	243	NLPRLNPKEIEILNRSIICNKIKAIIKS LLSKKSSGHNDVTAEFY*TFKEELITIL LKFYLTPKKKKKKKKKKKKKGGPF
2940	16841	A	2959	373	3	FSSLKKRVTPPPPPKTGFSLEGLHLLKK NFPQKPPPPKKSFSQKNPPPPKKKPPF* KKKPPPPPPI*HPPPKILQPPPPPPFFFF FFFPFFFFFFFFFFFFFFFFFFFTDMR GFIVRKFRTRG
2941	16842	A	2960	2	136	PRVRSTLPISYKWNNRALMKAHLIMK*F TEYFKTTDELYLHDNT
2942	16843	A	2962	1	358	HTPPVRKGL*YGIILFITSKVFFVPRFI *AVYHSSLCPTLQLGGLWPATGMTWLNP L*VPLCTTFVLLA**VSIT*AHHNLIDL NRCHVIYALVITILLRLYFTLLPASEYF

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						EAPLTIS
2943	16844	A	2963	2	373	RAYDIVRPRP*PLLGALSALLMTYGLAM *VHWDCITLLILGLLTNTLAIYQ*WRDV SRESTYQGHHTPPVQKGLRYGIILFITS EDVFFAGIV*AFYHYSLAPTPQLGGHWP PTGITPLNPLEV
2944	16845	A	2964	403	61	LFFPLEKNFLPPGFSAFFSPFSP*KFFF SPKALIFWGNFSPFFPPPKIRFLPKIPP WVFFSPPFWEKLFSSPPPLNFGPPRVLF KGPPLFFFFFFFFFFFFFFRFEGECW RL
2945	16846	A	2965	2	360	LIPNLAMVTR*GNHPQRLNAGTYLLFDT LDGSLALLIGLTYTRNTLGSLNVILLTI TAQELSNS*ANNLV*LAYTLAFIEKIPL YGLHL*LPKAHREAPIAGSIVLAAVLSK LGGSGKN
2946	16847	A	2966	321	2	STGMHFPHINMAINPPPPPRPPPPLFPP NPKTKPNPTQ*KGGFPPLGPF*KKLSPF LTLFFFFFFFFFGHHPGPWQKKKKKKVF FFCVCFSFQRVHNIYKNTHQQQ
2947	16848	A	2967	200	1	RRTYTSHLLACLRQGLAFSPRLECGGKI RAHCSLQLYGSSDPPT*APQTAGTKQHN QRIAQCNADN
2948	16849	A	2968	2	354	LLTASSSEIAPLQSSLGDRARLCLIK*K EGVLNSI*SGNQGKSYANVYRLLYLDPI PKIYAEAYTP*NVNSTNLETKSPKTIQK FPEDREFKNDFFEKTKNGDRETGAFHPF LLFLV
2949	16850	A	2969	99	400	ALGIHFIFTVSGLTGIGLANSSLHIVLH DTYYVVAHFHYVLSLGAAFAIIGGFIH* IPLYSCYTLDQTYAKIHFTIIFIGVNLT FFPQHFLGLSGMPRRY
2950	16851	A	2970	2	377	NILLLTLTAQELSNS*ANNLI*LAYTIA FIVKIPLYGLHL*LPKAHVEAPIAGSIV LAAVLLKLGGYGIIRLTLILNPLTKHIA YPFLVLSL*GIIITSSICLKKKKKKKKK KKKKKKKKRGGPF
2951	16852	A	2971	1	407	GTRSYTHLYRVFLELIKMSVYDLNHTVI MVISGHVRLAFYGIVHLTLILNLLTDHI LYPFLVLSLSGVIIISSIFLRRTDLESL IAYSSISHIALVVTAILIQTP*SFTGAD ILIIVHGLTSSLLCCLANSNYER
2952	16853	A	2972	10	259	SRSVAIYFKGMASA**RMFSSKKKKKKK KKKKKKKKKKKKKKTAITKKTTTAKWKN *RTEKIRHTRLPLISSRDAKCVDFLYT
2953	16854	A	2973	12	400	LNCRTPSLYLQRAGELLSVENPHIWCQK CVRKNNFFLFFFFFFKTDLYCPHICIAL SITCFLAISISGLFAFFLLNSFNYHFII VP*NFSLSIYLCLHSLFYVGFFFSFDMM IFSILT*TLFFCLLFHL
2954	16855	A	2974	125	3	RPRRPAAQVGVQ*KNLSSLQPVPPGFKL FFPLSLLSSWAS
2955	16856	A	2975	2	332	RECTNYPAQPPPPPLEAEEGFQPLPPTD TG*LECLPPLGGGQHRALGLGATWHLEN ACALVLADLGTGPKPSGPFSGQACGASG RLPLLSGPILPPLGQGHTLSAWGHHA
2956	16857	A	2976	7	329	SRDILVMTEDGEFF*GHV*P*DRSRRAD TPRLGGHWPPTGITPLNPL*VPLLNTSV

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						LLASGGSIT*THHRLIEYIRHQIIHALL ITILLGLYFTLLQASEYFESSFT
2957	16858	A	2977	2	339	AHHIFTARIDVDTRAYFTSATIIIAIPT GDKAFS*LATLHGSNMK*SAAVL*ALGF IFLFTVRGLTGIVLADSSLDIVLHDTYY VGAHFHYGLSIGAVFAIIGGFIH*CPLF
2958	16859	A	2978	394	0	QGCSEL*SCHCTPAWVTE*FPVSKKKKQ RK
2959	16860	A	2979	149	383	PLCFPSQHWGKSSNCLSSLKYFPSSGLP LRCKAELDDVKQKADKELDVVAHACNPS TLVGQGGRITLRSGV*DQPGQH
2960	16861	A	2980	2	378	ARVSIGFLGLIVGAHDMFTGRMDLYTRT YCTFATILIAIHTGVPVFI*LATLHGCN MK*SAAVL*ALRFIFISTVCGLTGIVLP N*SLDIVLHYMYYAVAHLHYVLSIGAVF AILGRFIHRLPVF
2961	16862	A	2982	2	409	PAVAEAYLKPVVDDSKGSFLWGKPDLDG IRECCQRNFGWNRTRTDESLFPVLKQLD AQQTQLRIDSFFTLAQQEKDDAKRIKSQ RLNRAVTCMLRIEIEAASSEIEAVSVD* QKELELIDKAVACHLEYMYETDP
2962	16863	A	2983	3	453	HASAHASAHASGQRKGAAPAEKKCGAEA QHEGLELRVENLQAVQTDFSSDPLQKVV CFNHDNTLLATGGTDGYVRVWKVPNLEK VLESKAHDGEIEDLVLVPEGML*IVCPD HYSPVGINDFMWLL*LNWGNRLYFPHIS VYLMFHFRTF
2963	16864	A	2984	3	417	LILPGFGIISHIVTYYSGKKEGFGYICM V*AMISIGFLGLIVRAHHIFTVGIDVYS RAYFTSATIIIAIPTGVKVFS*LSTLHG SNMK*SAAVL*ALRFIFLFTVSGLTGIV LANSSLDIALHDTYYV*THFHYVLSI
2964	16865	A	2985	273	408	MKIFIF*VSPPLFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFLAVFTFI
2965	16866	A	2986	176	335	TFQPSELWRTALLPRLECSGLIIAHCSL ELLGSSSPLASAS*IAGTTGSILRY
2966	16867	A	2987	65	398	KKEFKIGRKAAEKMTRNINNAFGPGTAN ECTVQWWFKKFCKGNKSLEDEECSGRPL EDDNDQWRAIIEADPLTTTREVAEELSV NHSMAVQHLK*VGKVKKLNKWVPHELS
2967	16868	A	2988	2	158	PGWSLTPDLR*STCLSLPKCWDYRHKRP SPTSRQTFDHAPNKNSSHSPPIYM
2968	16869	A	2989	435	23	GVVPPNPQKSFYFPQRLKIWGGGGRKRP PPKKKGFSQKTPEGF*KPPPKRRKKIFH DPGKKGPPKGIFKRGPPLFFFFYFFFFF FFFFFFFIITIECLHSRFPHRHHNKKFP PNPPSPRFWPQHLNTSLPNPKNKEP
2969	16870	A	2990	410	3	GGRGHFFSGAFFIKFPWNKKGISQPLCF PRGGGSPPPLGPVRGGGPPCWGPLCHKG PVKKTGAPRGKNGISPFFCFPPLGSFNR SGFFWALLGSPPLFFFFFF*DRVSLHHP GWNAVAQS*LTKTSTSWVQVILL
2970	16871	A	2991	371	132	KQSLPFKVKGFFFPPEVENAIYPDSHTA FYSW*KRSTFSKKKKKKKKERKRKKEE RKEGRKEGRKERKKEGKKEIENA
2971	16872	A	2992	336	1	CPRWSRTAGLK*STCFGLPKCWDNRHES PCPASSVLND*QLSTVQRAT*WQTKSLV LKAPPARGALPVSRAVSPPPSSHHFAYF

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						LHMI*QVSCLFLR*SLALVPQAGVQ*RD
2972	16873	A	2993	317	440	HLGRLRQEHHLSPG*LRKFFFFFGRDGV LMLSMLVFNSWTQVMLLPQPPQVLGLR
2973	16874	A	2994	2	181	FHHVGLDLLTL*SACLGLPKCWDYRREP LCPALVILLTAKFTNFRYRVKNVCTFHV ESN
2974	16875	A	2995	1	165	GFHCISRDGLDLLTS*YARLGLSNCWDY RHEPPSPAPLFISYSICLFLSKLIQFL
2975	16876	A	2996	405	2	KKGFPIFSRMFFLYKHIEKPPLASQKFG DPKWSPHPRPIFFFLLKKGVLYVWREGF KFHPP*FPPPGPPKRWE*RVKPPHPPPF FFFFFLYVEMGSHCVAQAGLKLLGSSTP PTSASQGAEIAGVSHRAQPHAS
2976	16877	A	2997	2	415	CLFTGGGLTGIGSAGSSLDIVLHDTYYV VAHFHYDLSIGAGFAIIGGLIH*FPLFS GYALDQTYARIHFTIIFIGVNLTFLPQH FLGLSGMPRRCSD*PDAYTT*SMLSSVG SVITLTAVIVLIIMIREAFDSKRTVL
2977	16878	A	2998	349	370	HHFY*SITAFRPFQHMELRNFFFFFLFF FFFFFFFFVFLFIFLFLFYFLFLYEIYL ILFFL*HHFYSAV
2978	16879	A	2999	36	139	LCHCTPAWETFSKEKKKKEKRKKKKKKK KKKKKKKPGGGS*KTALSHDCATVLQPG RLFQKKKKKRKKGKKKKRKKKKKKK
2979	16880	A	3000	104	373	SADREXXSKTDNLLGH*TNVNKCKVPRV IQSVFSSHSGLKLEINNRKMKEKSLNT* KINNISYWVQCSLYNLKSNSYTKSSDNT TTQYMY
2980	16881	A	3001	1	396	LDCSKISSYLQKSSSHVLFFSFSFFFFF GGGGGFALENPYPPAGLGPQKKKTLSPP WLVGGPPFPEKAPP*GGHFLGKKPQKNP GGQNPKRPSGEGNPFFQPPGGEKKQIGP PTGFGGKPFFSF*PREPPGP
2981	16882	A	3002	412	104	FFFFFLPVRQTFYPQPFSVFFPLFPFKF FFFP*AFNFFWGFFPIFSPPKFGFFSKI SRLVFFSLPFWEKFFFFLPPFFFAPLRF FFKGPPXFFFFFFFFFXXY
2982	16883	A	3003	400	46	LFFFFFYKLFPPPAFGGFFPPFPL*NFF FPPGPFFFLGGFPPFFPPPK*VFFPKIP PGFFFPPPF*KKFFFSPPPFFLPPPGFF FNPPPPFFFFFFFFFFFFFFFFFLCVV VQVEAY
2983	16884	A	3004	411	69	YSPLPPLFFSSPPSKFPWPPFSLFFLTR VYKGFFFFPFFPFELFGPPGLSLGSKPP PVFLGGDPAFFSIPHPRVGSLPPPPNWP FIGPSFW*ALFPAPPLFFFFFLSSFFFF F
2984	16885	A	3005	3	200	DAWG*LFSTNHKDIGTLYLLFGA*AGVL GTALSLLIRAELGQPGNLLGNDHIYNVI VTAHAFVII
2985	16886	A	3006	259	146	FFFFFFFFFFFFFFFFFFFFFFFFFFF FFGLLNDILL
2986	16887	A	3007	118	414	QNQPPQNKATHTVKIEKKEKPETKTVAK EHNKAKTAEKSEE*TKKEVKGGKQEKVN HTAAKVKEVQKTPSKPKEKEDNKKAAVS KHEQKDQYAFLRYMI
2987	16888	A	3008	427	111	FFFFSPVGNFSPPQQFPFFFPPFPPKIF FFPPPL*FFWGGFPPFPPPPKKVFFPKS

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						PPGFFFPPP*GKKFIFPPPP*FCPPPGF FLSPPPPFFFFFFFFFFFFS
2988	16889	A	3009	3	302	SLASCLSYLVCVIFLGQPKPTI*LQNST PHKK*NPTERYVKTCTQIFIALLFKKEK QPRCPSAGEWINKMLYACTIEYWLAIKR YEILIYATV*MYLEKI
2989	16890	A	3010	1	409	RLHDATFPIIEELITFHDHALVITFLIW LLVLCALFLTLTTKLTNTNISHAQEIET V*TILAAIILALMVLPSLRILYITDEDN DPSLTIKSIGHQWY*TYEYTDYGGLMFN SYILAPLFLEPGDLRLLDVDNRVV
2990	16891	A	3011	157	2	GRVDLKIQKLARCGGACLQSQHTQQNHL NPGEKGCSES*LPPCPPD*VTKQ
2991	16892	A	3012	2	423	ARAARAHIVTYYSGKKEPFGYIGMG*AM ISIGFLGFIGRAHHIFT**IDGHTRAYF TSATIIIAIPTGVKVFI*LATLHGSNMK *SAAVL*ALGFIFLFTECGLTGIVLANS SLYIVLHDTYYVVAHFHYVLSIGAVFAI
2992	16893	A	3013	2	140	ARANILLLTLTAQELWDPRANNLI*LAY TLAFIVKKPLYGLHL*LPKAHVETPMDG PILLAAKLLKLGGSGIIRLTLILNPMTK HIAYPLLGLSL*GIIITRSICLRQTELK WLIAYS*ISHIALVVTDILIQTP*SKHF TTNSHCPRTMGPQSQQLNMTSLHTSFYS KETSLRTPLMTP
2993	16894	A	3014	2	420	PVLAAGISILLTDRDLLTTLFDPGGGGD PILYQHLF*FFGHPDDYILILPGFGIIS HIVTDYYGRKEPSGYIGMV*AMTPVGFL GFIE*AHHIFTVGIDAHTRAYLTSVSIL IVIPTWRQVFS*LATLHGSNMT*YAALF
2994	16895	A	3015	6	292	AHHIFTV*IDVYTRAYFTSATIVIAIPT GVKVFS*LATLHGSNMK*SAAVL*ALGF I*LFTVGGLNGIV*SY*LLDIELHDTY* FVMGCPRKVYF
2995	16896	A	3016	3	422	TPIIIGGFGN*LFPLIISAPDMEFPRIS NISL*LLPPSILLLLASAIVEAGT*TD* TVYPPLAGNYSHPGASVDLTIFSLHLTG VSSILGAINFITPIINIRPPAITQYQTP LCA*CDLMTAVLLLLSLPDLAAGITILL
2996	16897	A	3017	21	490	TPFPGRHLTMFSLHLAGGCSILGAINYI TTLINIRPPAITQYQTPLFV*SVLITAV LHLLSLPGLTAGVTILLADQNLNTTFFD PAGGGDPILYQHLF*FFGHPEVYILILP GFGIISHIVTYYCGEKEPFGYIGMC*AM ISIGFLGIIV*AHHIF
2997	16898	A	3018	98	402	LRSQHSKSFQISGKPSQEEWPQISPDST DYIINT*HFNAQMLKNIY*HQPHGLHDF FPKKKKKKKKKKKKKKKKKKKKKKKKK KKASSSSSKKDPPGGGPT
2998	16899	A	3019	399	229	PPPPGGGGPQGPPPPRGGFLPKSPGGVF YPPPRGGKIFSPPPGFFGPPRGFF*GAP P
2999	16900	A	3020	2	401	SDAVL*ALGFIYLVLEGGLTGIVLADSF LDLELHDTYYVGAHFHYVLSIGAVFAII GGFVD*FPLFSGYTLDQTYAENHFTIIL IGANVTFLPQHFLGLSGMPRRYSDYPDA YTT*NILSSVGSFITLAAALL
3000	16901	A	3021	413	67	PPPPGKIFFKKTPKKKIFPPPQF*IFFP

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						PLPPKKFFFSPNP*FFLGGFSPFFPPQK KIFFPKIPPNFFFSPPLKKKIFFFPPP* IFPPPRFFLKPPPPFFFFFFFFFFFFFF FFF
3001	16902	A	3022	2	332	LTLSILSIIAGS*GGLNQTQLRKILAYS SITHIG*IIAVLPYNPNITILNLTIYII LTTTAFLLLNLNSSTTTLLLSRT*NKLT *LTPLIPSTLLSLGGLPPLTGFLPKW
3002	16903	A	3023	1	412	RGPPFFFFFCVFFFFFFFFFFFFNKGCR HSKRFFFFFKKKKKSSRPTRDRV*FYPK GWRSPLFLFFSPGGRGFFPLSHQVGFSN EVLVVFKKNLELFRGSPARKKKKKKKHL E
3003	16904	A	3024	279	1	LGRNTELWKSGKGMDILKTNCGKLANEP FRQPRVLGIGGEAPRAGSGPPSRAPPA* TPGPSSAGSWP*PPGTGRAPRGPAPSAP GARSPGRPG
3004	16905	A	3025	151	401	KKPLGGPNLTGEGKKKFFSLKGGKKKPP GKFLKKTFFLGGEKMGKTPPKKLKP*GK KKIFKGKRGKKNPKTLAVKKFSKKKKK
3005	16906	A	3026	416	140	YLSPLKKFFTPPPLRMFLPPNPLKNIFF PPQLKIFWGGWAQNSPPPKKGFFSKNPK RVFLPPPIRKRYNFPPHGKILAPPKNL* SAPPPIFF
3006	16907	A	3027	379	31	PPPRRAGVFFFKNPKPKPPPPREGGRF* PFPPLKF*FFPKPQNFLGGGGAIPTPPP KRGLGQIPTERFNLSPPTQKRINFPPPG KGGPPPPLLKPPPPPPFFFFFFFFFFSL NSFI
3007	16908	A	3028	28	420	MQQTTMAHIFLCNKFANCAHVPRT*SET KPMSTPLQFD*TYKGEKSCKYAEHERTW KQ*CVFSLYQIIPT*EKTWKCNQCGTNF NQFFKQTTHL*NHTRDNQICFSKIGLEY YYRITTRQHLLKLRTVCIL
3008	16909	A	3029	1	401	LGNNGEAVSEKRKEKSQKEKSHNVVVGF FFFFWGKPPFVPQAEGQGRNFC*PKPWP PGWGEFPGPAPRGGGNGRQKQPGRGNFG V*REKGGSMGGPRGA*NPGPKNPHPWPP QGPEITGGTTRPHPSGIFKKT
3009	16910	A	3030	285	397	MFIKGDGLNKLRPGAAAYACNPSTLGG* AGRITRSGD
3010	16911	A	3031	265	2	KKESSCIKATNSNSLFFLF*SVFFFFVF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFF*HFKSALLWVTDLGFLNSD PRV
3011	16912	A	3032	410	49	GFSPPPP*KFFFSPKPLNFWGGGGPNFP PPKKRFFPKNPPGVFYSPPKKKKKFFSP PP*NLAPPKIFLKSPPPFFFFFFFFFFF FFLSNVSNGLTNMYILPCKDPSCPTTFP ILGSLISL
3012	16913	A	3033	177	2	VTPPFFFFFETRSHSVARTGV**SDRCS LQPHPPSIK*SSHFSLPSSWDYRSMPPH AS
3013	16914	A	3034	75	395	MSYKHXXKKKKKKKKKGGAP*KKPWGG PKLTRDGKKKFFSLKGAKKKPTWKFWKK TLILGGRKMGTTPPKKLKPLRKKKIFKG *RGKKHPKSLPVEKFASRGRIKK
3014	16915	A	3035	400	83	KKEGPARVVSPVTPPLLEGPVGRSPQTR

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						NF*PTPPTHRKSLPS*KSKIDWRGIPLY PPPPRVKPKKSFNPGNRRFC*TKIFPCP SPWAPKTHPPFQKKKKKRVYK
3015	16916	A	3036	3	196	DSMPQT*NKSFAKARKKKKKKKKKKKKK KKKKKKKRGGPPLKKTLGGPKLPGGKKK NFFFFRGG
3016	16917	A	3037	1	411	FCYDVCVESGCADYSIVIIMKKKKEK*K KKKKKKGGGPLKKNPGGAQNYPGVEKKI FSLKGGLKKTPRGNFEKKPYFGGGKNGA PPPQKNKPLGEKKKFKREKGGKKLQFPW GKKISLPGFYLKKIYPPGRGFFNFS
3017	16918	A	3038	3	429	NFFFKKPRGGNFFPPPKKGFFSPPSPLK FFFFPPPFFFFGGGGPHFPPPPKRFFFQ KPPRGFFFPPL*EKNFFFPPPVFFAPPP VFFLTPPPP
3018	16919	A	3040	1	111	IGLSGMPRRFSDYPDAYAT*NILSSVGS FMYLQQDNK
3019	16920	A	3041	76	967	QLLKGGVSGVCPLLMFRCVRSFFLLVGS WSSLASGVKPQTFAVSVTVLKAARLELF IPPRGLVVSLASGVKLQTFAVSVTAHKS SVDPKNSGAQLASPSGSRTRAAGGAACQ SRCRVPALLSPWVVDGTGRRGAGGGARR GGSGRTGAHGVGGRLRHGGLHVPSPAPW KGS*GLARNRAQRRWAGTAGGPSTPSAA AGPGAKSLTALCEQGWPAAPSAGPTKPT PTRNSSWPASVARSPGSRSCLSLHTSLQ AEGVGSSLGQPSKGLPQCSGGAEGLLKC RQSGSPGRGGTESERGL*GLPQCSGGAE GLLKCRQSGSPGRGGTESERGL
3020	16921	A	3042	39	141	LSIRGLNIIIKRQRL*DWIKQQDSTLCC P*EIH
3021	16922	A	3043	2	405	LFSTNHIYIGTLYLLFSTRAGVLGTALS LLIPAELGQPGNLLGNDHIYNAIVTAHA FVIIFFIERPIIIGGYGN*LGPLIIGAP DMAVPRINNITF*LLPPSLLLLLASAIE EAGAGTG*TVYPPLAGNYSHPG
3022	16923	A	3044	3	134	HLNPGGRGCSEPRLHHCTPSWATE*DSV SKKKKSRKGWTGLFI
3023	16924	A	3045	44	187	DPRVRQYQTPLFV*SGLIFAGLLLLSLP TLGAGITILLTDRNLHTAVFDPDGGGDP ILYQHLF*FFGHPEVYILILPGFGIICH IVTYYSGKKEPFGYIGMV*AMISIGFLG FIAGAHHIFTGGIDVDTRAYFTSATIII AIPTGVKVFS*LRLIRPNLCRLTSPISP NPRGRHHYTTNRPQPPHRRV
3024	16925	A	3046	434	40	GAPPPPPGRFFFFLNPREDTFPPPPQKG GFSPPPPPKFFFSPPALFFFGGGWPNSP PPQKNFFF*KPPEFFFFPPFLKKKIFFP PPLFFPPPQIFF*TPPPLFFFFFFFFFF FFFFFFFRGCKINFIVRGF
3025	16926	A	3047	1	399	LFTGGGLTGIVLTNSSLDIVLHDTY*VV PHFHYGLSIGAGFAIIGGSIH*FPLFSG YTLDQTYAKIHFTIIFIGVKLTFFPQHF LGLSGMPRRYSDYPDAYTT*NILSSVGS LISLTAAILIIFMS*EAFASK
3026	16927	A	3048	116	367	GASMILSSMIFLECIVGGFPVFSVYLFK LQILRQSSTMCFVLFCFFEIRSCSVTQA GV*RRGHGSL*PQPPGLSHPSSRDHGHV

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3027	16928	A	3049	6	345	SQLLRRLRKENCLNLGGGGYSHQR*HQC PLAWATE*DYLKKKKKNFSLFLKTGGFY PFLKKAPLGTTLSPKNNLPLSPLYKKRT GPWNWERKNFGKKKGGVIGLQGGKTIPK
3028	16929	A	3050	261	2	NKKSPPVNLWWKMGFFFKFAKRVVLSWK GGGGFFFFSWRRSFTFVAQAGMQWRNLS SLQPRLPDLR*SACLGPPDC*DYRREPQ YP
3029	16930	A	3051	160	2	ICVDEQAGVQWRYLGSLQAPPPGLATLS CLSLMSSWECRQPPPLG*FFVCPR
3030	16931	A	3052	89	3	PLTSGLLLLT*QKLAPISIIYQISPSLN
3031	16932	A	3053	344	2	HVEAPIAGSIVLAAVLLKLGGYGIIRLT LILNPLTKHIAYPFLVLSL*GIIITSSI CLRQTDLKSLIAYSSISHIALVVTAILI QTP*SFTGAVILIIAHGLTSSLLFCLAN SN
3032	16933	A	3054	266	2	FQPPISAYTKISPSLNVSLLLTLSILSI IAGS*GGLNQTQLRKILAYSSITHVG*I IAVLPYNPNITILNLTIYIILTTTAFLL LNLN
3033	16934	A	3055	3	32	KYNSLIMPTMIATITLLNLYFYLSPLLY **SSCPP
3034	16935	A	3056	3	33	KNNSLIIPTTIATITLLNLYFYLSPLLY **SSSPPS
3035	16936	A	3057	57	445	ANVWAPHGPAKLTNKDNYHIWKSKRLKI ANMTIKKLNEVIGLTLPDFKTYVELVQ* RQNAID*RKHKQPVKQSPEA*PHSYSQL IFHWGAKANHGRKDSLFYK*CW*NWTIS SQKLNLHTDLTNFTKIN
3036	16937	A	3058	311	1	RVGLLLKLNKISWPPPPFYGPS*EKEPL CFSQIGLFLTRTMVLNNLHSPPVKTRPY NKIAPFRELFFFFKDRVSICLPGWSAVV *SQLTATSTSQASSDPGRV
3037	16938	A	3059	138	411	WERPWKAQEAVFWI*VSAFWAPPPLMEK QIPPDLEQHYRNVPGVNRNQPFVSFFLR WSLTVAQAGVWWRDLGSL*PLLPGFKRF LCLSLLS
3038	16939	A	3060	1	189	FCRVGQAGLKLLTSSDPPASAS*SAEIT GVSQRAWSKITILKSSSFSYFPNSCKMC FWLICLN
3039	16940	A	3061	3	406	DAWADAWVLILPRFGRTSHIVTYYSGKK EPFAYIGMV*AMISMGFLGFIV*AHHIF TVGIDVNTRAYFTSATIIIAIPTGVKGF S*LATLHGSNMK*SAAVL*ALRFIFLLK KKKKRGAVLKVPWGGPSLPGCG
3040	16941	A	3062	451	82	PPPTNYFSPPPAFLPGGGGPPRPPPPKK WSPPTPPPVVIMPPPKKKKKFFPPPRGW GPPPKIF*KPPPFFFF*KKNPPFSPPGE NRGVFFSTKPPPPWGKKNFAAPGAPPPP PFFFFFPRGGG
3041	16942	A	3063	430	1	FFPPKQLIFWGGGGPKSPPPKKKFFPKK PPGVFFSPPKKKKKFFPPPPLNLAPPKI FFKSPPPLSFLFFPFFFFFFFFFFFFF FFFFPLSVQTLLKRTRAPPQPPLLD*EK APAPRVP*TGEGMPAVNVAFAPPPFYKE RPS
3042	16943	A	3064	1	409	PTRPRESTYQGHHTPPVQKGLRYGIILF ITSEVFFFAGFF*AFYHSSLAPTPQLGG

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						HWPPTGITPLNPLEVPLLTT
3043	16944	A	3065	1	137	HTFNFSIYQKATVIKTVWYWYNNRHTVE SPEINPYIYS*LIFFLF
3044	16945	A	3066	4	426	KLEN*KMVLKEIKEDLNKQTDILFS*LQ RLITVRMSILPKLIYKFSAIPIQIPA*F L*IKIIIKCMRKGK*TRIAETIFFFFFL SQSFILSPKLDHRGGITANCTPPWAIKG KLLLKKKKKPPKTKPEKFFIQKATGAEG GVH
3045	16946	A	3067	411	187	RNLPNVPPRPTHFVLLVKTGVSQVGQGG GKLLASKNPPSPAPPKSWDYRGEPPRPA PRKFFF*LNKFKIYGGPKN
3046	16947	A	3068	193	471	QCTCIKVHSGQKTGSTPLVIGELQIKIT LGCYYTPTLMAQIKKTDRTKCW*GYGAI GMLILCWRECKIVQSL*KRVWQFII*LN IYLAIKLNI
3047	16948	A	3069	323	478	FFXFXFLFFFILXYFYYF*KLFYLYLFX YIFKIYFIYNFIYIILFYIIFIIF
3048	16949	A	3070	1	378	GTRRFFFHSITLLILGLLSNTLTIYQ*W RDVTRESTYQGHHTPPCQKGLLNGIILF ITSEVFFFAGFF*AFYHSSLAPTPQLGG HWPPTGITPLNPLEIPLLNTCVLLASGV SIT*AHHSLIENNR
3049	16950	A	3071	201	2	TTPIQLFLKHYHT*NFNYNFFFEIGSCS IAQAKVQWCDLCLLQPQTLGLKHSSHLS LQSSWDYRHA
3050	16951	A	3072	261	1	EKAMGGGPFKVKKSPGEGPTTKGWPLKG PLEGGQRGLTGPFKSNGRLFFFFFGSNE VSLCCPG*SRTPDFK*SACLSLPKCWDY RHG
3051	16952	A	3073	333	52	EIFKKKKKGGGRFFNKRVFPRPRVSNGR PRAQFFLETFFFFPERGFFFFFFFETES YSVTQAEV*WNYLGSQQPPRFKRFSHLS LPSSWNYRCK
3052	16953	A	3074	7	214	SQLQENRLNPGGGGCGEPRSCHCTPVWA TE*DSVSKKKKKKKKRGGWVPPSLGGGP KKKNPFFNQEGGL
3053	16954	A	3075	180	419	QKHLSILHYLFKRDVFFFFLKGSFVVSQ VGGQGHNLG*LKAPPPRLTHFSCLTLRE TWKNRPRYFFCFFIKTGFHHVTRE
3054	16955	A	3076	371	208	QKLSGHGGSRL*S*PF*EAKAG*QLVSG GRGCSQL*SHQCTPAWVTE*RLVCKR
3055	16956	A	3077	349	3	TFCWQKYTMCRSLCHPHPPRTWSTKKKR PPFQKGQGDAPPYKKVQRGNPPPPLKGR PSRGPPKKCKVFKAPVFLFPRFSPPPFF PPPLFFFFFF*DRVLFCCPGWSAVAQLT ATS
3056	16957	A	3078	124	1	ISSETPAVKSSFWPGVVVHACNPSTLGR *GKEITRSRDRDH
3057	16958	A	3079	205	1	CLVQNIWACVSHWRYIMSCKGC*RLGLM CVCVCVCVCVCVCVYFCCCCCCCYC*DE LSLCHSDCSAVA
3058	16959	A	3080	3	413	GHHTQPVQKGLLYGIILFIT*EGFFFSG FF*AFYHSSLAPTPQLGGHWPPTGITPL NPL*VPLLNTSVLLASGVSIT*AHHRLI *NNRNQIIQALLITILLGLYFTLLQASE YFETPFTISDGIYGSTFFVATGFHR
3059	16960	A	3081	1	321	NSLNPGDGGCS*PRLHYCTPAWGTELDS

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						ISKEKKYPYHVYHPSMKMTIYNYRQQNV NHIYIMLVEHSQTQENTCFMISGNFFFN LPIVLGEGEKNQHSISFKLFFNF
3060	16961	A	3082	117	484	VLKYFIDSEVNAVLFSISCSFVTDFVFL FFFFGKGVSFCPPAGIKGGGFGFLEPLA SGFKRIFFPNPLEKWE*RARPPPRGKFW NFFFFFFLKRELFFAPRWEGRGKILVYL KGPPWGYPHF
3061	16962	A	3083	381	227	CISRDGFYHLGQAGLELLTSSDPPALDS *SVGITGVSHRTRPLLLRLNVQF
3062	16963	A	3084	2	391	SHAYHIG*PSR*PVTGALSDLLMTSGLA M*IDFHSITLLILCLLTNTLSIYQ*WRD VTRESTYHGHHTPPVPKGLRYGIILFIT SEVFFFARFF*AFYHSSLAPTPQLRGHW PPTCITPRNTLDVPLLNT
3063	16964	A	3085	2	248	IMRSGDRDHPG*HGETPSLLKYKRLAGH GGMRLWSQLLGKGGTADSHHHVLLILET FYSLRERRHLTSVPTLGMNYWAQDIR
3064	16965	A	3086	276	243	EKWPD*SRAACPVLCRGNGQYSKGRCLC FSGWKGTECDVPTTQCIDPQCGGRGICI MGSCACNSGYKGESCEEAPRYIPEKE
3065	16966	A	3087	3	130	GFYHVGQAGLELLTL*SACLSLPKCWDY RREPPRPAHTPPHS
3066	16967	A	3088	277	2	SSSSVFCLLVWTSSSSSSSAARLPPLTG FLPKWAIIEEFTKNNSLIIPTIIATITL LNLYFYLRLIYSTSITLLPISNNVKIK* QFEHTKP
3067	16968	A	3089	404	60	FSHGKMRFFSPPSPKKIFFSPQSFYFLG GGGAKMPPPKKRFFFKKTPRGFYFPP*K KKNFFFPPPVKFGPPRGFLKSPPPFFFF FFFFFFFFFFFFFSPTFFTVFHLMLKSD ND
3068	16969	A	3090	405	186	INKKPEAFTNTVDQMVLTNSHRTFYPTA TACSLSGAHRTFSRMDHV*DHKTSLNKF KTEITLSTLSNHKLEP
3069	16970	A	3091	371	1	SPPLVQKGLRYGIILFITSEVFFFAGFF *AFYHSSLAPTPQLGGHWPPTGITPINP LEVPLLNTSVLLASGVSIT*AHHSLIEN
3070	16971	A	3092	263	3	NKRSPPVNLWWKMGSFFKFAKRVKISWK GGGGFFFFSWRRSFTFVAQAGMQWRNLS SLQPRLPDLR*SACLGPPDC*DYRREPQ YP
3071	16972	A	3093	1	392	FFFADFKKMFILINHFKMELTTYFELKR NEATASENC*DAVKAVLGGKFIVLSTYI RKEERPRINNISFQIKHWTKKN*T*GKQ KKKKKKKKVTGPEIPKFLIVKSGKPPKV ILTGAWGPIKFLSFITRL
3072	16973	A	3094	3	367	EM*IEITMRYHYNTARRLKF*KTDNIKC **GHGTSGTLIYHWQE*KMVQPLWKIV* QLL
3073	16974	A	3095	3	257	HEVSQDGLNLLTS*SARLGLPKCWDYRR EPPCLAWLILPDDCVIFQKLKLLHHNLL NLSCIDVLMGIYSLSNFSQSNFPFFFFF
3074	16975	A	3096	189	414	KGLVMVTS*CKMFFCLSIFFFFFERGFC FFAQAGVQGHNLSSLEPLPPQLKQFFCL TLPRS*KYRPAPPCPANFY
3075	16976	A	3097	1	299	ENYRPISFMNTDAKILNKILANQIQQCS KRITHRDQVGFLPGMQGQFYI*KSIKSI

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						NAIHHISRLKKRNHMIPSIEAKKAFNTH S*FMKKNKKLAFQET
3076	16977	A	3098	362	126	FIHTHTHTHTHTHTHIYIYIYIIASFQW NAIRGRMKCINKP*KDMEELKCILPSER SQSAKATYLLYDSNYITLEKAKL
3077	16978	A	3099	3	423	RHEHAYHIVKPTP*PLTGALSALLMTSG LAM*FHFHSITLLILGLLTNTLTIYQ*W RDVTRESTYQGRHTPPVQKGLRYGIILF ITSKVFFFAGFF*DFYHSSLAPTPQLRG HWAPTGITPLNPLEVPLLYTCVLLASGV
3078	16979	A	3100	392	83	LRNTNCGHGAPFKNSPFFPQFLVKNSPA YFQNKEKDVGKPPFFFRAPDGAPFFKKK KK*GLALSSRLEYGGMISLELLGSSDTF ASASRVARTTGQCHHAGPT
3079	16980	A	3101	81	247	GGWGGPPLKPPLF*KKTGKNFWPPFFKG KEKPPPNPRGGGKKGGPKPPPVIFFFF
3080	16981	A	3102	3	388	HEKKEPF*YIGMG*AMISIGFLGFIV*A HHIFTVGIYVDTRAYFTSASIIIAIPTG GKVFS*LATLHGNNMK*SAAVL*ALGFI FIFTESGLTGIVLSNSSLDIVLHDTCYL VAHLHYVLSIGAVFAI
3081	16982	A	3103	3	387	HERHEELSNS*ANNLI*LAYTIAFIVKI PLYGLHL*LPKAHVEAPIAGSIVLAAVL LKLGGYGIIRLTLILNPLTKHIAYPFLV LSL*GIIITSSICLRQTDLKSLIAYSSI SHIALVVTAILIQTP
3082	16983	A	3104	3	381	HEQSHAYHIVKPSP*PLTGALLALLMTS GLAMGFYFHFITLLILGLLTYTLTIYQ* WRDVSRESTYQGQHTPPVQKGLRYGIIL FIT*EAFFFARYF*AFYDFRLGPTPQLR GHWPPTGITPLNSL
3083	16984	A	3105	412	111	FLGHPLFKKKMGGKKRGLPKMGV*HPPA PKGKPPPLKKKKKKPGGGGAPLYSPFSG GEGKKNPLTPEGGGPKNPNSPPPPPPGG KKKNPPPLSPKKKKKK
3084	16985	A	3106	298	98	FFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF F*L*IIY*AICAINNIRGAGAELYRSRD FVCY
3085	16986	A	3107	2	417	ATHVGLQDVTSPMIEQLITFHDHALMNI LIICFLDLGALFLTLATKLTKTNM*YAQ EI*TD*TILPAIILNLMALPSLRMLYIT DEGDDPSLTIKSIGHQWY*TYEYTDYGG LIFNSYIRPPLFLEPGELRLLDVDNR
3086	16987	A	3108	8	430	VGLVLFLSELPLNGGILTFFHQGIYSPF PGGRTWALMVGSWGLVMASTDLLGPLCH AFTPATQLLLNLAVASPL*PAALRIGCH SKTTNALTHFLPRGTPTPPRPILVTIET MSLLIPPIAPDQRLAAGFTARHLLLHLS V
3087	16988	A	3109	3	453	PRAIKFYRDWPGHERKRIAWKGDPCHMV LIKDEKGLMCQKKKKKTPFFWAPKIPLV FPPAQKNQGS*PNPPGGGGNPPLRPGP* RKKPPALMGPPPSSPGGINPKSFFYLNP GPAH*PRGEN*LGPVFENLFLPLLKKIF LWGELRCSQT
3088	16989	A	3110	398	2	SLFQKNPNPLVG*KKKGKALPQGPPPLF PPLGGAGPGGSQGRGWGPPRPPWGNPFF

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						F*NPKIWPAKGGAPFSPPSEKG*AGGFF LPRGGGFPLTQIPPPPPHLGGKSKPPFQ KKKKKNRQGTSWMMQGWGPQ
3089	16990	A	3111	3	371	SSDPPTSAFQGSGTTDMCHHHHAQLIFN FFVETGSCYVAQAGVQWHDHGSLLSQTP GLR*SSGATVLNWAPALGPRRPDPTRME SLVLMKPRGSLIRSACPDCFLVFWFSFF HEAEGCASEC
3090	16991	A	3112	233	449	FALFS*LATLHGSNMK*SAAGL*ALGFI FLFTAGGLTGIVLANSSLDIGLHDTYYV EAHFHYGLSIGAEFAIIGGFIH*FALFS GYTLDQTYPKIHFTIIFIGGNITFLPQH FLGLSGMPRRYSDYPDAYTT*NILSSGG SFNALNAGSIT
3091	16992	A	3113	458	2	RGPPPPPPPKFFFF*TPGKNSPPPPPEG VFFPPSPPPNFFFSPPPLFFFGGVPPIS PPPPKSFSPQTPPRFFFPPPPPLKKNFFS PPPLFLPPPPFFFYPPPPFFFFFFFFFF FFFFFFFFFFCGDLEGELPGTGMLACVI LLRANRKARTRG
3092	16993	A	3114	1	418	LNTTFFYPDGGGDPNLYQHLY*F*GHPD PDIHILPRPGIRSHIDTDYSGKKEPYAY VGMGWAMTSIGFLWLMVRARPLFTVGVG VDAQAYSSFASITIAIPTGAEVFS*LCP LPLSGMK*TGAAVWALGLRFIFTCSGR
3093	16994	A	3115	1	425	PRINNISF*LLPPSLLLLLAYAIVEAGA GTG*TAYPPLAGNYSHPGASGNLTIFSL HLAGGSSILGAINFITTIINIKPPAITQ DQTPLFV*SVLITEDLLFLSLPGLAAGI TILLTDLNLSTTFFDPAGGGDPILYQHL F*FFDPAGGGDPILYQHLF
3094	16995	A	3116	2	383	GLSCTNHKDMGALYLLLGARAGVLSTAL SLLIRAELGQPGYLLGNDHIYNDIVTAH AFVIIFFIVIPTVLGGFGN*LGPLIIGA PDTAVPRINNISI*LLPPCLLLRLACAI EEAGAGTG*TVYPPL
3095	16996	A	3117	1	259	PTRPALVVTAILIQTP*SFTGAVILIIA HGLTSSLLFCLANSNYERTHSRIIILSQ GLQTLLPLIAF**LLASLANLPAPTPTP HQ
3096	16997	A	3118	3	174	LIRGGRGCHELRSRHCTPAWATRARTLS QKK*KTTNPKKKLCLIFFGGKKKKLKKG
3097	16998	A	3119	155	1	PDFFNKSMDKKKTARGWEDSSSSFCFFK RDRVLLCCPGWSAVAQS*LTAAS
3098	16999	A	3120	420	2	PPPKFFFPPTPPFLGEGGAKTPPPKKIF FLKKPPGVFFFPPLKKKKFFFSPP*FLA PPKIFFKRPPPFFFFFFFFFFFFFFFF FFFFFFFFFLVFIVLFQVKVHFLKKCFN IQFPLASDNS*PSMIHEKFYCESNIEF
3099	17000	A	3121	48	387	RDPVLQKKEKKKKKKPKNQKKKKKKGGP F*KIP*GAKIKPGKEKKNFSPKRGAKKK NPGNFEKKTNFGGGKKWGKPPPKN*RFK GKKKFLKGKGGKKTQIPWGLKIFFNGFD
3100	17001	A	3122	237	2	PFPVVLPPFPLKASSSP*SL*FLLGGWP NLPSSPNKGSFPKFPSWFLFRPP*GKNF YLALPR*PWPPQGFL*TAPP
3101	17002	A	3123	448	130	PPRFFPEFFYSGPPKPPFFKTPVFLGVK PGVFFFSPYQKKPTNFGPKMGAL*RIPL

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						FETPIWVFPIKGFHKKKPPVLN*PPTRK PPPDKILKKKKKDDCISRLARN
3102	17003	A	3124	453	3	SSAREGGGVPPPPPKIIFFPPPPIFSWG GGGTKSPPPEREVFPKNHGGCFFSPP*K RGKYFSPPPRMGPPPGVFFKGPPPNFFF FFFFFFFFFFIFFFFFFFFFFTKKKNWF FFKAFRMSPKPVPPFFFFCNYRVVFRPR VRPRVRPRV
3103	17004	A	3125	443	2	YFPPFGRVIWGDSLGAGVLNPPRPHKGT PFFPKKIFSIRPGWGGGPPLPPPQRQMW GGPPPPLFGLFRPQGKIPFPPKKKIKPP GGVCVGVGVCV*KKKKNPFPPFLWAGLK EPCFFFFFFFEMEFCSCCPGWSAMARSQ LNCNLHL
3104	17005	A	3126	3	186	PVIYSTIFAGTLITALSSH*FFT*VGLE INMLKKKKKKKKKKKKKKKKKKKKKR GGGL
3105	17006	A	3127	171	38	KKKKLFFPPREKWGPPKNFLKRAPPFFF FFFFFFFFFFFFFWSERSS*VA
3106	17007	A	3128	16	189	ILGEVIWV**FF*FIKKKKKKKKKKKKK KKKKKRGAPFKKTPGGPQITPGEKKKIF SL
3107	17008	A	3129	401	85	LVNFFSPQEKRGFFPPPPPKNFFFSPRG FFFLGGGGPIFPPPKKSFFSKNPPGVFF SPP*KKKIFFFPPPLFWAPPRFFFKGPP PFFFFFFFFFFFFFFFFFSQF
3108	17009	A	3130	2	312	ANNLI*LAYTIAFIVKIPLYGLHL*LPK AHVEAPIAGSIVLAAVLLKLGGYGIIRL TLIILNPLTKHIAYPFLVLSL*GGGVF
3109	17010	A	3131	449	3	FFFFFFFLGGPPEIFFFFFCPPKKPKPP LGGGKKKPPFF*NFPQKPLGVLGAPPPP LCFFIKKKKGGGKKFFSPPLF*KGGPFK KFFFFPPPPKGPPPFLKNLRGWVFFKPP PKKKALSFFKKKKKKKKKKKKKKRAAAR DLELADAW
3110	17011	A	3132	95	448	VINRE*KCVC*MKKKKKKKKKKKKKKK KKKERAGKGGG
3111	17012	A	3133	60	442	LGGFFFFGGKKGFCLWCPRWGAKAGIPV NGTPPRGV*RNFLAQPP*EGGITGPPPL PQ*FGFLRENGVPLRGPGGFEPPILGEP PPLPPQKGGKNGRNPPPPLKGFLVLFKK EFSSLVPSWKARGDP
3112	17013	A	3134	236	45	FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFGAAD*VILFRYFQ FEATIMGV
3113	17014	A	3135	441	88	KQQTPPGLIFF*KAPRREIFLPPPIMVF FSPPSPFKFFFFLSPFIFFGGVLPFFPP PKKGFFFKNPRRVFFCPPLKKKNFFFLP PFFFGPPRVFFYPPPPIFFFFFFFFFFF FFFFFF
3114	17015	A	3136	2	328	TMLSPKPQQLNQQNCSPEHYEPQLKTQR TWR*KKKKKKKKKKKKKKKKKKKKKK KKKKKRGGGQKKKMVGGEKKKPG*KIFF FFIKKVKKKTALGDKKKTQFWGGS
3115	17016	A	3137	281	2	KATKSGTPIPSQGQQSLAWSWAGIGSAQ PPALLHS*PIGKIFKNCMPVGRKSPQLP RNTSWQLGAVAHPSNSSTLGGRGGRITR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						SGVRDRTRG
3116	17017	A	3138	448	3	FFFLPPSPFFPY*KRGFSLFGRVVFNFP PPVFPPPWPSQIFGFQALIFLPPPPPLF FSFPVGFFQTALFPFNGFFPGFFHGLFP LLRFCPRK*VFWGGFFFFFFFFLRDKVS LCHPGWNAVAQSEFTTALTSKAQAPTRP PTRPPTRP
3117	17018	A	3139	2	436	DR*LFSTNHKEIGTLYLLFGA*AGVLST ALSLLILAELGQPGNLLGNDHIYNVIVT AHALGKIFFIAIPIIIGGFGN*LAPLII GAPEMAIPRINNIS*GLLPPSILLLLAS AIEEAGAGTG*TDYPPLAGNYCHPGASG DLIIF
3118	17019	A	3140	362	2	KPRRGKFFPPREGGGGFPPPPPKNFFFP KGGKFLGGGGGKNSPPQKKGFFQKNPGG VFFPPPKKKKNIFFPPGKMGAPPGFF*R GPPPFFFFFFFFFFFFFFFFFGQSGQVK LKSPKCKL
3119	17020	A	3141	440	102	PTPPPCCKFSFKRPPKKTLFFPTTNLVF FSPIPP*NFFFSPQALIFVGFLAPIFPP QKKFFFSKFPPLFFITPPLIKKFFVPPP PFILSPLKIFYKPPPPIFFFFFFFFFSF
3120	17021	A	3142	1	79	FKLDYFSIIFIPVALFVTWSIIEFSL*Y INSDPNINQF*KLDYFSIIFIPVALFVT WSIIEFSL
3121	17022	A	3143	3	441	FFFPPPLKKKKFFPPPPNIGPPPKSL*K PPPPPFFFFF
3122	17023	A	3144	223	3	LPYWKLPYLKH***LQDTNQESRG*HFL RPRPFKNQMKSGTVAHACNPSTLGGRGG RITRSGV*DHPGQHGEI
3123	17024	A	3145	65	414	KKKKKKKKKKKKKKKKKKKKKKKKRGGP PKKKTRGGPQNPPPKKKKFPPQKGGKKK PPLGF*KKTPPLGGEKIPPPPPKKNTPP KKKKKF*GGGGQTPPPPPPGKKFSPPRN KKKK
3124	17025	A	3146	410	31	RANQKAFRGKPLCDLAVGKNLSSRTQIA LTI*KWINWTILKLRTSGH*KTPIKTIK RYPIEGEKISDEELYLQY*KVL*IGKKK PDNPVEKWANDLKRSFMKGNILTVFKGM QR*LGSMAHICSLS
3125	17026	A	3147	182	241	SHPSHHSTINITNKGLL*TPLPIPNPLV NLNLGLLFILATSSLAVYSIL*SGGASN SNYALIGALRAVAQTISYEVTLAIILLS TLLIRGSFNL
3126	17027	A	3148	254	1	KTKKGLKIKDPLTRF*ISVC*ITKSI*F FKLLPFFPLLKEHIPLKYLFFFFFLFET EFRSCCPGWSTMV*SLLTATSTSQIQAI
3127	17028	A	3149	499	2	NTPPAAGGGCFFFFFFGEKNFPPPHPTP RFFPPPPLKNFFFFSRVFFFWGGGAQKA PPPKKVFF*KIPRGFFFPPPKKKKIFFF SPGFFGAPPGFFLSGPPSFFFFFFFFFF FFFFFFFFFFFFFFFFLINFLLSLQGFF LVSKELFLFGLTVKFTRGFRGFCGQ
3128	17029	A	3150	256	146	KNAKVTQVCPEFNKGPG*HTHTHTHSHT HTHTHTLQ
3129	17030	A	3151	333	1	TISCLCTRGEHPLSPRRAGPYTGSPLHC CVDVVDKVFSSWKDLTDWPLGDLDIEYF TDGSSFILRGVCRAGYAAVTLDSAVEVL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						SVSAETSA*KAELIALTRALWLGKEQK
3130	17031	A	3152	43	379	NKTSLFGWDYIWEWGAPEPETPPKRAAG ALHSLAQPFSVALPPCFFDPCAPSLSPG *HALRPLPLPGLASEIQTAPSWHVPPKS LSPAPQPCPIPTLVPVGYKTPP
3131	17032	A	3153	398	12	NTTPGGGKFFLKKTREEKFFPPKKKRGF FPPPPPKNFFFPQGGNFFGGGGGQISPP QKKGFFQKNPRGVFFTPPKKKKIFFSPP GKMGAPPGFF*RGPPPFFFFFFFFFFF FFFFFFLKKSWRPLAI
3132	17033	A	3154	371	105	SPSPQVNFIKGPKPPPPK*IL*RAPNPP LPKKKFSNPPTWGPGPQPPPSKFSKFAR FPFLPPPFPFKKEPPKKKIFFPTKEGTV I*KNPPFSGFQSPDSIK
3133	17034	A	3155	3	371	DVGADPILHTSTGL*LAMQY*PEA*TAF SSIAHIT*DVYYG*VIRYLHANGA*IFF ICLLLHIGRGLYYRPFLYSKT*KIGLIL LLATITTAFIGYVLP*GPI*F*GATVMT NLLSAIPYIGT
3134	17035	A	3156	1	398	IAIPTGVKVFS*LATLHGSNMK*SAAVL *ALRYIFLFTEGGLTGIVLPNSSLNIVL HDPYYVVAHFHYVLSIGAGFAIIGGFIH *FPLFSGYTLDQTYAIIHFTIFIGVNLT FFPQHFLGLSGMPRRYSDYP
3135	17036	A	3157	401	46	PPGGRNFFKKTPGKKIFSTKKKKGFFPP LPPKNFFFSPGGFFFGGGGGPNFPPPKK GFFSKNPRGVFFSPP*KKKIFFFPPG*I WAPPRVFLKGPPPFFFFFFFFFFFFFG KKSVRA
3136	17037	A	3158	404	18	FFSPPPPPPGGGVFPPNPNKNPFPPPPP PFFLGGGPPPPPPPPP*FPPPPTPPNVF FFSPPKKKNFFPPPPGPPPPPPKPPPPP PPPFFFFFFFFFFFFFFFFFFFLFFFEP MEKGPRPGDIGSNPPS
3137	17038	A	3159	3	192	SLVIAGCPR*NLSSTLNLPTEPSKSPCK FNC*KKKKKKKKKKKKKKKRGGALKKN PWGGKK
3138	17039	A	3160	205	80	VQRDNFGFLQPSPSGVKLFFCLSLPNKW DFRCGPPNPG*FFS
3139	17040	A	3161	3	384	LIVPTIILLPLT*LSKKHII*IINTTTHS LIISIIPLLFFNQINNNLFSCSPTFSSD HLSHPILKKKKKKKKKKKKKKKKGGGA FKRTPGGAAHWGGGGRETFFPKGGEKKN RPGVFWKQTFFWGGK
3140	17041	A	3162	348	70	GPPPKKRVFSKTPKVVLNKPPQKKKKFI FPPPVNLGPPKNFLKGPPPFFFFFFFF FFFFFYFFWMGCDR*CSWRHSSPPRLSG TPKCSPSVT
3141	17042	A	3163	2	353	LKTIPLTSTCLTIGSLALAGIPFLTGFY SEDHII*TANVLYTNA*ALSITLIATSL TSAYSTRIILLTLTGQPRFPTLTNIETK KKKGGPFNRYPLGAQVYGGGQNEKFFLI GREII
3142	17043	A	3164	1	221	PTRPRDCSELRSCHCTPAWATEGDSISR KKKKLSTRTAF*YTEAINSLIYSLNIGT FKTYFPKIKTYDRHFDF
3143	17044	A	3165	26	383	IPFYQ*SLI*YTRKKKKKKKKKKKKKKK KKKKRGG

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3144	17045	A	3166	251	381	GNLCAGWARWLTPVVPALWEAEAD*SRG QEIGAILANTVKPHL
3145	17046	A	3167	391	115	LFKKISPHAGIWGFFSPLTP*NFFFSLE PFIFGRGLAPIFPPPK*RFLSKNPPVVF IPPPLMGKPFPPPPPVRLGPPIYSFKGA PPFFFFFF
3146	17047	A	3168	94	389	SPGILGQKGQIGPIGNHVPGGLAAPVTP *FRFKPRLP*GFGPKASPPLALKPERAQ VGGTPPPGPRGPNGQPPPFKENQPGLGF RFRGKLAEKRGFHL
3147	17048	A	3169	3	363	WATALQPGQQSETQSQKKKKKKKKKKRG GPPFFFFFKKKIFFSPPGAKNKRGKFF* KPPKKKKKIFFFPPPPLKKKKKKKKKK KKKKKKMGGAFLKKPRGAPPPPGKRKLI FFFLKGV
3148	17049	A	3170	2	171	KEPLGYIRMV*AMISIGFLGGIV*AHHI FTVGIDVDTRAYFTSATIIIVIPTGVKV FS*LATLHGSNMK*SAAVL*ALGFIFLF TVGGLTGIVLTNSSLDIVLHDTYYVVAH FHYVLLIGG*FYLRYHNHCYPHRRQSI
3149	17050	A	3171	390	27	QSLTVKSPYPVVILIKTKGHH*VMNAGL TRYQSLLCENPHIRSEVCITLNPPPLLP VSESPVKHSCVQVLDSVYSSGPNL*DHP *TSVDWELYVDGISFANPCKVSLKKMTS PAPVTPRS
3150	17051	A	3172	127	310	KNPGGAKILRGGERKNFFLKRGGKKKHL GIFGKKTFFWGGKKWAKPPK*WRFFSPF SP*KFFFSLKALIFFGGFCPFFSPPKKS FFSKNSQVFFFSPPFKEKIFPFPPP*NF GPPRVFLKGPPPFFFLGVFFFFFFF
3151	17052	A	3173	376	3	FFFFFLRRQSLAVTLAGV*RCNLSSLQS PPPGIK
3152	17053	A	3174	365	14	RENFFSPEGGAPKNKPPPPPPPPGGKKK IFFQKKKKKKIFYPWKNFPPPPKKKKKN P*KPGPLKSQGFFFFKKNQNLPWGPPQI SFPKKKKKKKAKTVQERKYNSNTQLVSA ETQLL
3153	17054	A	3175	1	377	VPLHSSLGGKARLHLRKKKKKNPGFLKN FGPLALLGMGVGNIKGLKGQKGKNPAFG AHTGGGCFSLRGRNTPFPKRAEGIICYN SPH*KET*KALEPRGYKGL*QALALPNL KSGKMEHILRGAP
3154	17055	A	3176	352	125	GHEVLDSSDLPASASQSAGITGVSHHAL *EILLSMFETTWACDLLFQNISFIKSSI PCFIGLDFIMPHRYCRFFF
3155	17056	A	3177	139	366	TAHTS*GY*VKNYINLSFCFFFFFLERN HSALQPGGQGHNRSSLQPWFPGLKQFSC LSLPRSWDNGLVPQHLVNFF
3156	17057	A	3178	206	1	KGTLFKKDFFFKNFPKKVFLGVPKNSLF *KILTLPPVLNPYPFFFFFFFETVSLCH PGWNAVVPRLEP
3157	17058	A	3179	330	1	IVSTLETCYIAYNEEEKDTFITLRIYVI GGNGKFLGI*IKQHIKKIIHHDQVGFIP GMQGWFNICRSINVIHHISRIKGKSRAQ WLTPVIPALWEGDAGGSPEVRSSRPA
3158	17059	A	3180	3	399	HASAPLQSSLGYRARPCFKKKKKKKKGG GGGGFFFPKGGFGPLPKKGFFSGKGGLG KWGLGGAGKTPGIKKPLGKGPPKKRGGK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						KGQKGPHF*KKKKKKGGKKLKKGPF*KP FKKPLLGRGVQP*NPHLLGG
3159	17060	A	3181	2	204	CPTACPFW*NKELLMPKKKKKKKKKKKK KKKKKKKKKRGGAPFKNSLGGPHFPGAG KKNFFFFWGGY
3160	17061	A	3182	71	377	PKRGGQPKQKKIWGPPPPGAPPQKGMGF FNPRGFKKQITFFPPPPPPPPEKKPPFF* KKKKKKKKSNCSD
3161	17062	A	3183	151	2	FFFLEELVPLLLKLFQKIEEEGCSPNSF NEAFIILIPKPFR*TTKKENF
3162	17063	A	3184	152	387	YFQGFIYVVACICTSFLFFFFFLKREFC FVTQVEVQGPNFT*LNPPLFGLKKFFCL TLQIGWNNRPLPPPQVIFCFFK
3163	17064	A	3185	22	336	YEKCTALLQMVSSFIWMEREGTHQYSFY RKDFSLASKVNIVSYYLSPIVE*FFFFL RGSPFAPQAGGQGPNLGSWKPLPPGLMP FSCLTLPGGWNCRPPPPGPVN
3164	17065	A	3186	344	1	WVLKKIFFYPGRGGPPFIPPPLGGQGGP IPWARGF*PPRGPPPKNGF*KKKKKRGG GGPPPGFPPPGGPRGGVPFFLGGGGPRK PKKITKKKNPGEKKKTSFKNQKRKTKIK TT
3165	17066	A	3187	296	1	NPKKILTLPKKTKVYKCEGENQVPIIFQ GIKNIFWKGIF*PKKEREVCV*SMRHVI PVFPKKRGSKRSNKSCCYKDTCTRMFIV ALFTIGKTWKQPKY
3166	17067	A	3188	2134	1	GVAAHACNASILGGQGGRII*GWEFETS LANMVKPC
3167	17068	A	3189	1	159	LQDHPG*HGEPPSIVKIQKLARHGSLRL *S*LLGRLRQRMRQETCLNPGAR
3168	17069	A	3190	119	340	QIKKNRLVSARGKNNKRK*IYKP*VDIF FKEDIQMAGKQMKRDLISLIIREIQIKT TITCYLIHARMGTITRD
3169	17070	A	3191	75	1	LSVNNFWPGTVAHACNPSTLGG*GG
3170	17071	A	3192	343	1	IFILGGGPCCSPVFFQFFGGGGGGGFFLP QNFFPPRGKIFRPFFF*KKKLKRPNWGF F*NFFNPPLGFFNLFFFFFKKKPKNFFF LGGFFFFFFFFFFFFLAGGDSLALSPRL EC
3171	17072	A	3193	105	368	KFKDPPFPPPFFWPPPKQLPPPPGKIGA PHF*TPKGPPPPKKKKC*KKKILKGGRG KKKKKTPPKRPQKIWGPSKKKNPWGGGK TPPL
3172	17073	A	3194	1	365	FCRDEVLLFCPDWSPTPGLKQFSHLCLP KCWSYRC*PPYPAQGVFLK*HLTKSLSC LKLFMASLCLQDKVPAPQPCVKGLSKFF LCHLLSTLIPFTHSLFFLFLGWFLRQHR SVTQAGVQWR
3173	17074	A	3195	1	362	GNQPKRLNAGTYLLFYTLEGSVPLLIAL MYTHKTLWSLNILLLTLTGQELSNC*AN NLI*LAYTRALIVMIPLYGLHL*LPKAH VEAPIAGSI*LAAVLLKLGGYGIIRLTL ILNPLTNT
3174	17075	A	3196	137	3	KGQPRFPPISLKKGSQGKKGFFFFFF*Y RIPLCHPGWCPVVQSW
3175	17076	A	3197	1	266	EGRGCSEL*SCHCTPA*VTVRYPVSKKK KKKKKKGGGKGKKKGGEKNTLFGPKKGK LRGPQKRGKKIGPEKKVGNNLKKGIFFR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						EKTF
3176	17077	A	3198	217	446	YWSEHYAMTQVLEGFSYSLQDHFYFCFR SIRRIIFYSLIKPSIND*GERELEPITT SQALQIAGRAGRFSSRFKEG
3177	17078	A	3199	345	314	QPGPEGKIRFFLKIPNLTPSGGKSLKFP LFKRVKPENCLSLRG*GCN*PI
3178	17079	A	3200	2	330	SRHYTPAW*QSKTLSPKKKKKKKKKKKK PPFPKNTQKKPKKKKRGGLNWGVKTPPP LKTQKMGISPGKKLKKNLFPLKKKKPEG NPLF*FRGF*KKKKAPFKKKKNPPK
3179	17080	A	3201	2	385	FPPFLGGPQIPKFLKFFLRAN*NLFGLF FLGGVLKKIFLRKPFSLWIKPFPTPFKG KKIFFKTFFQKPLFFF*KKKFFFCFPPF FFLSRGFFVFFSPKKPFFFFFFFFFFL
3180	17081	A	3202	355	2	FFFFFSETESCSVAQAGVQWHYLGSG*A LPPRFTP
3181	17082	A	3203	156	1	LKSLLWEAKVGGLLEVRSSRPA*ATWRD FISTKN*KISQVWWYILVVVTTWE
3182	17083	A	3204	352	175	QPRGRPAPAHPP*CPLRLALPC*CPCPA CCPPWAEASPSGVQASPARAPACPARAL LNE
3183	17084	A	3205	280	373	QRGTRIFSDLQT*KKKNKSPFKILLLID NALGHSRVLTERYKDIFRPANTTSFLRP MVQELIPTFQS
3184	17085	A	3206	1	367	EIESIQIDGHTKNKFLGIHLTYLTKEVK DLCKKNYKTLLKEIIDDTEKYDMLMD*N NIVKMAILPKAIYRFDTISTKLLMSFFM ELEKIF*NLY*KA*MAETTISKKNKAGG ITLLDFKLYY
3185	17086	A	3207	368	12	FAQKKKKKKKKKKKKKKKKKRAPPQN* RAPQKPLKPPPRVFLIPPPLGSPPPPAF FWRGGGPPPGPFSKKKKKMRLTGGGRLF LLA
3186	17087	A	3208	2	356	KYLFSSIPEGKEKMKGIANLFNEIISEN CPSLARDLDIQKTRHANPYNLKKSSPQH IIVKLSKVKDKERILKTARKECFITYKR TPIRPGMVAYACNPSTLGG*GGWIMRSG DQDHPG
3187	17088	A	3209	359	170	INIKQLPRCGGTCLWSQLSRRLRRQDCY SLGGQGCSEL*SSQCSPAWATERDSVSK YKINNFL
3188	17089	A	3210	295	122	VIKTV*NWNKDRHIDQCSRIESPKIHLH IDDQLIFDKDVKTPE*RNNGLFNKWCWE N
3189	17090	A	3211	218	466	ATFDTTLPSCYQNAPNNRFDDLSD*EQE IDTMTVNIILPLRSLNIVITNPYNI*HH QHDLDYTYPDTTGQLVNCAYFINLLQP
3190	17091	A	3212	340	355	LGLQG*REGNFGSLQTSPPGFKRFSGLS LLSSWDYRV
3191	17092	A	3213	254	40	WPGTMAHACNLSTLGG*GGCITRPGDRD HPG*HNNNN
3192	17093	A	3214	198	25	YNEKEKPVKMLKIIANSLGAVAHAYNPS TLGGQGGRIMKSGDRDHPG*HADAWVET VL
3193	17094	A	3215	376	3	PPGVF*RGPPGFRTLPPKSSSSSPPPKI LGGPPFLAFFGGAPPQKKPPSSSSSASS PPSSSSRAPLKKGGPFNPAGGFPLFGGP PRGGPPFSSSSSSSSSSSSSSSGRRSR

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						SRTSRTRGRTRG
3194	17095	A	3216	393	260	VSQDGLDLLTS*STRLGLPKCWDYRREP PRPACTLCISSTYNDP
3195	17096	A	3217	3	387	HASASSGSRAPPFFFFFNKKTGSKELET TRGTVLKTCLFFKKKKKVLGGPKPPLGN PKGVGKPLKGFPGPNPWPPP*KGPGCHF *KNGF*DPGPKKSHIPSWVGGKGSSLLP GPLGGPSEVYFSPLRA
3196	17097	A	3218	77	406	RMARPELGLPGNLLSNDHIYNGIVTAHA FVIIFLIVIPIINGGFGN*LIPLIIGAP DMAFPRINNISF*LLPPSLLLLLASAIV EAGAGTG*TVYPPLAGNYSHPGASVK
3197	17098	A	3219	394	2	KRRYFPDGLNFFWGPGILKIFVKKKVSS LKKKKKKNFPPVFLQGWGGNKNFKGGGL KFSKPNLI*FFFPQKEAR*KVFFFFFRS PQKDPLREFFFFFLRQVSLCHPDWSAVA RSQLTSASISRAQGAGRV
3198	17099	A	3220	376	157	KFFFSP*KFFFSPKPLKFGGGVGPIIPP PKKRFFFKNPQGVFKKPPQKKKKIPFQP PVNFGPPRDFLKGPPPFFFFFFFF
3199	17100	A	3221	394	1	VPPPQKFKTPGPPPPPREFFFF*KKKGF PPLGGFLNPAPKNPPPGPPKKVGFPGGP PPPPGGFFFSPPLSF*NPGERVFFGPKI PKRKFLLKWGKGGKFFPKKPIFPPPPKK KKKKKKRAAARDLELADAW
3200	17101	A	3222	207	402	SILM*LCCLFPLPGVTPIDGAPHRSYRE CYPVLLDGVMVGWVDKDLAPGIADSLRH FKVMREKRI
3201	17102	A	3223	309	3	YPFFHLIDLAIHPCVCFTKFYKATVTQT AWSWYQIRYIDQ*NGTEISEIPPHIYNH VICDKHDKNKQWGKDSLFNKWCWEN*LA ICRKLKLDPFPTPYAKI
3202	17103	A	3224	3	382	LDRERPPFFFWGARHMDIPQLVNLSINK GHWANFNFLGYKKKGGWEKKKKKKKKKK RGGPP*KKPPGGPK*PPGGKR*IFPYMG GKKKPPGGFLEKPPPLGGAHLGNPPPQK YTPPGKKKNLKRET
3203	17104	A	3225	133	2	FFFETESHSVTRLECSGTISAYCNLCLP GSSDSPASAS*AAGI
3204	17105	A	3226	349	2	AGVPPGNPPLWGGEGGGSPRGGGLKPGF PQRGNPFFFKKSQPTPPGGGPPLIPPPW GGGAGGSPLPQGQRFQ*TKIGPFPSPRG KKKKPPFPKKKKKKKKRKEKSEMPGFMV LNA
3205	17106	A	3227	3	239	LNKVGRGCSEPRSRHCTPAWATE*DSIS EKKKKKPESRGILKVKGLTQALFYLALW LYYLHPTAKQQIWGFFIYFSKP
3206	17107	A	3228	205	1	IGLKIQNSCPLKDSLKKIKRQATDWRKY LQNTSDKASVFIIYKEHLQLSNYKAVDP IK*WAKEMNKLH
3207	17108	A	3229	174	1	VQMLEDKSFEETP*FSSETLVLKIPHVQ PGAVAHTCNPSTLGGRGGRITRSGDRDH PG
3208	17109	A	3230	2	340	KNHSVYLLCVFSIPFPTFCFF*F*VFNT F*FKLN*IN*FTYIDRVLLCHPGWSAVA *S*LTAALNSWAQAVPCLSLLLAHHHAW LIIFKKTAYIIHIWYVWYDTTYPFKVYN S

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3209	17110	A	3231	1	313	KKSTPYQRGFDPISPARVPFSIKFFLEA ITFLLFDLEDALLLPLP*ALRFIFLFTV GGLTGVVLANSSLDIVLHDTYYVAPHFH YVLSIGAVLAIIGGFIH*FP
3210	17111	A	3232	207	355	ELSPFRLKKTLY*LGMVAHACNPSTLGA RGGQIA*AQEFKTSLGNMAKP
3211	17112	A	3233	3	355	TTQQ*LIKLTCKQTIAIHNTKGRT*ALI LISLIIFIATTNLLGLLPYSLTPTTQLC INLAMAIPL*ADAEVIGFRSKIKNALAH LLPQGTPTPLIPILVIMETINLLIEPIA LARRL
3212	17113	A	3234	2	355	KYLINNRLITNQQ*LIKLTSKQMITIHN TKGRT*SLILISLIIFIATTNHLGLLPY SFTPTTQLSINLAMDIPL*SGAMVIGFR SKIKNALAHFLPQGTPTPLIPILAIIET ISLLI
3213	17114	A	3235	43	370	QGCVKGWVLEEQVRRGWILDSSEGKTDL KQRGSPGSWPEHVGGWSGVMG*SEAWTG QARWLTPIITALWEAEVGGSLRPGVQWH NLGSLQPLPPRFKRFSYFSLPSSWD
3214	17115	A	3236	15	356	LIQPSLKLMISIHNTKGRT*SVILLSLI IFIATTNLLGLRPYLFTPTTQLSINLSM VIHL*AGAMVIGFRSNIKNALAHLLPQG TPTPLMPILVIIETIRPLILPIALAVRL TA
3215	17116	A	3237	1	376	GTRTNTLTIYQ*WGDGTRESTYQGHHTP PVQKGLRYGIILFITSEVFFFAGFF*AF YHSSLAPTPQL*GHWPPTGITPLNPLEV PLLNTCVLLASGVSIT*AHHSLIENNRD QIIQALLITIVLG
3216	17117	A	3238	1	358	GTRNG*YTNA*ALSITVIGASLTSAQGS RIILLTLTGQPRFPTLTNINENNPTLLN PIKRLAAGSRFAGFLITNNISPGCPFQT TIPLYLKITDLGVTFLGLLTGLDLNYLT NKLIIKA
3217	17118	A	3239	258	390	RQGLLMLAGLVLNSWPLQSSHLGFPKCW DYGREPPCLGN*LIL
3218	17119	A	3240	2	372	ARARFHHVSRDGLDLLT**NTHLRLPKC WDYRREPLRPGKTFFLKKKKKNSIFLFF REGFKEKSILGIKFFRPTGGVLILTGNH GWGCKTGTELLVPSRFPGLAFKICGLWA HDTPHRVRNWL
3219	17120	A	3241	3	283	HERLWGGWKTGAAGLGRTSSRPTASLTQ T*TTMTH*SRTTGCSTGSGRTWTRSRHS CAWGMAGLYRVAVASRGPRGMM*PTPPH WLCWAWKVP
3220	17121	A	3242	170	3	IKSQAGLVGFLGPFSFQDSLNLVFVFGF FCF*DRVSFCSPGWSAVVQSEFTAALV
3221	17122	A	3243	2	385	ARADVDTPSYLTSDTIMRDIPTGGQVFS *LSTLHGSNMK*TAAPLLTLGFIFLFTA GGLTGLELTNSWLDIVLHDTYYVGPDFH YVLSIGAVFAIIGGLLH*YPLFSGYTLY RTYAQIHFAIIFIGEN
3222	17123	A	3244	1	106	GTRYVGQAHLKCLTSSDSPASTSQSAGI TGVSHSA*PASTSQSAGITGVSHSA
3223	17124	A	3245	2	360	ARANTLTIYQ*WSDVSLENTYQGHHTPP VQKGLRYRIILFITSEDYFFSGFL*AF* HSSLSPTPQL*GHWPPTGITPLNPLKMP

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						LLNTSVLLASGVSIT*AHHSLIENNRNQ IIQALLI
3224	17125	A	3246	17	160	GG*GCSCSEL*SCHCSPAWVTEQDFDSK KKPAILASCLKHLNPLSSH
3225	17126	A	3247	236	2	WAHIYMTPLSPPSFLKPVQ*KNFYIYST YSLDN*NPSSPKAKRAPKKSYTLPYLHL CVCVCECV*VCVCVCVCVCVWV
3226	17127	A	3248	2	2220	FFGGGRPSPPQGYFLLNNHSSPSPPVKL NPGPA*FYPPTKGKNFPPPQR*PSPPKN IKTPPPSFFFSS
3227	17128	A	3249	2	372	AYTISFIGKISFYGLH**LPKAHVEAPI VGSIVLAAELLKLGGFGIIHLTLIFNPL TKHIAYPFLGLSL*GISITSSMWLRQTD LKSLIAYSSISHIALVVTAILIQTP*SF TGAFFLIIDHG
3228	17129	A	3250	293	56	EGSPKVIFNKSPPHHLFLFLFFFFIFFF *FFFFFFFFFFFFFFFFFFFFFFFLYL LAMFYLSFFFKQDNQRYRQYSIK
3229	17130	A	3251	169	370	LKMTELRGAPASKPRGQEPPPHYPCHHH HHHHHHFL*VTKGQGPHHWPSPTRDPGW L*SPS*EDQRR
3230	17131	A	3252	22	156	GERIGLGLGGQGCSEP*LCHCTLAWVGD TVRPCLKKKKKKKGPPF
3231	17132	A	3253	3	400	QNQTPLLD*GGLITAVLLLLYLAVLTGG ITILLADRSLDSTLFYPAGGGDPILYQH LF*FFGHPEVYILILPGFGIVSHIETNY WGGKEPFGFVGMV*AMIAMGFLGFIG*A HHIFTVGVDVHTRA*FTSAT
3232	17133	A	3254	373	31	REVGPPTP*KIFFFPKGLNFWGGGGPKF PPPKKKGFFKKSPVGVFPPPGG*KSGPG PGFKKPPQKGKNISFPAGGKIGPPRGTL KRAPPFFFFFFFFFFFLLWVVVQVERP TL
3233	17134	A	3255	1	379	LNLIQRQ*R*V*KFL*LPPQT*KKKKKK KKKKKGGGAFKKNLGGAKFNGGRKKKIF FLKGGVKKKKAGGGFKKRGKGKKCYLGI FEKKPFFGGGKNWENPPKKIKGLREKKK F*GEKGEKKPEKAG
3234	17135	A	3256	42	376	FCYISLVHHCIYNDLSFERKKNIFVPGQ INSISSIA*EAHCKNKSLLHAVKKKKKK KKKKKKKKKKKKKKKKEKKRGEKKKKK KEGRSSLKKEK
3235	17136	A	3257	353	67	CYPLSPLKFFFSPRSLKFWKGVGPIISP PKKKVPSQNSQEAGFPSPNVLKRRPGPN FKTTP*KEKKNPFPPPVKFGPPKESLKR PPLFFFFCGLQ
3236	17137	A	3258	2	129	FHRISQDGLDLLSS*SARLGLPKCWDYR CEPPRPAKNKILLS
3237	17138	A	3259	205	415	QQKNRRLLHFKGARTHNSYNRGQPTTPS ITAHMYPRLRQSHTIYVLRVHHP*VPSA IEGPVSV*ALLHSSTIVVAGNLLLIRFH PLAEKSPLIQTVTLCLGANTTLVAGGWA LTQNDSKRIAAFSTSRGLGLIIVTIGVN QPHLALLHICTHAFVKAILFMCSGSIIH NLSKEQDIRKIGGLLITIP
3238	17139	A	3260	3	393	SFNLSTLITTQEHL*LLLPS*PLAII*F ISTLAETNRTPFDLAEGEAELVSGFNIE YAAGPFALFLIAEYTNIIIINTLTTTIL

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						LGTTYDALSPELYTTYFVTKTLLLTSLL L*IRTAYPRFRYDQLIHL
3239	17140	A	3261	2	400	ISDLSEK*FKRLVVKLIMEAPEKGKAQC KEIQKMTQEVKGEIFKE*IA*RKKKSKF QETLDTLIEMQSALESFSNRIKQVEERN SELKDKIFELTQSNKDKGKRIRKYEQSL *VAWDYIQ*PNLGIIGIPEEE
3240	17141	A	3262	450	129	NNLAFN*V*EFCVLAIKLLKVKRYPIEW EKMFANHISDKGLVSGIYKELFRLSNKQ AIDLTF*KWAAGHGGSPL
3241	17142	A	3263	238	3	KEKKIGLKKCLQGSHFSIHTAWSIIIYM FSPLTIISRKRMGQPGIVAHTCNPST*G G*GRWITRSGVRDQTGQHGKTP
3242	17143	A	3264	350	3	SPTLLGSKDPNLLGFRFPLWKKGKIIRA PLSLGLN*RFFSEVVLIP*KPPKNWPGG TFLVVCFLKRGFPFLSQKKKKKNPGAVA HACNPSTLGGRGGRSQGQELETSLANTV KTR
3243	17144	A	3265	69	200	RLECSGVISAHCNLNLPGSGDSPASAS* LAGITVMVKLPVIAK
3244	17145	A	3266	223	408	GGFPFFPPGGGEGGNFGELEPLPPGLRK FFCLGPPRRGD*GPRSSSPGSFWVFKKN GVSP
3245	17146	A	3267	185	420	DQGLWGFIIYFYRQSLA*VHWNNPSSL* PRTPGLKHTPVPSLLISWDYGRTPPHLT NFCIFFDRGSFFF*DRVSATHA
3246	17147	A	3268	3	392	TGCHSIPQAGVQWHNHGLLQPQPPGLR* SSCLSLPSSWHY
3247	17148	A	3269	1	398	KFSCISSKHQKLKLTPKPPKPPPKKSPL VLPIGKKIRETFWGAFKSPPPNQPKGAQ TLPLKIWDKMGGGGGLALVV*KAPPGNF KGPPGGKPMEQP*LGPGPPLKWKGGLPH QKGGFSKAPGEKKKGGEGRL
3248	17149	A	3270	422	183	ETEVVSLFKVIITEKSPNLEKDTNIQVQ ESYRTPSRFILMKTTSRHLIIILPKVNN TERIL*MQQDRGNNIQWSSGCSA
3249	17150	A	3271	3	35	KNNSLIIPTIIATITLLNLYFYLSPLLY **SSSPPS
3250	17151	A	3272	155	1	KDFFFFFLRQSFTLVAQAAAEWCDLCSL QPKPPGFK*FSYNSLSSSWDYIG
3251	17152	A	3273	413	71	PPSTGLFLTEEYEVSFPPFPL*KFFFPP SGLFFGGGVPPFFPPPKKGFFPKYPRLV FKGPLLGGGGLPPPPP*ILPPLGSFLPA PPLFFFFLFFL
3252	17153	A	3274	336	45	DRVLSCSPAWRAMARSHDFG*LQLPPPR VKVFSCLSNPSSWDPRHVPPRKGNFVFL VKTGNPWNLGGQGCRERRLCPCIPAWGT DKDSVSKKKKKS
3253	17154	A	3275	206	366	SVFFFVLFGFFYGALLCFPNPWLECSGT ILVHCNLHFPGSKDSSASPS*VAGT
3254	17155	A	3276	334	75	ENTRRVERRRRTHIIYYNFF*EFMNRFF FFIFFDGRFSCVFFFFFLFYFFFFFFFF FFFFFFFFFFFFFFWFSARSFIYFLFPRH VT
3255	17156	A	3277	144	17	KAPPLFFFFFFFFFFFFFFW*FRG*T HWNGDACMCNLTKS
3256	17157	A	3278	2	109	YHIVKPSP*PLTGALSALLMTSGLAM*F HFHSITL